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(54) Title: NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

## (57) Abstract

The invention provides proteins from Neisseria meningitidis, including the amino acid sequences and the corresponding nucleotide sequences. The proteins are predicted to be useful antigens for vaccines and/or diagnostics.

**919 (46 kDa)****A) PURIFICATION****M1 919**



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## NEISSERIA MENINGITIDIS ANTIGENS AND COMPOSITIONS

This application is a continuation-in-part of the following U.S. Provisional Patent applications, from each of which priority is claimed, and each of which is incorporated by reference in its entirety: 60/083,758 (filed May 1, 1998); 60/094,869 (filed July 31, 1998); 60/098,994 (filed September 2, 1998); 60/099,062 (filed September 2, 1998); 60/103,749 (filed October 9, 1998); 60/103,794 (filed October 9, 1998); 60/103,796 (filed October 9, 1998); and 60/121,528 (filed February 25, 1999).

This invention relates to antigens from the bacterial species: *Neisseria meningitidis* and *Neisseria gonorrhoeae*.

### BACKGROUND

*Neisseria meningitidis* is a non-motile, gram negative diplococcus human pathogen. It colonizes the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. It is closely related to *N. gonorrhoea*, although one feature that clearly differentiates meningococcus from gonococcus is the presence of a polysaccharide capsule that is present in all pathogenic meningococci.

*N. meningitidis* causes both endemic and epidemic disease. In the United States the attack rate is 0.6-1 per 100,000 persons per year, and it can be much greater during outbreaks. (see Lieberman *et al.* (1996) Safety and Immunogenicity of a Serogroups A/C *Neisseria meningitidis* Oligosaccharide-Protein Conjugate Vaccine in Young Children. *JAMA* 275(19):1499-1503; Schuchat *et al* (1997) Bacterial Meningitis in the United States in 1995. *N Engl J Med* 337(14):970-976). In developing countries, endemic disease rates are much higher and during epidemics incidence rates can reach 500 cases per 100,000 persons per year. Mortality is extremely high, at 10-20% in the United States, and much higher in developing countries. Following the introduction of the conjugate vaccine against *Haemophilus influenzae*, *N. meningitidis* is the major cause of bacterial meningitis at all ages in the United States (Schuchat *et al* (1997) *supra*).

Based on the organism's capsular polysaccharide, 12 serogroups of *N. meningitidis* have been identified. Group A is the pathogen most often implicated in epidemic disease in sub-Saharan Africa. Serogroups B and C are responsible for the vast majority of cases in the

United States and in most developed countries. Serogroups W135 and Y are responsible for the rest of the cases in the United States and developed countries. The meningococcal vaccine currently in use is a tetravalent polysaccharide vaccine composed of serogroups A, C, Y and W135. Although efficacious in adolescents and adults, it induces a poor immune response and short duration of protection, and cannot be used in infants [eg. Morbidity and Mortality weekly report, Vol.46, No. RR-5 (1997)]. This is because polysaccharides are T-cell independent antigens that induce a weak immune response that cannot be boosted by repeated immunization. Following the success of the vaccination against *H.influenzae*, conjugate vaccines against serogroups A and C have been developed and are at the final stage of clinical testing (Zollinger WD "New and Improved Vaccines Against Meningococcal Disease". In: *New Generation Vaccines, supra*, pp. 469-488; Lieberman *et al* (1996) *supra*; Costantino *et al* (1992) Development and phase I clinical testing of a conjugate vaccine against meningococcus A and C. *Vaccine* 10:691-698).

Meningococcus B (menB) remains a problem, however. This serotype currently is responsible for approximately 50% of total meningitis in the United States, Europe, and South America. The polysaccharide approach cannot be used because the menB capsular polysaccharide is a polymer of  $\alpha(2-8)$ -linked *N*-acetyl neuraminic acid that is also present in mammalian tissue. This results in tolerance to the antigen; indeed, if an immune response were elicited, it would be anti-self, and therefore undesirable. In order to avoid induction of autoimmunity and to induce a protective immune response, the capsular polysaccharide has, for instance, been chemically modified substituting the *N*-acetyl groups with *N*-propionyl groups, leaving the specific antigenicity unaltered (Romero & Outschoorn (1994) Current status of Meningococcal group B vaccine candidates: capsular or non-capsular? *Clin Microbiol Rev* 7(4):559-575).

Alternative approaches to menB vaccines have used complex mixtures of outer membrane proteins (OMPs), containing either the OMPs alone, or OMPs enriched in porins, or deleted of the class 4 OMPs that are believed to induce antibodies that block bactericidal activity. This approach produces vaccines that are not well characterized. They are able to protect against the homologous strain, but are not effective at large where there are many antigenic variants of the outer membrane proteins. To overcome the antigenic variability, multivalent vaccines containing up to nine different porins have been constructed (eg. Poolman JT (1992) Development of a meningococcal vaccine. *Infect. Agents Dis.* 4:13-28).

Additional proteins to be used in outer membrane vaccines have been the opa and opc proteins, but none of these approaches have been able to overcome the antigenic variability (eg. Ala'Aldeen & Borriello (1996) The meningococcal transferrin-binding proteins 1 and 2 are both surface exposed and generate bactericidal antibodies capable of killing homologous and heterologous strains. *Vaccine* 14(1):49-53).

A certain amount of sequence data is available for meningococcal and gonococcal genes and proteins (e.g. EP-A-0467714, WO96/29412), but this is by no means complete. Other men B proteins may include those listed in WO 97/28273, WO 96/29412, WO 95/03413, US 5,439,808, and US 5,879,686.

The provision of further sequences could provide an opportunity to identify secreted or surface-exposed proteins that are presumed targets for the immune system and which are not antigenically variable. For instance, some of the identified proteins could be components of efficacious vaccines against meningococcus B, some could be components of vaccines against all meningococcal serotypes, and others could be components of vaccines against all pathogenic *Neisseriae* including *Neisseria meningitidis* or *Neisseria gonorrhoeae*. Those sequences specific to *N. meningitidis* or *N. gonorrhoeae* that are more highly conserved are further preferred sequences.

It is thus an object of the invention is to provide Neisserial DNA sequences which encode proteins that are antigenic or immunogenic.

## BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 illustrates the products of protein expression and purification of the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 2 illustrates the products of protein expression and purification of the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 3 illustrates the products of protein expression and purification of the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 4 illustrates the products of protein expression and purification of the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 5 illustrates the products of protein expression and purification of the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 6 illustrates the products of protein expression and purification of the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 7 illustrates the products of protein expression and purification of the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 8 illustrates the products of protein expression and purification of the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 9 illustrates the products of protein expression and purification of the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 10 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 919 as cloned and expressed in *E. coli*.

Fig. 11 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 279 as cloned and expressed in *E. coli*.

Fig. 12 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 576-1 as cloned and expressed in *E. coli*.

Fig. 13 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 519-1 as cloned and expressed in *E. coli*.

Fig. 14 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 121-1 as cloned and expressed in *E. coli*.

Fig. 15 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 128-1 as cloned and expressed in *E. coli*.

Fig. 16 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 206 as cloned and expressed in *E. coli*.

Fig. 17 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 287 as cloned and expressed in *E. coli*.

Fig. 18 illustrates the hydrophilicity plot, antigenic index and AMPHI regions of the products of protein expression the predicted ORF 406 as cloned and expressed in *E. coli*.

Fig. 19 shows an alignment comparison of amino acid sequences for ORF 225 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 20 shows an alignment comparison of amino acid sequences for ORF 235 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 21 shows an alignment comparison of amino acid sequences for ORF 287 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 22 shows an alignment comparison of amino acid sequences for ORF 519 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

Fig. 23 shows an alignment comparison of amino acid sequences for ORF 919 for several strains of *Neisseria*. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. The Figure demonstrates a high degree of conservation among the various strains, further confirming its utility as an antigen for both vaccines and diagnostics.

## THE INVENTION

The invention provides proteins comprising the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples.

It also provides proteins comprising sequences homologous (i.e., those having sequence identity) to the *N. meningitidis* amino acid sequences disclosed in the examples. Depending on the particular sequence, the degree of homology (sequence identity) is preferably greater than 50% (eg. 60%, 70%, 80%, 90%, 95%, 99% or more). These proteins include mutants and allelic variants of the sequences disclosed in the examples. Typically, 50% identity or more between two proteins is considered to be an indication of functional equivalence. Identity between proteins is preferably determined by the Smith-Waterman

homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with parameters: gap penalty 12, gap extension penalty 1.

The invention further provides proteins comprising fragments of the *N. meningitidis* amino acid sequences and *N. gonorrhoeae* amino acid sequences disclosed in the examples. The fragments should comprise at least  $n$  consecutive amino acids from the sequences and, depending on the particular sequence,  $n$  is 7 or more (eg. 8, 10, 12, 14, 16, 18, 20 or more). Preferably the fragments comprise an epitope from the sequence.

The proteins of the invention can, of course, be prepared by various means (eg. recombinant expression, purification from cell culture, chemical synthesis *etc.*) and in various forms (eg. native, fusions *etc.*). They are preferably prepared in substantially pure or isolated form (*ie.* substantially free from other *N. meningitidis* or *N. gonorrhoeae* host cell proteins)

According to a further aspect, the invention provides antibodies which bind to these proteins. These may be polyclonal or monoclonal and may be produced by any suitable means.

According to a further aspect, the invention provides nucleic acid comprising the *N. meningitidis* nucleotide sequences and *N. gonorrhoeae* nucleotide sequences disclosed in the examples.

According to a further aspect, the invention comprises nucleic acids having sequence identity of greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) to the nucleic acid sequences herein. Sequence identity is determined as above-discussed.

According to a further aspect, the invention comprises nucleic acid that hybridizes to the sequences provided herein. Conditions for hybridization are set forth herein.

Nucleic acid comprising fragments of these sequences are also provided. These should comprise at least  $n$  consecutive nucleotides from the *N. meningitidis* sequences or *N. gonorrhoeae* sequences and depending on the particular sequence,  $n$  is 10 or more (eg 12, 14, 15, 18, 20, 25, 30, 35, 40 or more).

According to a further aspect, the invention provides nucleic acid encoding the proteins and protein fragments of the invention.

It should also be appreciated that the invention provides nucleic acid comprising sequences complementary to those described above (eg. for antisense or probing purposes).

Nucleic acid according to the invention can, of course, be prepared in many ways (eg. by chemical synthesis, in part or in whole, from genomic or cDNA libraries, from the

organism itself *etc.*) and can take various forms (*eg.* single stranded, double stranded, vectors, probes *etc.*).

In addition, the term "nucleic acid" includes DNA and RNA, and also their analogues, such as those containing modified backbones, and also protein nucleic acids (PNA) *etc.*

According to a further aspect, the invention provides vectors comprising nucleotide sequences of the invention (*eg.* expression vectors) and host cells transformed with such vectors.

According to a further aspect, the invention provides compositions comprising protein, antibody, and/or nucleic acid according to the invention. These compositions may be suitable as vaccines, for instance, or as diagnostic reagents or as immunogenic compositions.

The invention also provides nucleic acid, protein, or antibody according to the invention for use as medicaments (*eg.* as vaccines) or as diagnostic reagents. It also provides the use of nucleic acid, protein, or antibody according to the invention in the manufacture of (I) a medicament for treating or preventing infection due to Neisserial bacteria (ii) a diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised against Neisserial bacteria or (iii) for raising antibodies. Said Neisserial bacteria may be any species or strain (such as *N. gonorrhoeae*) but are preferably *N. meningitidis*, especially strain B or strain C.

The invention also provides a method of treating a patient, comprising administering to the patient a therapeutically effective amount of nucleic acid, protein, and/or antibody according to the invention.

According to further aspects, the invention provides various processes.

A process for producing proteins of the invention is provided, comprising the step of culturing a host cell according to the invention under conditions which induce protein expression.

A process for detecting polynucleotides of the invention is provided, comprising the steps of: (a) contacting a nucleic probe according to the invention with a biological sample under hybridizing conditions to form duplexes; and (b) detecting said duplexes.

A process for detecting proteins of the invention is provided, comprising the steps of: (a) contacting an antibody according to the invention with a biological sample under conditions suitable for the formation of an antibody-antigen complexes; and (b) detecting said complexes.



Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

#### Methodology - Summary of standard procedures and techniques.

##### General

This invention provides *Neisseria meningitidis* menB nucleotide sequences, amino acid sequences encoded therein. With these disclosed sequences, nucleic acid probe assays and expression cassettes and vectors can be produced. The expression vectors can be transformed into host cells to produce proteins. The purified or isolated polypeptides (which may also be chemically synthesized) can be used to produce antibodies to detect menB proteins. Also, the host cells or extracts can be utilized for biological assays to isolate agonists or antagonists. In addition, with these sequences one can search to identify open reading frames and identify amino acid sequences. The proteins may also be used in immunogenic compositions, antigenic compositions and as vaccine components.

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature e.g., Sambrook *Molecular Cloning; A Laboratory Manual, Second Edition* (1989); *DNA Cloning, Volumes I and ii* (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); *Transcription and Translation* (B.D. Hames & S.J. Higgins eds. 1984); *Animal Cell Culture* (R.I. Freshney ed. 1986); *Immobilized Cells and Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide to Molecular Cloning* (1984); the *Methods in Enzymology* series (Academic Press, Inc.), especially volumes 154 & 155; *Gene Transfer Vectors for Mammalian Cells* (J.H. Miller and M.P. Calos eds. 1987, Cold Spring Harbor Laboratory); Mayer and Walker, eds. (1987), *Immunochemical Methods in Cell and Molecular Biology* (Academic Press, London); Scopes, (1987) *Protein Purification: Principles and Practice*, Second Edition (Springer-Verlag, N.Y.), and *Handbook of Experimental Immunology, Volumes I-IV* (D.M. Weir and C.C. Blackwell eds 1986).

Standard abbreviations for nucleotides and amino acids are used in this specification.

All publications, patents, and patent applications cited herein are incorporated in full by reference.

### Expression systems

The *Neisseria* menB nucleotide sequences can be expressed in a variety of different expression systems; for example those used with mammalian cells, plant cells, baculoviruses, bacteria, and yeast.

#### i. Mammalian Systems

Mammalian expression systems are known in the art. A mammalian promoter is any DNA sequence capable of binding mammalian RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiating region, which is usually placed proximal to the 5' end of the coding sequence, and a TATA box, usually located 25-30 base pairs (bp) upstream of the transcription initiation site. The TATA box is thought to direct RNA polymerase II to begin RNA synthesis at the correct site. A mammalian promoter will also contain an upstream promoter element, usually located within 100 to 200 bp upstream of the TATA box. An upstream promoter element determines the rate at which transcription is initiated and can act in either orientation (Sambrook et al. (1989) "Expression of Cloned Genes in Mammalian Cells." In *Molecular Cloning: A Laboratory Manual*, 2nd ed.).

Mammalian viral genes are often highly expressed and have a broad host range; therefore sequences encoding mammalian viral genes provide particularly useful promoter sequences. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter (Ad MLP), and herpes simplex virus promoter. In addition, sequences derived from non-viral genes, such as the murine metallothionein gene, also provide useful promoter sequences. Expression may be either constitutive or regulated (inducible). Depending on the promoter selected, many promoters may be inducible using known substrates, such as the use of the mouse mammary tumor virus (MMTV) promoter with the glucocorticoid responsive element (GRE) that is induced by glucocorticoid in hormone-responsive transformed cells (see for example, U.S. Patent 5,783,681).

The presence of an enhancer element (enhancer), combined with the promoter elements described above, will usually increase expression levels. An enhancer is a

regulatory DNA sequence that can stimulate transcription up to 1000-fold when linked to homologous or heterologous promoters, with synthesis beginning at the normal RNA start site. Enhancers are also active when they are placed upstream or downstream from the transcription initiation site, in either normal or flipped orientation, or at a distance of more than 1000 nucleotides from the promoter (Maniatis et al. (1987) *Science* 236:1237; Alberts et al. (1989) *Molecular Biology of the Cell*, 2nd ed.). Enhancer elements derived from viruses may be particularly useful, because they usually have a broader host range. Examples include the SV40 early gene enhancer (Dijkema et al (1985) *EMBO J.* 4:761) and the enhancer/promoters derived from the long terminal repeat (LTR) of the Rous Sarcoma Virus (Gorman et al. (1982b) *Proc. Natl. Acad. Sci.* 79:6777) and from human cytomegalovirus (Boshart et al. (1985) *Cell* 41:521). Additionally, some enhancers are regulatable and become active only in the presence of an inducer, such as a hormone or metal ion (Sassone-Corsi and Borelli (1986) *Trends Genet.* 2:215; Maniatis et al. (1987) *Science* 236:1237).

A DNA molecule may be expressed intracellularly in mammalian cells. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in mammalian cells. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The adenovirus tripartite leader is an example of a leader sequence that provides for secretion of a foreign protein in mammalian cells.

Usually, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. The 3' terminus of the mature mRNA is formed by site-specific post-transcriptional cleavage and polyadenylation (Birnstiel et al. (1985) *Cell* 41:349; Proudfoot and Whitelaw (1988) "Termination and 3' end processing of eukaryotic RNA. In *Transcription and splicing* (ed. B.D. Hames and D.M.

Glover); Proudfoot (1989) *Trends Biochem. Sci.* 14:105). These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator/polyadenylation signals include those derived from SV40 (Sambrook et al (1989) "Expression of cloned genes in cultured mammalian cells." In *Molecular Cloning: A Laboratory Manual*).

Usually, the above described components, comprising a promoter, polyadenylation signal, and transcription termination sequence are put together into expression constructs. Enhancers, introns with functional splice donor and acceptor sites, and leader sequences may also be included in an expression construct, if desired. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as mammalian cells or bacteria. Mammalian replication systems include those derived from animal viruses, which require trans-acting factors to replicate. For example, plasmids containing the replication systems of papovaviruses, such as SV40 (Gluzman (1981) *Cell* 23:175) or polyomavirus, replicate to extremely high copy number in the presence of the appropriate viral T antigen. Additional examples of mammalian replicons include those derived from bovine papillomavirus and Epstein-Barr virus. Additionally, the replicon may have two replication systems, thus allowing it to be maintained, for example, in mammalian cells for expression and in a prokaryotic host for cloning and amplification. Examples of such mammalian-bacteria shuttle vectors include pMT2 (Kaufman et al. (1989) *Mol. Cell. Biol.* 9:946) and pHEBO (Shimizu et al. (1986) *Mol. Cell. Biol.* 6:1074).

The transformation procedure used depends upon the host to be transformed. Methods for introduction of heterologous polynucleotides into mammalian cells are known in the art and include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

Mammalian cell lines available as hosts for expression are known in the art and include many immortalized cell lines available from the American Type Culture Collection (ATCC), including but not limited to, Chinese hamster ovary (CHO) cells, HeLa cells, baby hamster kidney (BHK) cells, monkey kidney cells (COS), human hepatocellular carcinoma cells (e.g., Hep G2), and a number of other cell lines.

## ii. Plant Cellular Expression Systems

There are many plant cell culture and whole plant genetic expression systems known in the art. Exemplary plant cellular genetic expression systems include those described in patents, such as: U.S. 5,693,506; US 5,659,122; and US 5,608,143. Additional examples of genetic expression in plant cell culture has been described by Zenk, *Phytochemistry* 30:3861-3863 (1991). Descriptions of plant protein signal peptides may be found in addition to the references described above in Vaulcombe et al., *Mol. Gen. Genet.* 209:33-40 (1987); Chandler et al., *Plant Molecular Biology* 3:407-418 (1984); Rogers, *J. Biol. Chem.* 260:3731-3738 (1985); Rothstein et al., *Gene* 55:353-356 (1987); Whittier et al., *Nucleic Acids Research* 15:2515-2535 (1987); Wirsal et al., *Molecular Microbiology* 3:3-14 (1989); Yu et al., *Gene* 122:247-253 (1992). A description of the regulation of plant gene expression by the phytohormone, gibberellic acid and secreted enzymes induced by gibberellic acid can be found in R.L. Jones and J. MacMillin, Gibberellins: in: *Advanced Plant Physiology*, Malcolm B. Wilkins, ed., 1984 Pitman Publishing Limited, London, pp. 21-52. References that describe other metabolically-regulated genes: Sheen, *Plant Cell*, 2:1027-1038(1990); Maas et al., *EMBO J.* 9:3447-3452 (1990); Benkel and Hickey, *Proc. Natl. Acad. Sci.* 84:1337-1339 (1987)

Typically, using techniques known in the art, a desired polynucleotide sequence is inserted into an expression cassette comprising genetic regulatory elements designed for operation in plants. The expression cassette is inserted into a desired expression vector with companion sequences upstream and downstream from the expression cassette suitable for expression in a plant host. The companion sequences will be of plasmid or viral origin and provide necessary characteristics to the vector to permit the vectors to move DNA from an original cloning host, such as bacteria, to the desired plant host. The basic bacterial/plant vector construct will preferably provide a broad host range prokaryote replication origin; a prokaryote selectable marker; and, for *Agrobacterium* transformations, T DNA sequences for *Agrobacterium*-mediated transfer to plant chromosomes. Where the heterologous gene is not readily amenable to detection, the construct will preferably also have a selectable marker gene suitable for determining if a plant cell has been transformed. A general review of suitable markers, for example for the members of the grass family, is found in Wilmink and Dons, 1993, *Plant Mol. Biol. Repr.* 11(2):165-185.

Sequences suitable for permitting integration of the heterologous sequence into the plant genome are also recommended. These might include transposon sequences and the like for homologous recombination as well as Ti sequences which permit random insertion of a heterologous expression cassette into a plant genome. Suitable prokaryote selectable markers include resistance toward antibiotics such as ampicillin or tetracycline. Other DNA sequences encoding additional functions may also be present in the vector, as is known in the art.

The nucleic acid molecules of the subject invention may be included into an expression cassette for expression of the protein(s) of interest. Usually, there will be only one expression cassette, although two or more are feasible. The recombinant expression cassette will contain in addition to the heterologous protein encoding sequence the following elements, a promoter region, plant 5' untranslated sequences, initiation codon depending upon whether or not the structural gene comes equipped with one, and a transcription and translation termination sequence. Unique restriction enzyme sites at the 5' and 3' ends of the cassette allow for easy insertion into a pre-existing vector.

A heterologous coding sequence may be for any protein relating to the present invention. The sequence encoding the protein of interest will encode a signal peptide which allows processing and translocation of the protein, as appropriate, and will usually lack any sequence which might result in the binding of the desired protein of the invention to a membrane. Since, for the most part, the transcriptional initiation region will be for a gene which is expressed and translocated during germination, by employing the signal peptide which provides for translocation, one may also provide for translocation of the protein of interest. In this way, the protein(s) of interest will be translocated from the cells in which they are expressed and may be efficiently harvested. Typically secretion in seeds are across the aleurone or scutellar epithelium layer into the endosperm of the seed. While it is not required that the protein be secreted from the cells in which the protein is produced, this facilitates the isolation and purification of the recombinant protein.

Since the ultimate expression of the desired gene product will be in a eucaryotic cell it is desirable to determine whether any portion of the cloned gene contains sequences which will be processed out as introns by the host's splicosome machinery. If so, site-directed mutagenesis of the "intron" region may be conducted to prevent losing a portion of the genetic message as a false intron code, Reed and Maniatis, *Cell* 41:95-105, 1985.

The vector can be microinjected directly into plant cells by use of micropipettes to mechanically transfer the recombinant DNA. Crossway, *Mol. Gen. Genet*, 202:179-185, 1985. The genetic material may also be transferred into the plant cell by using polyethylene glycol, Krens, et al., *Nature*, 296, 72-74, 1982. Another method of introduction of nucleic acid segments is high velocity ballistic penetration by small particles with the nucleic acid either within the matrix of small beads or particles, or on the surface, Klein, et al., *Nature*, 327, 70-73, 1987 and Knudsen and Muller, 1991, *Planta*, 185:330-336 teaching particle bombardment of barley endosperm to create transgenic barley. Yet another method of introduction would be fusion of protoplasts with other entities, either minicells, cells, lysosomes or other fusible lipid-surfaced bodies, Fraley, et al., *Proc. Natl. Acad. Sci. USA*, 79, 1859-1863, 1982.

The vector may also be introduced into the plant cells by electroporation. (Fromm et al., *Proc. Natl Acad. Sci. USA* 82:5824, 1985). In this technique, plant protoplasts are electroporated in the presence of plasmids containing the gene construct. Electrical impulses of high field strength reversibly permeabilize biomembranes allowing the introduction of the plasmids. Electroporated plant protoplasts reform the cell wall, divide, and form plant callus.

All plants from which protoplasts can be isolated and cultured to give whole regenerated plants can be transformed by the present invention so that whole plants are recovered which contain the transferred gene. It is known that practically all plants can be regenerated from cultured cells or tissues, including but not limited to all major species of sugarcane, sugar beet, cotton, fruit and other trees, legumes and vegetables. Some suitable plants include, for example, species from the genera *Fragaria*, *Lotus*, *Medicago*, *Onobrychis*, *Trifolium*, *Trigonella*, *Vigna*, *Citrus*, *Linum*, *Geranium*, *Manihot*, *Daucus*, *Arabidopsis*, *Brassica*, *Raphanus*, *Sinapis*, *Atropa*, *Capsicum*, *Datura*, *Hyoscyamus*, *Lycopersion*, *Nicotiana*, *Solanum*, *Petunia*, *Digitalis*, *Majorana*, *Cichorium*, *Helianthus*, *Lactuca*, *Bromus*, *Asparagus*, *Antirrhinum*, *Hererocallis*, *Nemesia*, *Pelargonium*, *Panicum*, *Pennisetum*, *Ranunculus*, *Senecio*, *Salpiglossis*, *Cucumis*, *Browaalia*, *Glycine*, *Lolium*, *Zea*, *Triticum*, *Sorghum*, and *Datura*.

Means for regeneration vary from species to species of plants, but generally a suspension of transformed protoplasts containing copies of the heterologous gene is first provided. Callus tissue is formed and shoots may be induced from callus and subsequently rooted. Alternatively, embryo formation can be induced from the protoplast suspension.

These embryos germinate as natural embryos to form plants. The culture media will generally contain various amino acids and hormones, such as auxin and cytokinins. It is also advantageous to add glutamic acid and proline to the medium, especially for such species as corn and alfalfa. Shoots and roots normally develop simultaneously. Efficient regeneration will depend on the medium, on the genotype, and on the history of the culture. If these three variables are controlled, then regeneration is fully reproducible and repeatable.

In some plant cell culture systems, the desired protein of the invention may be excreted or alternatively, the protein may be extracted from the whole plant. Where the desired protein of the invention is secreted into the medium, it may be collected. Alternatively, the embryos and embryoless-half seeds or other plant tissue may be mechanically disrupted to release any secreted protein between cells and tissues. The mixture may be suspended in a buffer solution to retrieve soluble proteins. Conventional protein isolation and purification methods will be then used to purify the recombinant protein. Parameters of time, temperature pH, oxygen, and volumes will be adjusted through routine methods to optimize expression and recovery of heterologous protein.

### iii. Baculovirus Systems

The polynucleotide encoding the protein can also be inserted into a suitable insect expression vector, and is operably linked to the control elements within that vector. Vector construction employs techniques which are known in the art. Generally, the components of the expression system include a transfer vector, usually a bacterial plasmid, which contains both a fragment of the baculovirus genome, and a convenient restriction site for insertion of the heterologous gene or genes to be expressed; a wild type baculovirus with a sequence homologous to the baculovirus-specific fragment in the transfer vector (this allows for the homologous recombination of the heterologous gene in to the baculovirus genome); and appropriate insect host cells and growth media.

After inserting the DNA sequence encoding the protein into the transfer vector, the vector and the wild type viral genome are transfected into an insect host cell where the vector and viral genome are allowed to recombine. The packaged recombinant virus is expressed and recombinant plaques are identified and purified. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *inter alia*, Invitrogen, San Diego CA ("MaxBac" kit). These techniques are generally known to



those skilled in the art and fully described in Summers and Smith, *Texas Agricultural Experiment Station Bulletin No. 1555* (1987) (hereinafter "Summers and Smith").

Prior to inserting the DNA sequence encoding the protein into the baculovirus genome, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are usually assembled into an intermediate transplacement construct (transfer vector). This construct may contain a single gene and operably linked regulatory elements; multiple genes, each with its own set of operably linked regulatory elements; or multiple genes, regulated by the same set of regulatory elements. Intermediate transplacement constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as a bacterium. The replicon will have a replication system, thus allowing it to be maintained in a suitable host for cloning and amplification.

Currently, the most commonly used transfer vector for introducing foreign genes into AcNPV is pAc373. Many other vectors, known to those of skill in the art, have also been designed. These include, for example, pVL985 (which alters the polyhedrin start codon from ATG to ATT, and which introduces a BamHI cloning site 32 basepairs downstream from the ATT; see Luckow and Summers, *Virology* (1989) 17:31.

The plasmid usually also contains the polyhedrin polyadenylation signal (Miller et al. (1988) *Ann. Rev. Microbiol.*, 42:177) and a prokaryotic ampicillin-resistance (*amp*) gene and origin of replication for selection and propagation in *E. coli*.

Baculovirus transfer vectors usually contain a baculovirus promoter. A baculovirus promoter is any DNA sequence capable of binding a baculovirus RNA polymerase and initiating the downstream (5' to 3') transcription of a coding sequence (e.g., structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A baculovirus transfer vector may also have a second domain called an enhancer, which, if present, is usually distal to the structural gene. Expression may be either regulated or constitutive.

Structural genes, abundantly transcribed at late times in a viral infection cycle, provide particularly useful promoter sequences. Examples include sequences derived from the gene encoding the viral polyhedron protein, Friesen et al., (1986) "The Regulation of Baculovirus Gene Expression," in: *The Molecular Biology of Baculoviruses* (ed. Walter Doerfler); EPO

Publ. Nos. 127 839 and 155 476; and the gene encoding the p10 protein, Vlak et al., (1988), *J. Gen. Virol.* 69:765.

DNA encoding suitable signal sequences can be derived from genes for secreted insect or baculovirus proteins, such as the baculovirus polyhedrin gene (Carbonell et al. (1988) *Gene*, 73:409). Alternatively, since the signals for mammalian cell posttranslational modifications (such as signal peptide cleavage, proteolytic cleavage, and phosphorylation) appear to be recognized by insect cells, and the signals required for secretion and nuclear accumulation also appear to be conserved between the invertebrate cells and vertebrate cells, leaders of non-insect origin, such as those derived from genes encoding human (alpha)  $\alpha$ -interferon, Maeda et al., (1985), *Nature* 315:592; human gastrin-releasing peptide, Lebacqz-Verheyden et al., (1988), *Molec. Cell. Biol.* 8:3129; human IL-2, Smith et al., (1985) *Proc. Nat'l Acad. Sci. USA*, 82:8404; mouse IL-3, (Miyajima et al., (1987) *Gene* 58:273; and human glucocerebrosidase, Martin et al. (1988) *DNA*, 7:99, can also be used to provide for secretion in insects.

A recombinant polypeptide or polyprotein may be expressed intracellularly or, if it is expressed with the proper regulatory sequences, it can be secreted. Good intracellular expression of nonfused foreign proteins usually requires heterologous genes that ideally have a short leader sequence containing suitable translation initiation signals preceding an ATG start signal. If desired, methionine at the N-terminus may be cleaved from the mature protein by *in vitro* incubation with cyanogen bromide.

Alternatively, recombinant polyproteins or proteins which are not naturally secreted can be secreted from the insect cell by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provides for secretion of the foreign protein in insects. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the translocation of the protein into the endoplasmic reticulum.

After insertion of the DNA sequence and/or the gene encoding the expression product precursor of the protein, an insect cell host is co-transformed with the heterologous DNA of the transfer vector and the genomic DNA of wild type baculovirus -- usually by co-transfection. The promoter and transcription termination sequence of the construct will usually comprise a 2-5kb section of the baculovirus genome. Methods for introducing heterologous DNA into the desired site in the baculovirus virus are known in the art. (See

Summers and Smith *supra*; Ju et al. (1987); Smith et al., *Mol. Cell. Biol.* (1983) 3:2156; and Luckow and Summers (1989)). For example, the insertion can be into a gene such as the polyhedrin gene, by homologous double crossover recombination; insertion can also be into a restriction enzyme site engineered into the desired baculovirus gene. Miller et al., (1989), *Bioessays* 4:91. The DNA sequence, when cloned in place of the polyhedrin gene in the expression vector, is flanked both 5' and 3' by polyhedrin-specific sequences and is positioned downstream of the polyhedrin promoter.

The newly formed baculovirus expression vector is subsequently packaged into an infectious recombinant baculovirus. Homologous recombination occurs at low frequency (between about 1% and about 5%); thus, the majority of the virus produced after cotransfection is still wild-type virus. Therefore, a method is necessary to identify recombinant viruses. An advantage of the expression system is a visual screen allowing recombinant viruses to be distinguished. The polyhedrin protein, which is produced by the native virus, is produced at very high levels in the nuclei of infected cells at late times after viral infection. Accumulated polyhedrin protein forms occlusion bodies that also contain embedded particles. These occlusion bodies, up to 15  $\mu\text{m}$  in size, are highly refractile, giving them a bright shiny appearance that is readily visualized under the light microscope. Cells infected with recombinant viruses lack occlusion bodies. To distinguish recombinant virus from wild-type virus, the transfection supernatant is plaqued onto a monolayer of insect cells by techniques known to those skilled in the art. Namely, the plaques are screened under the light microscope for the presence (indicative of wild-type virus) or absence (indicative of recombinant virus) of occlusion bodies. *Current Protocols in Microbiology* Vol. 2 (Ausubel et al. eds) at 16.8 (Supp. 10, 1990); Summers and Smith, *supra*; Miller et al. (1989).

Recombinant baculovirus expression vectors have been developed for infection into several insect cells. For example, recombinant baculoviruses have been developed for, *inter alia*: *Aedes aegypti*, *Autographa californica*, *Bombyx mori*, *Drosophila melanogaster*, *Spodoptera frugiperda*, and *Trichoplusia ni* (PCT Pub. No. WO 89/046699; Carbonell et al., (1985) *J. Virol.* 56:153; Wright (1986) *Nature* 321:718; Smith et al., (1983) *Mol. Cell. Biol.* 3:2156; and see generally, Fraser, et al. (1989) *In Vitro Cell. Dev. Biol.* 25:225).

Cells and cell culture media are commercially available for both direct and fusion expression of heterologous polypeptides in a baculovirus/expression system; cell culture technology is generally known to those skilled in the art. See, e.g., Summers and Smith *supra*.

The modified insect cells may then be grown in an appropriate nutrient medium, which allows for stable maintenance of the plasmid(s) present in the modified insect host. Where the expression product gene is under inducible control, the host may be grown to high density, and expression induced. Alternatively, where expression is constitutive, the product will be continuously expressed into the medium and the nutrient medium must be continuously circulated, while removing the product of interest and augmenting depleted nutrients. The product may be purified by such techniques as chromatography, e.g., HPLC, affinity chromatography, ion exchange chromatography, etc.; electrophoresis; density gradient centrifugation; solvent extraction, or the like. As appropriate, the product may be further purified, as required, so as to remove substantially any insect proteins which are also secreted in the medium or result from lysis of insect cells, so as to provide a product which is at least substantially free of host debris, e.g., proteins, lipids and polysaccharides.

In order to obtain protein expression, recombinant host cells derived from the transformants are incubated under conditions which allow expression of the recombinant protein encoding sequence. These conditions will vary, dependent upon the host cell selected. However, the conditions are readily ascertainable to those of ordinary skill in the art, based upon what is known in the art.

#### iv. Bacterial Systems

Bacterial expression techniques are known in the art. A bacterial promoter is any DNA sequence capable of binding bacterial RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site and a transcription initiation site. A bacterial promoter may also have a second domain called an operator, that may overlap an adjacent RNA polymerase binding site at which RNA synthesis begins. The operator permits negative regulated (inducible) transcription, as a gene repressor protein may bind the operator and thereby inhibit transcription of a specific gene. Constitutive expression may occur in the absence of negative regulatory elements, such as the operator. In addition, positive regulation may be achieved by a gene activator protein binding sequence, which, if present is usually proximal (5') to the RNA polymerase binding sequence. An example of a gene activator protein is the catabolite activator protein (CAP), which helps

initiate transcription of the lac operon in *Escherichia coli* (*E. coli*) (Raibaud *et al.* (1984) *Annu. Rev. Genet.* 18:173). Regulated expression may therefore be either positive or negative, thereby either enhancing or reducing transcription.

Sequences encoding metabolic pathway enzymes provide particularly useful promoter sequences. Examples include promoter sequences derived from sugar metabolizing enzymes, such as galactose, lactose (*lac*) (Chang *et al.* (1977) *Nature* 198:1056), and maltose. Additional examples include promoter sequences derived from biosynthetic enzymes such as tryptophan (*trp*) (Goeddel *et al.* (1980) *Nuc. Acids Res.* 8:4057; Yelverton *et al.* (1981) *Nucl. Acids Res.* 9:731; U.S. Patent 4,738,921; EPO Publ. Nos. 036 776 and 121 775). The beta-lactamase (*bla*) promoter system (Weissmann (1981) "The cloning of interferon and other mistakes." In *Interferon 3* (ed. I. Gresser)), bacteriophage lambda PL (Shimatake *et al.* (1981) *Nature* 292:128) and T5 (U.S. Patent 4,689,406) promoter systems also provide useful promoter sequences.

In addition, synthetic promoters which do not occur in nature also function as bacterial promoters. For example, transcription activation sequences of one bacterial or bacteriophage promoter may be joined with the operon sequences of another bacterial or bacteriophage promoter, creating a synthetic hybrid promoter (U.S. Patent 4,551,433). For example, the *tac* promoter is a hybrid *trp-lac* promoter comprised of both *trp* promoter and *lac* operon sequences that is regulated by the *lac* repressor (Amann *et al.* (1983) *Gene* 25:167; de Boer *et al.* (1983) *Proc. Natl. Acad. Sci.* 80:21). Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. A naturally occurring promoter of non-bacterial origin can also be coupled with a compatible RNA polymerase to produce high levels of expression of some genes in prokaryotes. The bacteriophage T7 RNA polymerase/promoter system is an example of a coupled promoter system (Studier *et al.* (1986) *J. Mol. Biol.* 189:113; Tabor *et al.* (1985) *Proc Natl. Acad. Sci.* 82:1074). In addition, a hybrid promoter can also be comprised of a bacteriophage promoter and an *E. coli* operator region (EPO Publ. No. 267 851).

In addition to a functioning promoter sequence, an efficient ribosome binding site is also useful for the expression of foreign genes in prokaryotes. In *E. coli*, the ribosome binding site is called the Shine-Dalgarno (SD) sequence and includes an initiation codon (ATG) and a sequence 3-9 nucleotides in length located 3-11 nucleotides upstream of the initiation codon

(Shine *et al.* (1975) *Nature* 254:34). The SD sequence is thought to promote binding of mRNA to the ribosome by the pairing of bases between the SD sequence and the 3' end of *E. coli* 16S rRNA (Steitz *et al.* (1979) "Genetic signals and nucleotide sequences in messenger RNA." In *Biological Regulation and Development: Gene Expression* (ed. R.F. Goldberg)). To express eukaryotic genes and prokaryotic genes with weak ribosome-binding site, it is often necessary to optimize the distance between the SD sequence and the ATG of the eukaryotic gene (Sambrook *et al.* (1989) "Expression of cloned genes in *Escherichia coli*." In *Molecular Cloning: A Laboratory Manual*).

A DNA molecule may be expressed intracellularly. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide or by either *in vivo* or *in vitro* incubation with a bacterial methionine N-terminal peptidase (EPO Publ. No. 219 237).

Fusion proteins provide an alternative to direct expression. Usually, a DNA sequence encoding the N-terminal portion of an endogenous bacterial protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the bacteriophage lambda cell gene can be linked at the 5' terminus of a foreign gene and expressed in bacteria. The resulting fusion protein preferably retains a site for a processing enzyme (factor Xa) to cleave the bacteriophage protein from the foreign gene (Nagai *et al.* (1984) *Nature* 309:810). Fusion proteins can also be made with sequences from the *lacZ* (Jia *et al.* (1987) *Gene* 60:197), *trpE* (Allen *et al.* (1987) *J. Biotechnol.* 5:93; Makoff *et al.* (1989) *J. Gen. Microbiol.* 135:11), and *Chey* (EPO Publ. No. 324 647) genes. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin specific processing-protease) to cleave the ubiquitin from the foreign protein. Through this method, native foreign protein can be isolated (Miller *et al.* (1989) *Bio/Technology* 7:698).

Alternatively, foreign proteins can also be secreted from the cell by creating chimeric DNA molecules that encode a fusion protein comprised of a signal peptide sequence fragment that provides for secretion of the foreign protein in bacteria (U.S. Patent 4,336,336). The

signal sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). Preferably there are processing sites, which can be cleaved either *in vivo* or *in vitro* encoded between the signal peptide fragment and the foreign gene.

DNA encoding suitable signal sequences can be derived from genes for secreted bacterial proteins, such as the *E. coli* outer membrane protein gene (*ompA*) (Masui *et al.* (1983), in: *Experimental Manipulation of Gene Expression*; Ghrayeb *et al.* (1984) *EMBO J.* 3:2437) and the *E. coli* alkaline phosphatase signal sequence (*phoA*) (Oka *et al.* (1985) *Proc. Natl. Acad. Sci.* 82:7212). As an additional example, the signal sequence of the alpha-amylase gene from various *Bacillus* strains can be used to secrete heterologous proteins from *B. subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. No. 244 042).

Usually, transcription termination sequences recognized by bacteria are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Transcription termination sequences frequently include DNA sequences of about 50 nucleotides capable of forming stem loop structures that aid in terminating transcription. Examples include transcription termination sequences derived from genes with strong promoters, such as the *trp* gene in *E. coli* as well as other biosynthetic genes.

Usually, the above described components, comprising a promoter, signal sequence (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as bacteria. The replicon will have a replication system, thus allowing it to be maintained in a prokaryotic host either for expression or for cloning and amplification. In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably contain at least about 10, and more preferably at least about 20 plasmids. Either a high or low copy number

vector may be selected, depending upon the effect of the vector and the foreign protein on the host.

Alternatively, the expression constructs can be integrated into the bacterial genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to the bacterial chromosome that allows the vector to integrate. Integrations appear to result from recombinations between homologous DNA in the vector and the bacterial chromosome. For example, integrating vectors constructed with DNA from various *Bacillus* strains integrate into the *Bacillus* chromosome (EPO Publ. No. 127 328). Integrating vectors may also be comprised of bacteriophage or transposon sequences.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of bacterial strains that have been transformed. Selectable markers can be expressed in the bacterial host and may include genes which render bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin (neomycin), and tetracycline (Davies *et al.* (1978) *Annu. Rev. Microbiol.* 32:469). Selectable markers may also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways.

Alternatively, some of the above described components can be put together in transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extra-chromosomal replicons or integrating vectors, have been developed for transformation into many bacteria. For example, expression vectors have been developed for, *inter alia*, the following bacteria: *Bacillus subtilis* (Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541), *Escherichia coli* (Shimatake *et al.* (1981) *Nature* 292:128; Amann *et al.* (1985) *Gene* 40:183; Studier *et al.* (1986) *J. Mol. Biol.* 189:113; EPO Publ. Nos. 036 776, 136 829 and 136 907), *Streptococcus cremoris* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655); *Streptococcus lividans* (Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655), *Streptomyces lividans* (U.S. Patent 4,745,056).

Methods of introducing exogenous DNA into bacterial hosts are well-known in the art, and usually include either the transformation of bacteria treated with  $\text{CaCl}_2$  or other agents, such as divalent cations and DMSO. DNA can also be introduced into bacterial cells by



electroporation. Transformation procedures usually vary with the bacterial species to be transformed. (See e.g., use of *Bacillus*: Masson *et al.* (1989) *FEMS Microbiol. Lett.* 60:273; Palva *et al.* (1982) *Proc. Natl. Acad. Sci. USA* 79:5582; EPO Publ. Nos. 036 259 and 063 953; PCT Publ. No. WO 84/04541; use of *Campylobacter*: Miller *et al.* (1988) *Proc. Natl. Acad. Sci.* 85:856; and Wang *et al.* (1990) *J. Bacteriol.* 172:949; use of *Escherichia coli*: Cohen *et al.* (1973) *Proc. Natl. Acad. Sci.* 69:2110; Dower *et al.* (1988) *Nucleic Acids Res.* 16:6127; Kushner (1978) "An improved method for transformation of *Escherichia coli* with ColE1-derived plasmids. In *Genetic Engineering: Proceedings of the International Symposium on Genetic Engineering* (eds. H.W. Boyer and S. Nicosia); Mandel *et al.* (1970) *J. Mol. Biol.* 53:159; Taketo (1988) *Biochim. Biophys. Acta* 949:318; use of *Lactobacillus*: Chassy *et al.* (1987) *FEMS Microbiol. Lett.* 44:173; use of *Pseudomonas*: Fiedler *et al.* (1988) *Anal. Biochem* 170:38; use of *Staphylococcus*: Augustin *et al.* (1990) *FEMS Microbiol. Lett.* 66:203; use of *Streptococcus*: Barany *et al.* (1980) *J. Bacteriol.* 144:698; Harlander (1987) "Transformation of *Streptococcus lactis* by electroporation, in: *Streptococcal Genetics* (ed. J. Ferretti and R. Curtiss III); Perry *et al.* (1981) *Infect. Immun.* 32:1295; Powell *et al.* (1988) *Appl. Environ. Microbiol.* 54:655; Somkuti *et al.* (1987) *Proc. 4th Evr. Cong. Biotechnology* 1:412.

#### v. Yeast Expression

Yeast expression systems are also known to one of ordinary skill in the art. A yeast promoter is any DNA sequence capable of binding yeast RNA polymerase and initiating the downstream (3') transcription of a coding sequence (e.g. structural gene) into mRNA. A promoter will have a transcription initiation region which is usually placed proximal to the 5' end of the coding sequence. This transcription initiation region usually includes an RNA polymerase binding site (the "TATA Box") and a transcription initiation site. A yeast promoter may also have a second domain called an upstream activator sequence (UAS), which, if present, is usually distal to the structural gene. The UAS permits regulated (inducible) expression. Constitutive expression occurs in the absence of a UAS. Regulated expression may be either positive or negative, thereby either enhancing or reducing transcription.

Yeast is a fermenting organism with an active metabolic pathway, therefore sequences encoding enzymes in the metabolic pathway provide particularly useful promoter sequences.

Examples include alcohol dehydrogenase (ADH) (EPO Publ. No. 284 044), enolase, glucokinase, glucose-6-phosphate isomerase, glyceraldehyde-3-phosphate-dehydrogenase (GAP or GAPDH), hexokinase, phosphofructokinase, 3-phosphoglycerate mutase, and pyruvate kinase (PyK) (EPO Publ. No. 329 203). The yeast *PHO5* gene, encoding acid phosphatase, also provides useful promoter sequences (Myanohara *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:1).

In addition, synthetic promoters which do not occur in nature also function as yeast promoters. For example, UAS sequences of one yeast promoter may be joined with the transcription activation region of another yeast promoter, creating a synthetic hybrid promoter. Examples of such hybrid promoters include the ADH regulatory sequence linked to the GAP transcription activation region (U.S. Patent Nos. 4,876,197 and 4,880,734). Other examples of hybrid promoters include promoters which consist of the regulatory sequences of either the *ADH2*, *GAL4*, *GAL10*, OR *PHO5* genes, combined with the transcriptional activation region of a glycolytic enzyme gene such as GAP or PyK (EPO Publ. No. 164 556). Furthermore, a yeast promoter can include naturally occurring promoters of non-yeast origin that have the ability to bind yeast RNA polymerase and initiate transcription. Examples of such promoters include, *inter alia*, (Cohen *et al.* (1980) *Proc. Natl. Acad. Sci. USA* 77:1078; Henikoff *et al.* (1981) *Nature* 283:835; Hollenberg *et al.* (1981) *Curr. Topics Microbiol. Immunol.* 96:119; Hollenberg *et al.* (1979) "The Expression of Bacterial Antibiotic Resistance Genes in the Yeast *Saccharomyces cerevisiae*," in: *Plasmids of Medical, Environmental and Commercial Importance* (eds. K.N. Timmis and A. Puhler); Mercerau-Puigalon *et al.* (1980) *Gene* 11:163; Panthier *et al.* (1980) *Curr. Genet.* 2:109;).

A DNA molecule may be expressed intracellularly in yeast. A promoter sequence may be directly linked with the DNA molecule, in which case the first amino acid at the N-terminus of the recombinant protein will always be a methionine, which is encoded by the ATG start codon. If desired, methionine at the N-terminus may be cleaved from the protein by *in vitro* incubation with cyanogen bromide.

Fusion proteins provide an alternative for yeast expression systems, as well as in mammalian, plant, baculovirus, and bacterial expression systems. Usually, a DNA sequence encoding the N-terminal portion of an endogenous yeast protein, or other stable protein, is fused to the 5' end of heterologous coding sequences. Upon expression, this construct will provide a fusion of the two amino acid sequences. For example, the yeast or human

superoxide dismutase (SOD) gene, can be linked at the 5' terminus of a foreign gene and expressed in yeast. The DNA sequence at the junction of the two amino acid sequences may or may not encode a cleavable site. See e.g., EPO Publ. No. 196056. Another example is a ubiquitin fusion protein. Such a fusion protein is made with the ubiquitin region that preferably retains a site for a processing enzyme (e.g. ubiquitin-specific processing protease) to cleave the ubiquitin from the foreign protein. Through this method, therefore, native foreign protein can be isolated (e.g., WO88/024066).

Alternatively, foreign proteins can also be secreted from the cell into the growth media by creating chimeric DNA molecules that encode a fusion protein comprised of a leader sequence fragment that provide for secretion in yeast of the foreign protein. Preferably, there are processing sites encoded between the leader fragment and the foreign gene that can be cleaved either *in vivo* or *in vitro*. The leader sequence fragment usually encodes a signal peptide comprised of hydrophobic amino acids which direct the secretion of the protein from the cell.

DNA encoding suitable signal sequences can be derived from genes for secreted yeast proteins, such as the yeast invertase gene (EPO Publ. No. 012 873; JPO Publ. No. 62:096,086) and the A-factor gene (U.S. Patent 4,588,684). Alternatively, leaders of non-yeast origin, such as an interferon leader, exist that also provide for secretion in yeast (EPO Publ. No. 060 057).

A preferred class of secretion leaders are those that employ a fragment of the yeast alpha-factor gene, which contains both a "pre" signal sequence, and a "pro" region. The types of alpha-factor fragments that can be employed include the full-length pre-pro alpha factor leader (about 83 amino acid residues) as well as truncated alpha-factor leaders (usually about 25 to about 50 amino acid residues) (U.S. Patent Nos. 4,546,083 and 4,870,008; EPO Publ. No. 324 274). Additional leaders employing an alpha-factor leader fragment that provides for secretion include hybrid alpha-factor leaders made with a presequence of a first yeast, but a pro-region from a second yeast alphafactor. (See e.g., PCT Publ. No. WO 89/02463.)

Usually, transcription termination sequences recognized by yeast are regulatory regions located 3' to the translation stop codon, and thus together with the promoter flank the coding sequence. These sequences direct the transcription of an mRNA which can be translated into the polypeptide encoded by the DNA. Examples of transcription terminator

sequence and other yeast-recognized termination sequences, such as those coding for glycolytic enzymes.

Usually, the above described components, comprising a promoter, leader (if desired), coding sequence of interest, and transcription termination sequence, are put together into expression constructs. Expression constructs are often maintained in a replicon, such as an extrachromosomal element (e.g., plasmids) capable of stable maintenance in a host, such as yeast or bacteria. The replicon may have two replication systems, thus allowing it to be maintained, for example, in yeast for expression and in a prokaryotic host for cloning and amplification. Examples of such yeast-bacteria shuttle vectors include YEp24 (Botstein *et al.* (1979) *Gene* 8:17-24), pCI/1 (Brake *et al.* (1984) *Proc. Natl. Acad. Sci. USA* 81:4642-4646), and YRp17 (Stinchcomb *et al.* (1982) *J. Mol. Biol.* 158:157). In addition, a replicon may be either a high or low copy number plasmid. A high copy number plasmid will generally have a copy number ranging from about 5 to about 200, and usually about 10 to about 150. A host containing a high copy number plasmid will preferably have at least about 10, and more preferably at least about 20. Enter a high or low copy number vector may be selected, depending upon the effect of the vector and the foreign protein on the host. See e.g., Brake *et al.*, *supra*.

Alternatively, the expression constructs can be integrated into the yeast genome with an integrating vector. Integrating vectors usually contain at least one sequence homologous to a yeast chromosome that allows the vector to integrate, and preferably contain two homologous sequences flanking the expression construct. Integrations appear to result from recombinations between homologous DNA in the vector and the yeast chromosome (Orr-Weaver *et al.* (1983) *Methods in Enzymol.* 101:228-245). An integrating vector may be directed to a specific locus in yeast by selecting the appropriate homologous sequence for inclusion in the vector. See Orr-Weaver *et al.*, *supra*. One or more expression construct may integrate, possibly affecting levels of recombinant protein produced (Rine *et al.* (1983) *Proc. Natl. Acad. Sci. USA* 80:6750). The chromosomal sequences included in the vector can occur either as a single segment in the vector, which results in the integration of the entire vector, or two segments homologous to adjacent segments in the chromosome and flanking the expression construct in the vector, which can result in the stable integration of only the expression construct.

Usually, extrachromosomal and integrating expression constructs may contain selectable markers to allow for the selection of yeast strains that have been transformed. Selectable markers may include biosynthetic genes that can be expressed in the yeast host, such as *ADE2*, *HIS4*, *LEU2*, *TRP1*, and *ALG7*, and the G418 resistance gene, which confer resistance in yeast cells to tunicamycin and G418, respectively. In addition, a suitable selectable marker may also provide yeast with the ability to grow in the presence of toxic compounds, such as metal. For example, the presence of *CUP1* allows yeast to grow in the presence of copper ions (Butt *et al.* (1987) *Microbiol. Rev.* 51:351).

Alternatively, some of the above described components can be put together into transformation vectors. Transformation vectors are usually comprised of a selectable marker that is either maintained in a replicon or developed into an integrating vector, as described above.

Expression and transformation vectors, either extrachromosomal replicons or integrating vectors, have been developed for transformation into many yeasts. For example, expression vectors and methods of introducing exogenous DNA into yeast hosts have been developed for, *inter alia*, the following yeasts: *Candida albicans* (Kurtz, *et al.* (1986) *Mol. Cell. Biol.* 6:142); *Candida maltosa* (Kunze, *et al.* (1985) *J. Basic Microbiol.* 25:141); *Hansenula polymorpha* (Gleeson, *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302); *Kluyveromyces fragilis* (Das, *et al.* (1984) *J. Bacteriol.* 158:1165); *Kluyveromyces lactis* (De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:737; Van den Berg *et al.* (1990) *Bio/Technology* 8:135); *Pichia guilliermondii* (Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141); *Pichia pastoris* (Cregg, *et al.* (1985) *Mol. Cell. Biol.* 5:3376; U.S. Patent Nos. 4,837,148 and 4,929,555); *Saccharomyces cerevisiae* (Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163); *Schizosaccharomyces pombe* (Beach and Nurse (1981) *Nature* 300:706); and *Yarrowia lipolytica* (Davidow, *et al.* (1985) *Curr. Genet.* 10:380471 Gaillardin, *et al.* (1985) *Curr. Genet.* 10:49).

Methods of introducing exogenous DNA into yeast hosts are well-known in the art, and usually include either the transformation of spheroplasts or of intact yeast cells treated with alkali cations. Transformation procedures usually vary with the yeast species to be transformed. See e.g., [Kurtz *et al.* (1986) *Mol. Cell. Biol.* 6:142; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; *Candida*]; [Gleeson *et al.* (1986) *J. Gen. Microbiol.* 132:3459; Roggenkamp *et al.* (1986) *Mol. Gen. Genet.* 202:302; *Hansenula*]; [Das *et al.* (1984) *J.*

*Bacteriol.* 158:1165; De Louvencourt *et al.* (1983) *J. Bacteriol.* 154:1165; Van den Berg *et al.* (1990) *Bio/Technology* 8:135; Kluyveromyces]; [Cregg *et al.* (1985) *Mol. Cell. Biol.* 5:3376; Kunze *et al.* (1985) *J. Basic Microbiol.* 25:141; U.S. Patent Nos. 4,837,148 and 4,929,555; Pichia]; [Hinnen *et al.* (1978) *Proc. Natl. Acad. Sci. USA* 75:1929; Ito *et al.* (1983) *J. Bacteriol.* 153:163 *Saccharomyces*]; [Beach and Nurse (1981) *Nature* 300:706; *Schizosaccharomyces*]; [Davidow *et al.* (1985) *Curr. Genet.* 10:39; Gaillardin *et al.* (1985) *Curr. Genet.* 10:49; *Yarrowia*].

### Definitions

A composition containing X is "substantially free of" Y when at least 85% by weight of the total X+Y in the composition is X. Preferably, X comprises at least about 90% by weight of the total of X+Y in the composition, more preferably at least about 95% or even 99% by weight.

A "conserved" *Neisseria* amino acid fragment or protein is one that is present in a particular *Neisserial* protein in at least x% of *Neisseria*. The value of x may be 50% or more, e.g., 66%, 75%, 80%, 90%, 95% or even 100% (i.e. the amino acid is found in the protein in question in all *Neisseria*). In order to determine whether an amino acid is "conserved" in a particular *Neisserial* protein, it is necessary to compare that amino acid residue in the sequences of the protein in question from a plurality of different *Neisseria* (a reference population). The reference population may include a number of different *Neisseria* species or may include a single species. The reference population may include a number of different serogroups of a particular species or a single serogroup. A preferred reference population consists of the 5 most common *Neisseria* strains.

The term "heterologous" refers to two biological components that are not found together in nature. The components may be host cells, genes, or regulatory regions, such as promoters. Although the heterologous components are not found together in nature, they can function together, as when a promoter heterologous to a gene is operably linked to the gene. Another example is where a *Neisserial* sequence is heterologous to a mouse host cell.

"Epitope" means antigenic determinant, and may elicit a cellular and/or humoral response.

Conditions for "high stringency" are 65 degrees C in 0.1 xSSC 0.5% SDS solution.

An "origin of replication" is a polynucleotide sequence that initiates and regulates replication of polynucleotides, such as an expression vector. The origin of replication behaves as an autonomous unit of polynucleotide replication within a cell, capable of replication under its own control. An origin of replication may be needed for a vector to replicate in a particular host cell. With certain origins of replication, an expression vector can be reproduced at a high copy number in the presence of the appropriate proteins within the cell. Examples of origins are the autonomously replicating sequences, which are effective in yeast; and the viral T-antigen, effective in COS-7 cells.

A "mutant" sequence is defined as a DNA, RNA or amino acid sequence differing from but having homology with the native or disclosed sequence. Depending on the particular sequence, the degree of homology (sequence identity) between the native or disclosed sequence and the mutant sequence is preferably greater than 50% (e.g., 60%, 70%, 80%, 90%, 95%, 99% or more) which is calculated as described above. As used herein, an "allelic variant" of a nucleic acid molecule, or region, for which nucleic acid sequence is provided herein is a nucleic acid molecule, or region, that occurs at essentially the same locus in the genome of another or second isolate, and that, due to natural variation caused by, for example, mutation or recombination, has a similar but not identical nucleic acid sequence. A coding region allelic variant typically encodes a protein having similar activity to that of the protein encoded by the gene to which it is being compared. An allelic variant can also comprise an alteration in the 5' or 3' untranslated regions of the gene, such as in regulatory control regions. (see, for example, U.S. Patent 5,753,235).

#### Antibodies

As used herein, the term "antibody" refers to a polypeptide or group of polypeptides composed of at least one antibody combining site. An "antibody combining site" is the three-dimensional binding space with an internal surface shape and charge distribution complementary to the features of an epitope of an antigen, which allows a binding of the antibody with the antigen. "Antibody" includes, for example, vertebrate antibodies, hybrid antibodies, chimeric antibodies, humanized antibodies, altered antibodies, univalent antibodies, Fab proteins, and single domain antibodies.

Antibodies against the proteins of the invention are useful for affinity chromatography, immunoassays, and distinguishing/identifying *Neisseria menB* proteins.

Antibodies elicited against the proteins of the present invention bind to antigenic polypeptides or proteins or protein fragments that are present and specifically associated with strains of *Neisseria meningitidis* menB. In some instances, these antigens may be associated with specific strains, such as those antigens specific for the menB strains. The antibodies of the invention may be immobilized to a matrix and utilized in an immunoassay or on an affinity chromatography column, to enable the detection and/or separation of polypeptides, proteins or protein fragments or cells comprising such polypeptides, proteins or protein fragments. Alternatively, such polypeptides, proteins or protein fragments may be immobilized so as to detect antibodies bindably specific thereto.

Antibodies to the proteins of the invention, both polyclonal and monoclonal, may be prepared by conventional methods. In general, the protein is first used to immunize a suitable animal, preferably a mouse, rat, rabbit or goat. Rabbits and goats are preferred for the preparation of polyclonal sera due to the volume of serum obtainable, and the availability of labeled anti-rabbit and anti-goat antibodies. Immunization is generally performed by mixing or emulsifying the protein in saline, preferably in an adjuvant such as Freund's complete adjuvant, and injecting the mixture or emulsion parenterally (generally subcutaneously or intramuscularly). A dose of 50-200 µg/injection is typically sufficient. Immunization is generally boosted 2-6 weeks later with one or more injections of the protein in saline, preferably using Freund's incomplete adjuvant. One may alternatively generate antibodies by *in vitro* immunization using methods known in the art, which for the purposes of this invention is considered equivalent to *in vivo* immunization. Polyclonal antisera is obtained by bleeding the immunized animal into a glass or plastic container, incubating the blood at 25°C for one hour, followed by incubating at 4°C for 2-18 hours. The serum is recovered by centrifugation (e.g., 1,000g for 10 minutes). About 20-50 ml per bleed may be obtained from rabbits.

Monoclonal antibodies are prepared using the standard method of Kohler & Milstein (*Nature* (1975) 256:495-96), or a modification thereof. Typically, a mouse or rat is immunized as described above. However, rather than bleeding the animal to extract serum, the spleen (and optionally several large lymph nodes) is removed and dissociated into single cells. If desired, the spleen cells may be screened (after removal of nonspecifically adherent cells) by applying a cell suspension to a plate or well coated with the protein antigen. B-cells that express membrane-bound immunoglobulin specific for the antigen bind to the plate, and



are not rinsed away with the rest of the suspension. Resulting B-cells, or all dissociated spleen cells, are then induced to fuse with myeloma cells to form hybridomas, and are cultured in a selective medium (e.g., hypoxanthine, aminopterin, thymidine medium, "HAT"). The resulting hybridomas are plated by limiting dilution, and are assayed for the production of antibodies which bind specifically to the immunizing antigen (and which do not bind to unrelated antigens). The selected MAb-secreting hybridomas are then cultured either *in vitro* (e.g., in tissue culture bottles or hollow fiber reactors), or *in vivo* (as ascites in mice).

If desired, the antibodies (whether polyclonal or monoclonal) may be labeled using conventional techniques. Suitable labels include fluorophores, chromophores, radioactive atoms (particularly  $^{32}\text{P}$  and  $^{125}\text{I}$ ), electron-dense reagents, enzymes, and ligands having specific binding partners. Enzymes are typically detected by their activity. For example, horseradish peroxidase is usually detected by its ability to convert 3,3',5,5'-tetramethylbenzidine (TMB) to a blue pigment, quantifiable with a spectrophotometer. "Specific binding partner" refers to a protein capable of binding a ligand molecule with high specificity, as for example in the case of an antigen and a monoclonal antibody specific therefor. Other specific binding partners include biotin and avidin or streptavidin, IgG and protein A, and the numerous receptor-ligand couples known in the art. It should be understood that the above description is not meant to categorize the various labels into distinct classes, as the same label may serve in several different modes. For example,  $^{125}\text{I}$  may serve as a radioactive label or as an electron-dense reagent. HRP may serve as enzyme or as antigen for a MAb. Further, one may combine various labels for desired effect. For example, MAbs and avidin also require labels in the practice of this invention: thus, one might label a MAb with biotin, and detect its presence with avidin labeled with  $^{125}\text{I}$ , or with an anti-biotin MAb labeled with HRP. Other permutations and possibilities will be readily apparent to those of ordinary skill in the art, and are considered as equivalents within the scope of the instant invention.

Antigens, immunogens, polypeptides, proteins or protein fragments of the present invention elicit formation of specific binding partner antibodies. These antigens, immunogens, polypeptides, proteins or protein fragments of the present invention comprise immunogenic compositions of the present invention. Such immunogenic compositions may further comprise or include adjuvants, carriers, or other compositions that promote or enhance

or stabilize the antigens, polypeptides, proteins or protein fragments of the present invention. Such adjuvants and carriers will be readily apparent to those of ordinary skill in the art.

#### Pharmaceutical Compositions

Pharmaceutical compositions can comprise (include) either polypeptides, antibodies, or nucleic acid of the invention. The pharmaceutical compositions will comprise a therapeutically effective amount of either polypeptides, antibodies, or polynucleotides of the claimed invention.

The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature, when given to a patient that is febrile. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation can be determined by routine experimentation and is within the judgment of the clinician.

For purposes of the present invention, an effective dose will be from about 0.01 mg/kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which may be administered without undue toxicity. Suitable carriers may be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

Pharmaceutically acceptable salts can be used therein, for example, mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of

organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in Remington's Pharmaceutical Sciences (Mack Pub. Co., N.J. 1991).

Pharmaceutically acceptable carriers in therapeutic compositions may contain liquids such as water, saline, glycerol and ethanol. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier.

#### Delivery Methods

Once formulated, the compositions of the invention can be administered directly to the subject. The subjects to be treated can be animals; in particular, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal and transcutaneous applications, needles, and gene guns or hyposprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

#### Vaccines

Vaccines according to the invention may either be prophylactic (i.e., to prevent infection) or therapeutic (i.e., to treat disease after infection).

Such vaccines comprise immunizing antigen(s) or immunogen(s), immunogenic polypeptide, protein(s) or protein fragments, or nucleic acids (e.g., ribonucleic acid or deoxyribonucleic acid), usually in combination with "pharmaceutically acceptable carriers," which include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, lipid aggregates (such as oil droplets or

liposomes), and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Additionally, these carriers may function as immunostimulating agents ("adjuvants"). Furthermore, the immunogen or antigen may be conjugated to a bacterial toxoid, such as a toxoid from diphtheria, tetanus, cholera, *H. pylori*, etc. pathogens.

Preferred adjuvants to enhance effectiveness of the composition include, but are not limited to: (1) aluminum salts (alum), such as aluminum hydroxide, aluminum phosphate, aluminum sulfate, etc; (2) oil-in-water emulsion formulations (with or without other specific immunostimulating agents such as muramyl peptides (see below) or bacterial cell wall components), such as for example (a) MF59 (PCT Publ. No. WO 90/14837), containing 5% Squalene, 0.5% Tween 80, and 0.5% Span 85 (optionally containing various amounts of MTP-PE (see below), although not required) formulated into submicron particles using a microfluidizer such as Model 110Y microfluidizer (Microfluidics, Newton, MA), (b) SAF, containing 10% Squalene, 0.4% Tween 80, 5% pluronic-blocked polymer L121, and thr-MDP (see below) either microfluidized into a submicron emulsion or vortexed to generate a larger particle size emulsion, and (c) Ribi<sup>TM</sup> adjuvant system (RAS), (Ribi Immunochem, Hamilton, MT) containing 2% Squalene, 0.2% Tween 80, and one or more bacterial cell wall components from the group consisting of monophosphorylipid A (MPL), trehalose dimycolate (TDM), and cell wall skeleton (CWS), preferably MPL + CWS (Detox<sup>TM</sup>); (3) saponin adjuvants, such as Stimulon<sup>TM</sup> (Cambridge Bioscience, Worcester, MA) may be used or particles generated therefrom such as ISCOMs (immunostimulating complexes); (4) Complete Freund's Adjuvant (CFA) and Incomplete Freund's Adjuvant (IFA); (5) cytokines, such as interleukins (e.g., IL-1, IL-2, IL-4, IL-5, IL-6, IL-7, IL-12, etc.), interferons (e.g., gamma interferon), macrophage colony stimulating factor (M-CSF), tumor necrosis factor (TNF), etc; (6) detoxified mutants of a bacterial ADP-ribosylating toxin such as a cholera toxin (CT), a pertussis toxin (PT), or an *E. coli* heat-labile toxin (LT), particularly LT-K63, LT-R72, CT-S109, PT-K9/G129; see, e.g., WO 93/13302 and WO 92/19265; and (7) other substances that act as immunostimulating agents to enhance the effectiveness of the composition. Alum and MF59 are preferred.

As mentioned above, muramyl peptides include, but are not limited to, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-normuramyl-L-alanyl-D-isoglutamine (nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-*sn*-glycero-3-hydroxyphosphoryloxy)-ethylamine (MTP-PE), etc.

The vaccine compositions comprising immunogenic compositions (e.g., which may include the antigen, pharmaceutically acceptable carrier, and adjuvant) typically will contain diluents, such as water, saline, glycerol, ethanol, etc. Additionally, auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, may be present in such vehicles. Alternatively, vaccine compositions comprising immunogenic compositions may comprise an antigen, polypeptide, protein, protein fragment or nucleic acid in a pharmaceutically acceptable carrier.

More specifically, vaccines comprising immunogenic compositions comprise an immunologically effective amount of the immunogenic polypeptides, as well as any other of the above-mentioned components, as needed. By "immunologically effective amount", it is meant that the administration of that amount to an individual, either in a single dose or as part of a series, is effective for treatment or prevention. This amount varies depending upon the health and physical condition of the individual to be treated, the taxonomic group of individual to be treated (e.g., nonhuman primate, primate, *etc.*), the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials.

Typically, the vaccine compositions or immunogenic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection may also be prepared. The preparation also may be emulsified or encapsulated in liposomes for enhanced adjuvant effect, as discussed above under pharmaceutically acceptable carriers.

The immunogenic compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Additional formulations suitable for other modes of administration include oral and pulmonary formulations, suppositories, and transdermal and transcutaneous applications. Dosage treatment may be a single dose schedule or a multiple dose schedule. The vaccine may be administered in conjunction with other immunoregulatory agents.

As an alternative to protein-based vaccines, DNA vaccination may be employed (e.g., Robinson & Torres (1997) *Seminars in Immunology* 9:271-283; Donnelly *et al.* (1997) *Annu Rev Immunol* 15:617-648).

### Gene Delivery Vehicles

Gene therapy vehicles for delivery of constructs, including a coding sequence of a therapeutic of the invention, to be delivered to the mammal for expression in the mammal, can be administered either locally or systemically. These constructs can utilize viral or non-viral vector approaches in *in vivo* or *ex vivo* modality. Expression of such coding sequence can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence *in vivo* can be either constitutive or regulated.

The invention includes gene delivery vehicles capable of expressing the contemplated nucleic acid sequences. The gene delivery vehicle is preferably a viral vector and, more preferably, a retroviral, adenoviral, adeno-associated viral (AAV), herpes viral, or alphavirus vector. The viral vector can also be an astrovirus, coronavirus, orthomyxovirus, papovavirus, paramyxovirus, parvovirus, picornavirus, poxvirus, or togavirus viral vector. See generally, Jolly (1994) *Cancer Gene Therapy* 1:51-64; Kimura (1994) *Human Gene Therapy* 5:845-852; Connelly (1995) *Human Gene Therapy* 6:185-193; and Kaplitt (1994) *Nature Genetics* 6:148-153.

Retroviral vectors are well known in the art, including B, C and D type retroviruses, xenotropic retroviruses (for example, NZB-X1, NZB-X2 and NZB9-1 (see O'Neill (1985) *J. Virol.* 53:160) polytropic retroviruses e.g., MCF and MCF-MLV (see Kelly (1983) *J. Virol.* 45:291), spumaviruses and lentiviruses. See RNA Tumor Viruses, Second Edition, Cold Spring Harbor Laboratory, 1985.

Portions of the retroviral gene therapy vector may be derived from different retroviruses. For example, retrovector LTRs may be derived from a Murine Sarcoma Virus, a tRNA binding site from a Rous Sarcoma Virus, a packaging signal from a Murine Leukemia Virus, and an origin of second strand synthesis from an Avian Leukosis Virus.

These recombinant retroviral vectors may be used to generate transduction competent retroviral vector particles by introducing them into appropriate packaging cell lines (see US patent 5,591,624). Retrovirus vectors can be constructed for site-specific integration into host cell DNA by incorporation of a chimeric integrase enzyme into the retroviral particle (see WO96/37626). It is preferable that the recombinant viral vector is a replication defective recombinant virus.

Packaging cell lines suitable for use with the above-described retrovirus vectors are well known in the art, are readily prepared (see WO95/30763 and WO92/05266), and can be used to create producer cell lines (also termed vector cell lines or "VCLs") for the production of recombinant vector particles. Preferably, the packaging cell lines are made from human parent cells (e.g., HT1080 cells) or mink parent cell lines, which eliminates inactivation in human serum.

Preferred retroviruses for the construction of retroviral gene therapy vectors include Avian Leukosis Virus, Bovine Leukemia Virus, Murine Leukemia Virus, Mink-Cell Focus-Inducing Virus, Murine Sarcoma Virus, Reticuloendotheliosis Virus and Rous Sarcoma Virus. Particularly preferred Murine Leukemia Viruses include 4070A and 1504A (Hartley and Rowe (1976) *J Virol* 19:19-25), Abelson (ATCC No. VR-999), Friend (ATCC No. VR-245), Graffi, Gross (ATCC No. VR-590), Kirsten, Harvey Sarcoma Virus and Rauscher (ATCC No. VR-998) and Moloney Murine Leukemia Virus (ATCC No. VR-190). Such retroviruses may be obtained from depositories or collections such as the American Type Culture Collection ("ATCC") in Rockville, Maryland or isolated from known sources using commonly available techniques.

Exemplary known retroviral gene therapy vectors employable in this invention include those described in patent applications GB2200651, EP0415731, EP0345242, EP0334301, WO89/02468; WO89/05349, WO89/09271, WO90/02806, WO90/07936, WO94/03622, WO93/25698, WO93/25234, WO93/11230, WO93/10218, WO91/02805, WO91/02825, WO95/07994, US 5,219,740, US 4,405,712, US 4,861,719, US 4,980,289, US 4,777,127, US 5,591,624. See also Vile (1993) *Cancer Res* 53:3860-3864; Vile (1993) *Cancer Res* 53:962-967; Ram (1993) *Cancer Res* 53 (1993) 83-88; Takamiya (1992) *J Neurosci Res* 33:493-503; Baba (1993) *J Neurosurg* 79:729-735; Mann (1983) *Cell* 33:153; Cane (1984) *Proc Natl Acad Sci* 81:6349; and Miller (1990) *Human Gene Therapy* 1.

Human adenoviral gene therapy vectors are also known in the art and employable in this invention. See, for example, Berkner (1988) *Biotechniques* 6:616 and Rosenfeld (1991) *Science* 252:431, and WO93/07283, WO93/06223, and WO93/07282. Exemplary known adenoviral gene therapy vectors employable in this invention include those described in the above referenced documents and in WO94/12649, WO93/03769, WO93/19191, WO94/28938, WO95/11984, WO95/00655, WO95/27071, WO95/29993, WO95/34671, WO96/05320, WO94/08026, WO94/11506, WO93/06223, WO94/24299, WO95/14102,

WO95/24297, WO95/02697, WO94/28152, WO94/24299, WO95/09241, WO95/25807, WO95/05835, WO94/18922 and WO95/09654. Alternatively, administration of DNA linked to killed adenovirus as described in Curiel (1992) *Hum. Gene Ther.* 3:147-154 may be employed. The gene delivery vehicles of the invention also include adenovirus associated virus (AAV) vectors. Leading and preferred examples of such vectors for use in this invention are the AAV-2 based vectors disclosed in Srivastava, WO93/09239. Most preferred AAV vectors comprise the two AAV inverted terminal repeats in which the native D-sequences are modified by substitution of nucleotides, such that at least 5 native nucleotides and up to 18 native nucleotides, preferably at least 10 native nucleotides up to 18 native nucleotides, most preferably 10 native nucleotides are retained and the remaining nucleotides of the D-sequence are deleted or replaced with non-native nucleotides. The native D-sequences of the AAV inverted terminal repeats are sequences of 20 consecutive nucleotides in each AAV inverted terminal repeat (i.e., there is one sequence at each end) which are not involved in HP formation. The non-native replacement nucleotide may be any nucleotide other than the nucleotide found in the native D-sequence in the same position. Other employable exemplary AAV vectors are pWP-19, pWN-1, both of which are disclosed in Nahreini (1993) *Gene* 124:257-262. Another example of such an AAV vector is psub201 (see Samulski (1987) *J. Virol.* 61:3096). Another exemplary AAV vector is the Double-D ITR vector. Construction of the Double-D ITR vector is disclosed in US Patent 5,478,745. Still other vectors are those disclosed in Carter US Patent 4,797,368 and Muzyczka US Patent 5,139,941, Chartejee US Patent 5,474,935, and Kotin WO94/288157. Yet a further example of an AAV vector employable in this invention is SSV9AFABTKneo, which contains the AFP enhancer and albumin promoter and directs expression predominantly in the liver. Its structure and construction are disclosed in Su (1996) *Human Gene Therapy* 7:463-470. Additional AAV gene therapy vectors are described in US 5,354,678, US 5,173,414, US 5,139,941, and US 5,252,479.

The gene therapy vectors comprising sequences of the invention also include herpes vectors. Leading and preferred examples are herpes simplex virus vectors containing a sequence encoding a thymidine kinase polypeptide such as those disclosed in US 5,288,641 and EP0176170 (Roizman). Additional exemplary herpes simplex virus vectors include HFEM/ICP6-LacZ disclosed in WO95/04139 (Wistar Institute), pHSVlac described in Geller (1988) *Science* 241:1667-1669 and in WO90/09441 and WO92/07945, HSV Us3::pgC-lacZ



described in Fink (1992) *Human Gene Therapy* 3:11-19 and HSV 7134, 2 RH 105 and GAL4 described in EP 0453242 (Breakefield), and those deposited with the ATCC as accession numbers ATCC VR-977 and ATCC VR-260.

Also contemplated are alpha virus gene therapy vectors that can be employed in this invention. Preferred alpha virus vectors are Sindbis viruses vectors. Togaviruses, Semliki Forest virus (ATCC VR-67; ATCC VR-1247), Middleberg virus (ATCC VR-370), Ross River virus (ATCC VR-373; ATCC VR-1246), Venezuelan equine encephalitis virus (ATCC VR923; ATCC VR-1250; ATCC VR-1249; ATCC VR-532), and those described in US patents 5,091,309, 5,217,879, and WO92/10578. More particularly, those alpha virus vectors described in U.S. Serial No. 08/405,627, filed March 15, 1995, WO94/21792, WO92/10578, WO95/07994, US 5,091,309 and US 5,217,879 are employable. Such alpha viruses may be obtained from depositories or collections such as the ATCC in Rockville, Maryland or isolated from known sources using commonly available techniques. Preferably, alphavirus vectors with reduced cytotoxicity are used (see USSN 08/679640).

DNA vector systems such as eukaryotic layered expression systems are also useful for expressing the nucleic acids of the invention. See WO95/07994 for a detailed description of eukaryotic layered expression systems. Preferably, the eukaryotic layered expression systems of the invention are derived from alphavirus vectors and most preferably from Sindbis viral vectors.

Other viral vectors suitable for use in the present invention include those derived from poliovirus, for example ATCC VR-58 and those described in Evans, *Nature* 339 (1989) 385 and Sabin (1973) *J. Biol. Standardization* 1:115; rhinovirus, for example ATCC VR-1110 and those described in Arnold (1990) *J Cell Biochem* L401; pox viruses such as canary pox virus or vaccinia virus, for example ATCC VR-111 and ATCC VR-2010 and those described in Fisher-Hoch (1989) *Proc Natl Acad Sci* 86:317; Flexner (1989) *Ann NY Acad Sci* 569:86, Flexner (1990) *Vaccine* 8:17; in US 4,603,112 and US 4,769,330 and WO89/01973; SV40 virus, for example ATCC VR-305 and those described in Mulligan (1979) *Nature* 277:108 and Madzak (1992) *J Gen Virol* 73:1533; influenza virus, for example ATCC VR-797 and recombinant influenza viruses made employing reverse genetics techniques as described in US 5,166,057 and in Enami (1990) *Proc Natl Acad Sci* 87:3802-3805; Enami & Palese (1991) *J Virol* 65:2711-2713 and Luytjes (1989) *Cell* 59:110, (see also McMichael (1983) *NEJ Med* 309:13, and Yap (1978) *Nature* 273:238 and *Nature* (1979) 277:108); human

immunodeficiency virus as described in EP-0386882 and in Buchschacher (1992) *J. Virol.* 66:2731; measles virus, for example ATCC VR-67 and VR-1247 and those described in EP-0440219; Aura virus, for example ATCC VR-368; Bebaru virus, for example ATCC VR-600 and ATCC VR-1240; Cabassou virus, for example ATCC VR-922; Chikungunya virus, for example ATCC VR-64 and ATCC VR-1241; Fort Morgan Virus, for example ATCC VR-924; Getah virus, for example ATCC VR-369 and ATCC VR-1243; Kyzylagach virus, for example ATCC VR-927; Mayaro virus, for example ATCC VR-66; Mucambo virus, for example ATCC VR-580 and ATCC VR-1244; Ndumu virus, for example ATCC VR-371; Pixuna virus, for example ATCC VR-372 and ATCC VR-1245; Tonate virus, for example ATCC VR-925; Trinita virus, for example ATCC VR-469; Una virus, for example ATCC VR-374; Whataroa virus, for example ATCC VR-926; Y-62-33 virus, for example ATCC VR-375; O'Nyong virus, Eastern encephalitis virus, for example ATCC VR-65 and ATCC VR-1242; Western encephalitis virus, for example ATCC VR-70, ATCC VR-1251, ATCC VR-622 and ATCC VR-1252; and coronavirus, for example ATCC VR-740 and those described in Hamre (1966) *Proc Soc Exp Biol Med* 121:190.

Delivery of the compositions of this invention into cells is not limited to the above mentioned viral vectors. Other delivery methods and media may be employed such as, for example, nucleic acid expression vectors, polycationic condensed DNA linked or unlinked to killed adenovirus alone, for example see US Serial No. 08/366,787, filed December 30, 1994 and Curiel (1992) *Hum Gene Ther* 3:147-154 ligand linked DNA, for example see Wu (1989) *J Biol Chem* 264:16985-16987, eucaryotic cell delivery vehicles cells, for example see US Serial No.08/240,030, filed May 9, 1994, and US Serial No. 08/404,796, deposition of photopolymerized hydrogel materials, hand-held gene transfer particle gun, as described in US Patent 5,149,655, ionizing radiation as described in US5,206,152 and in WO92/11033, nucleic charge neutralization or fusion with cell membranes. Additional approaches are described in Philip (1994) *Mol Cell Biol* 14:2411-2418 and in Woffendin (1994) *Proc Natl Acad Sci* 91:1581-1585.

Particle mediated gene transfer may be employed, for example see US Serial No. 60/023,867. Briefly, the sequence can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, as described in Wu &

Wu (1987) *J. Biol. Chem.* 262:4429-4432, insulin as described in Hucked (1990) *Biochem Pharmacol* 40:253-263, galactose as described in Plank (1992) *Bioconjugate Chem* 3:533-539, lactose or transferrin.

Naked DNA may also be employed to transform a host cell. Exemplary naked DNA introduction methods are described in WO 90/11092 and US 5,580,859. Uptake efficiency may be improved using biodegradable latex beads. DNA coated latex beads are efficiently transported into cells after endocytosis initiation by the beads. The method may be improved further by treatment of the beads to increase hydrophobicity and thereby facilitate disruption of the endosome and release of the DNA into the cytoplasm.

Liposomes that can act as gene delivery vehicles are described in U.S. 5,422,120, WO95/13796, WO94/23697, WO91/14445 and EP-524,968. As described in USSN. 60/023,867, on non-viral delivery, the nucleic acid sequences encoding a polypeptide can be inserted into conventional vectors that contain conventional control sequences for high level expression, and then be incubated with synthetic gene transfer molecules such as polymeric DNA-binding cations like polylysine, protamine, and albumin, linked to cell targeting ligands such as asialoorosomucoid, insulin, galactose, lactose, or transferrin. Other delivery systems include the use of liposomes to encapsulate DNA comprising the gene under the control of a variety of tissue-specific or ubiquitously-active promoters. Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al* (1994) *Proc. Natl. Acad. Sci. USA* 91(24):11581-11585. Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials. Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun, as described in U.S. 5,149,655; use of ionizing radiation for activating transferred gene, as described in U.S. 5,206,152 and WO92/11033.

Exemplary liposome and polycationic gene delivery vehicles are those described in US 5,422,120 and 4,762,915; in WO 95/13796; WO94/23697; and WO91/14445; in EP-0524968; and in Stryer, *Biochemistry*, pages 236-240 (1975) W.H. Freeman, San Francisco; Szoka (1980) *Biochem Biophys Acta* 600:1; Bayer (1979) *Biochem Biophys Acta* 550:464; Rivnay (1987) *Meth Enzymol* 149:119; Wang (1987) *Proc Natl Acad Sci* 84:7851; Plant (1989) *Anal Biochem* 176:420.

A polynucleotide composition can comprises therapeutically effective amount of a gene therapy vehicle, as the term is defined above. For purposes of the present invention, an effective dose will be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

### **Delivery Methods**

Once formulated, the polynucleotide compositions of the invention can be administered (1) directly to the subject; (2) delivered *ex vivo*, to cells derived from the subject; or (3) *in vitro* for expression of recombinant proteins. The subjects to be treated can be mammals or birds. Also, human subjects can be treated.

Direct delivery of the compositions will generally be accomplished by injection, either subcutaneously, intraperitoneally, intravenously or intramuscularly or delivered to the interstitial space of a tissue. The compositions can also be administered into a tumor or lesion. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hypodermic sprays. Dosage treatment may be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in *eg.* WO93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells.

Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by the following procedures, for example, dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

### **Polynucleotide and polypeptide pharmaceutical compositions**

In addition to the pharmaceutically acceptable carriers and salts described above, the following additional agents can be used with polynucleotide and/or polypeptide compositions.

#### **A. Polypeptides**

One example are polypeptides which include, without limitation: asialoglycoprotein (ASOR); transferrin; asialoglycoproteins; antibodies; antibody fragments; ferritin; interleukins; interferons, granulocyte, macrophage colony stimulating factor (GM-CSF),

granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), stem cell factor and erythropoietin. Viral antigens, such as envelope proteins, can also be used. Also, proteins from other invasive organisms, such as the 17 amino acid peptide from the circumsporozoite protein of plasmodium falciparum known as RII.

#### B.Hormones, Vitamins, Etc.

Other groups that can be included are, for example: hormones, steroids, androgens, estrogens, thyroid hormone, or vitamins, folic acid.

#### C.Polyalkylenes, Polysaccharides, etc.

Also, polyalkylene glycol can be included with the desired polynucleotides or polypeptides. In a preferred embodiment, the polyalkylene glycol is polyethylene glycol. In addition, mono-, di-, or polysaccharides can be included. In a preferred embodiment of this aspect, the polysaccharide is dextran or DEAE-dextran. Also, chitosan and poly(lactide-co-glycolide)

#### D.Lipids, and Liposomes

The desired polynucleotide or polypeptide can also be encapsulated in lipids or packaged in liposomes prior to delivery to the subject or to cells derived therefrom.

Lipid encapsulation is generally accomplished using liposomes which are able to stably bind or entrap and retain nucleic acid. The ratio of condensed polynucleotide or polypeptide to lipid preparation can vary but will generally be around 1:1 (mg DNA:micromoles lipid), or more of lipid. For a review of the use of liposomes as carriers for delivery of nucleic acids, see, Hug and Sleight (1991) *Biochim. Biophys. Acta.* 1097:1-17; Straubinger (1983) *Meth. Enzymol.* 101:512-527.

Liposomal preparations for use in the present invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner (1987) *Proc. Natl. Acad. Sci. USA* 84:7413-7416); mRNA (Malone (1989) *Proc. Natl. Acad. Sci. USA* 86:6077-6081); and purified transcription factors (Debs (1990) *J. Biol. Chem.* 265:10189-10192), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleoyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, NY. (See, also, Felgner *supra*). Other commercially available liposomes include transfectace (DDAB/DOPE) and

DOTAP/DOPE (Boehringer). Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, eg. Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; WO90/11092 for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, AL), or can be easily prepared using readily available materials. Such materials include phosphatidyl choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphosphatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs). The various liposome-nucleic acid complexes are prepared using methods known in the art. See eg. Straubinger (1983) *Meth. Immunol.* 101:512-527; Szoka (1978) *Proc. Natl. Acad. Sci. USA* 75:4194-4198; Papahadjopoulos (1975) *Biochim. Biophys. Acta* 394:483; Wilson (1979) *Cell* 17:77; Deamer & Bangham (1976) *Biochim. Biophys. Acta* 443:629; Ostro (1977) *Biochem. Biophys. Res. Commun.* 76:836; Fraley (1979) *Proc. Natl. Acad. Sci. USA* 76:3348; Enoch & Strittmatter (1979) *Proc. Natl. Acad. Sci. USA* 76:145; Fraley (1980) *J. Biol. Chem.* (1980) 255:10431; Szoka & Papahadjopoulos (1978) *Proc. Natl. Acad. Sci. USA* 75:145; and Schaefer-Ridder (1982) *Science* 215:166.

#### E.Lipoproteins

In addition, lipoproteins can be included with the polynucleotide or polypeptide to be delivered. Examples of lipoproteins to be utilized include: chylomicrons, HDL, IDL, LDL, and VLDL. Mutants, fragments, or fusions of these proteins can also be used. Also, modifications of naturally occurring lipoproteins can be used, such as acetylated LDL. These lipoproteins can target the delivery of polynucleotides to cells expressing lipoprotein receptors. Preferably, if lipoproteins are including with the polynucleotide to be delivered, no other targeting ligand is included in the composition.

Naturally occurring lipoproteins comprise a lipid and a protein portion. The protein portion are known as apoproteins. At the present, apoproteins A, B, C, D, and E have been

isolated and identified. At least two of these contain several proteins, designated by Roman numerals, AI, AII, AIV; CI, CII, CIII.

A lipoprotein can comprise more than one apoprotein. For example, naturally occurring chylomicrons comprises of A, B, C, and E, over time these lipoproteins lose A and acquire C and E apoproteins. VLDL comprises A, B, C, and E apoproteins, LDL comprises apoprotein B; and HDL comprises apoproteins A, C, and E.

The amino acid of these apoproteins are known and are described in, for example, Breslow (1985) *Annu Rev. Biochem* 54:699; Law (1986) *Adv. Exp Med. Biol.* 151:162; Chen (1986) *J Biol Chem* 261:12918; Kane (1980) *Proc Natl Acad Sci USA* 77:2465; and Utermann (1984) *Hum Genet* 65:232.

Lipoproteins contain a variety of lipids including, triglycerides, cholesterol (free and esters), and phospholipids. The composition of the lipids varies in naturally occurring lipoproteins. For example, chylomicrons comprise mainly triglycerides. A more detailed description of the lipid content of naturally occurring lipoproteins can be found, for example, in *Meth. Enzymol.* 128 (1986). The composition of the lipids are chosen to aid in conformation of the apoprotein for receptor binding activity. The composition of lipids can also be chosen to facilitate hydrophobic interaction and association with the polynucleotide binding molecule.

Naturally occurring lipoproteins can be isolated from serum by ultracentrifugation, for instance. Such methods are described in *Meth. Enzymol.* (*supra*); Pitas (1980) *J. Biochem.* 255:5454-5460 and Mahey (1979) *J Clin. Invest* 64:743-750.

Lipoproteins can also be produced by *in vitro* or recombinant methods by expression of the apoprotein genes in a desired host cell. See, for example, Atkinson (1986) *Annu Rev Biophys Chem* 15:403 and Radding (1958) *Biochim Biophys Acta* 30: 443.

Lipoproteins can also be purchased from commercial suppliers, such as Biomedical Technologies, Inc., Stoughton, Massachusetts, USA.

Further description of lipoproteins can be found in Zuckermann et al., PCT. Appln. No. US97/14465.

#### F. Polycationic Agents

Polycationic agents can be included, with or without lipoprotein, in a composition with the desired polynucleotide or polypeptide to be delivered.

Polycationic agents, typically, exhibit a net positive charge at physiological relevant pH and are capable of neutralizing the electrical charge of nucleic acids to facilitate delivery to a desired location. These agents have both in vitro, ex vivo, and in vivo applications. Polycationic agents can be used to deliver nucleic acids to a living subject either intramuscularly, subcutaneously, etc.

The following are examples of useful polypeptides as polycationic agents: polylysine, polyarginine, polyornithine, and protamine. Other examples include histones, protamines, human serum albumin, DNA binding proteins, non-histone chromosomal proteins, coat proteins from DNA viruses, such as (X174, transcriptional factors also contain domains that bind DNA and therefore may be useful as nucleic acid condensing agents. Briefly, transcriptional factors such as C/CEBP, c-jun, c-fos, AP-1, AP-2, AP-3, CPF, Prot-1, Sp-1, Oct-1, Oct-2, CREP, and TFIID contain basic domains that bind DNA sequences.

Organic polycationic agents include: spermine, spermidine, and putrescine.

The dimensions and of the physical properties of a polycationic agent can be extrapolated from the list above, to construct other polypeptide polycationic agents or to produce synthetic polycationic agents.

#### Synthetic Polycationic Agents

Synthetic polycationic agents which are useful include, for example, DEAE-dextran, polybrene. Lipofectin<sup>®</sup>, and lipofectAMINE<sup>®</sup> are monomers that form polycationic complexes when combined with polynucleotides or polypeptides.

#### Immunodiagnostic Assays

Neisserial antigens of the invention can be used in immunoassays to detect antibody levels (or, conversely, anti-Neisserial antibodies can be used to detect antigen levels). Immunoassays based on well defined, recombinant antigens can be developed to replace invasive diagnostics methods. Antibodies to Neisserial proteins within biological samples, including for example, blood or serum samples, can be detected. Design of the immunoassays is subject to a great deal of variation, and a variety of these are known in the art. Protocols for the immunoassay may be based, for example, upon competition, or direct reaction, or sandwich type assays. Protocols may also, for example, use solid supports, or may be by immunoprecipitation. Most assays involve the use of labeled antibody or polypeptide; the labels may be, for example, fluorescent, chemiluminescent, radioactive, or dye molecules. Assays which amplify the signals from the probe are also known; examples of which are



assays which utilize biotin and avidin, and enzyme-labeled and mediated immunoassays, such as ELISA assays.

Kits suitable for immunodiagnosis and containing the appropriate labeled reagents are constructed by packaging the appropriate materials, including the compositions of the invention, in suitable containers, along with the remaining reagents and materials (for example, suitable buffers, salt solutions, *etc.*) required for the conduct of the assay, as well as suitable set of assay instructions.

### **Nucleic Acid Hybridisation**

"Hybridization" refers to the association of two nucleic acid sequences to one another by hydrogen bonding. Typically, one sequence will be fixed to a solid support and the other will be free in solution. Then, the two sequences will be placed in contact with one another under conditions that favor hydrogen bonding. Factors that affect this bonding include: the type and volume of solvent; reaction temperature; time of hybridization; agitation; agents to block the non-specific attachment of the liquid phase sequence to the solid support (Denhardt's reagent or BLOTTO); concentration of the sequences; use of compounds to increase the rate of association of sequences (dextran sulfate or polyethylene glycol); and the stringency of the washing conditions following hybridization. See Sambrook *et al.* [*supra*] Volume 2, chapter 9, pages 9.47 to 9.57.

"Stringency" refers to conditions in a hybridization reaction that favor association of very similar sequences over sequences that differ. For example, the combination of temperature and salt concentration should be chosen that is approximately 120 to 200°C below the calculated  $T_m$  of the hybrid under study. The temperature and salt conditions can often be determined empirically in preliminary experiments in which samples of genomic DNA immobilized on filters are hybridized to the sequence of interest and then washed under conditions of different stringencies. See Sambrook *et al.* at page 9.50.

Variables to consider when performing, for example, a Southern blot are (1) the complexity of the DNA being blotted and (2) the homology between the probe and the sequences being detected. The total amount of the fragment(s) to be studied can vary a magnitude of 10, from 0.1 to 1 µg for a plasmid or phage digest to  $10^{-9}$  to  $10^{-8}$  g for a single copy gene in a highly complex eukaryotic genome. For lower complexity polynucleotides, substantially shorter blotting, hybridization, and exposure times, a smaller amount of starting polynucleotides, and lower specific activity of probes can be used. For example, a single-copy

yeast gene can be detected with an exposure time of only 1 hour starting with 1  $\mu\text{g}$  of yeast DNA, blotting for two hours, and hybridizing for 4-8 hours with a probe of  $10^8$  cpm/ $\mu\text{g}$ . For a single-copy mammalian gene a conservative approach would start with 10  $\mu\text{g}$  of DNA, blot overnight, and hybridize overnight in the presence of 10% dextran sulfate using a probe of greater than  $10^8$  cpm/ $\mu\text{g}$ , resulting in an exposure time of ~24 hours.

Several factors can affect the melting temperature ( $T_m$ ) of a DNA-DNA hybrid between the probe and the fragment of interest, and consequently, the appropriate conditions for hybridization and washing. In many cases the probe is not 100% homologous to the fragment. Other commonly encountered variables include the length and total G+C content of the hybridizing sequences and the ionic strength and formamide content of the hybridization buffer. The effects of all of these factors can be approximated by a single equation:

$$T_m = 81 + 16.6(\log_{10} C_i) + 0.4[\%(G + C)] - 0.6(\%\text{formamide}) - 600/n - 1.5(\%\text{mismatch}).$$

where  $C_i$  is the salt concentration (monovalent ions) and  $n$  is the length of the hybrid in base pairs (slightly modified from Meinkoth & Wahl (1984) *Anal. Biochem.* 138: 267-284).

In designing a hybridization experiment, some factors affecting nucleic acid hybridization can be conveniently altered. The temperature of the hybridization and washes and the salt concentration during the washes are the simplest to adjust. As the temperature of the hybridization increases (*ie.* stringency), it becomes less likely for hybridization to occur between strands that are nonhomologous, and as a result, background decreases. If the radiolabeled probe is not completely homologous with the immobilized fragment (as is frequently the case in gene family and interspecies hybridization experiments), the hybridization temperature must be reduced, and background will increase. The temperature of the washes affects the intensity of the hybridizing band and the degree of background in a similar manner. The stringency of the washes is also increased with decreasing salt concentrations.

In general, convenient hybridization temperatures in the presence of 50% formamide are  $42^\circ\text{C}$  for a probe which is 95% to 100% homologous to the target fragment,  $37^\circ\text{C}$  for 90% to 95% homology, and  $32^\circ\text{C}$  for 85% to 90% homology. For lower homologies, formamide content should be lowered and temperature adjusted accordingly, using the equation above. If the homology between the probe and the target fragment are not known, the simplest approach is to start with both hybridization and wash conditions which are nonstringent. If non-specific bands or high background are observed after autoradiography, the filter can be

washed at high stringency and reexposed. If the time required for exposure makes this approach impractical, several hybridization and/or washing stringencies should be tested in parallel.

### **Nucleic Acid Probe Assays**

Methods such as PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes according to the invention can determine the presence of cDNA or mRNA. A probe is said to "hybridize" with a sequence of the invention if it can form a duplex or double stranded complex, which is stable enough to be detected.

The nucleic acid probes will hybridize to the Neisserial nucleotide sequences of the invention (including both sense and antisense strands). Though many different nucleotide sequences will encode the amino acid sequence, the native Neisserial sequence is preferred because it is the actual sequence present in cells. mRNA represents a coding sequence and so a probe should be complementary to the coding sequence; single-stranded cDNA is complementary to mRNA, and so a cDNA probe should be complementary to the non-coding sequence.

The probe sequence need not be identical to the Neisserial sequence (or its complement) — some variation in the sequence and length can lead to increased assay sensitivity if the nucleic acid probe can form a duplex with target nucleotides, which can be detected. Also, the nucleic acid probe can include additional nucleotides to stabilize the formed duplex. Additional Neisserial sequence may also be helpful as a label to detect the formed duplex. For example, a non-complementary nucleotide sequence may be attached to the 5' end of the probe, with the remainder of the probe sequence being complementary to a Neisserial sequence. Alternatively, non-complementary bases or longer sequences can be interspersed into the probe, provided that the probe sequence has sufficient complementarity with the a Neisserial sequence in order to hybridize therewith and thereby form a duplex which can be detected.

The exact length and sequence of the probe will depend on the hybridization conditions, such as temperature, salt condition and the like. For example, for diagnostic applications, depending on the complexity of the analyte sequence, the nucleic acid probe typically contains at least 10-20 nucleotides, preferably 15-25, and more preferably at least 30 nucleotides, although it may be shorter than this. Short primers generally require cooler temperatures to form sufficiently stable hybrid complexes with the template.

Probes may be produced by synthetic procedures, such as the triester method of Matteucci *et al.* [*J. Am. Chem. Soc.* (1981) 103:3185], or according to Urdea *et al.* [*Proc. Natl. Acad. Sci. USA* (1983) 80: 7461], or using commercially available automated oligonucleotide synthesizers.

The chemical nature of the probe can be selected according to preference. For certain applications, DNA or RNA are appropriate. For other applications, modifications may be incorporated *eg.* backbone modifications, such as phosphorothioates or methylphosphonates, can be used to increase *in vivo* half-life, alter RNA affinity, increase nuclease resistance *etc.* [*eg.* see Agrawal & Iyer (1995) *Curr Opin Biotechnol* 6:12-19; Agrawal (1996) *TIBTECH* 14:376-387]; analogues such as peptide nucleic acids may also be used [*eg.* see Corey (1997) *TIBTECH* 15:224-229; Buchardt *et al.* (1993) *TIBTECH* 11:384-386].

One example of a nucleotide hybridization assay is described by Urdea *et al.* in international patent application WO92/02526 [see also US patent 5,124,246].

Alternatively, the polymerase chain reaction (PCR) is another well-known means for detecting small amounts of target nucleic acids. The assay is described in: Mullis *et al.* [*Meth. Enzymol.* (1987) 155: 335-350]; US patent 4,683,195; and US patent 4,683,202. Two "primer" nucleotides hybridize with the target nucleic acids and are used to prime the reaction. The primers can comprise sequence that does not hybridize to the sequence of the amplification target (or its complement) to aid with duplex stability or, for example, to incorporate a convenient restriction site. Typically, such sequence will flank the desired Neisserial sequence.

A thermostable polymerase creates copies of target nucleic acids from the primers using the original target nucleic acids as a template. After a threshold amount of target nucleic acids are generated by the polymerase, they can be detected by more traditional methods, such as Southern blots. When using the Southern blot method, the labelled probe will hybridize to the Neisserial sequence (or its complement).

Also, mRNA or cDNA can be detected by traditional blotting techniques described in Sambrook *et al.* [*supra*]. mRNA, or cDNA generated from mRNA using a polymerase enzyme, can be purified and separated using gel electrophoresis. The nucleic acids on the gel are then blotted onto a solid support, such as nitrocellulose. The solid support is exposed to a labelled probe and then washed to remove any unhybridized probe. Next, the duplexes

containing the labeled probe are detected. Typically, the probe is labelled with a radioactive moiety.

## EXAMPLES

The examples describe nucleic acid sequences which have been identified in *N. meningitidis*, and *N. gonorrhoeae* along with their respective and putative translation products. Not all of the nucleic acid sequences are complete *ie.* they encode less than the full-length wild-type protein.

The examples are generally in the following format:

- a nucleotide sequence which has been identified in *N. meningitidis*
- the putative translation product of said *N. meningitidis* sequence
- a computer analysis of said translation product based on database comparisons
- a corresponding nucleotide sequence identified from *N. gonorrhoeae*
- the putative translation product of said *N. gonorrhoeae* sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a corresponding nucleotide sequence identified from strain A of *N. meningitidis*
- the putative translation product of said *N. meningitidis* strain A sequence
- a comparison of the percentage of identity between the translation product of the *N. meningitidis* sequence and the *N. gonorrhoeae* sequence.
- a description of the characteristics of the protein which indicates that it might be suitably antigenic or immunogenic.

Sequence comparisons were performed at NCBI (<http://www.ncbi.nlm.nih.gov>) using the algorithms BLAST, BLAST2, BLASTn, BLASTp, tBLASTn, BLASTx, & tBLASTx [eg. see also Altschul *et al.* (1997) Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. *Nucleic Acids Research* 25:2289-3402]. Searches were performed against the following databases: non-redundant GenBank+EMBL+DDBJ+PDB sequences and non-redundant GenBank CDS translations+PDB+SwissProt+SPupdate+PIR sequences.

Dots within nucleotide sequences represent nucleotides which have been arbitrarily introduced in order to maintain a reading frame. In the same way, double-underlined nucleotides were removed. Lower case letters represent ambiguities which arose during

alignment of independent sequencing reactions (some of the nucleotide sequences in the examples are derived from combining the results of two or more experiments).

Nucleotide sequences were scanned in all six reading frames to predict the presence of hydrophobic domains using an algorithm based on the statistical studies of Esposti *et al.* [Critical evaluation of the hydropathy of membrane proteins (1990) *Eur J Biochem* 190:207-219]. These domains represent potential transmembrane regions or hydrophobic leader sequences.

Open reading frames were predicted from fragmented nucleotide sequences using the program ORFFINDER (NCBI).

Underlined amino acid sequences indicate possible transmembrane domains or leader sequences in the ORFs, as predicted by the PSORT algorithm (<http://www.psort.nibb.ac.jp>). Functional domains were also predicted using the MOTIFS program (GCG Wisconsin & PROSITE).

For each of the following examples: based on the presence of a putative leader sequence and/or several putative transmembrane domains (single-underlined) in the gonococcal protein, it is predicted that the proteins from *N. meningitidis* and *N. gonorrhoeae*, and their respective epitopes, could be useful antigens or immunogenic compositions for vaccines or diagnostics.

The standard techniques and procedures which may be employed in order to perform the invention (*e.g.* to utilize the disclosed sequences for vaccination or diagnostic purposes) were summarized above. This summary is not a limitation on the invention but, rather, gives examples that may be used, but are not required.

In particular, the following methods were used to express, purify and biochemically characterize the proteins of the invention.

#### **Chromosomal DNA Preparation**

*N.meningitidis* strain 2996 was grown to exponential phase in 100ml of GC medium, harvested by centrifugation, and resuspended in 5ml buffer (20%(w/v) Sucrose, 50mM Tris-HCl, 50mM EDTA, pH8). After 10 minutes incubation on ice, the bacteria were lysed by adding 10ml of lysis solution (50mM NaCl, 1% Na-Sarkosyl, 50µg/ml Proteinase K), and the suspension incubated at 37°C for 2 hours. Two phenol extractions (equilibrated to pH 8) and one CHCl<sub>3</sub>/isoamylalcohol (24:1) extraction were performed. DNA was precipitated by addition of 0.3M sodium acetate and 2 volumes of ethanol, and collected by centrifugation.

The pellet was washed once with 70%(v/v) ethanol and redissolved in 4.0ml TE buffer (10mM Tris-HCl, 1mM EDTA, pH 8.0). The DNA concentration was measured by reading the OD at 260 nm.

### Oligonucleotide design

Synthetic oligonucleotide primers were designed on the basis of the coding sequence of each ORF, using (a) the meningococcus B sequence when available, or (b) the gonococcus/meningococcus A sequence, adapted to the codon preference usage of meningococcus as necessary. Any predicted signal peptides were omitted, by designing the 5' primers to sequence immediately downstream from the predicted leader sequence.

For most ORFs, the 5' primers included two restriction enzyme recognition sites (*Bam*HI-*Nde*I, *Bam*HI-*Nhe*I, *Eco*RI-*Nde*I or *Eco*RI-*Nhe*I), depending on the restriction pattern of the gene of interest. The 3' primers included a *Xho*I or a *Hind*III restriction site (table 1). This procedure was established in order to direct the cloning of each amplification product (corresponding to each ORF) into two different expression systems: pGEX-KG (using *Bam*HI-*Xho*I, *Bam*HI-*Hind*III, *Eco*RI-*Xho*I or *Eco*RI-*Hind*III), and pET21b+ (using *Nde*I-*Xho*I, *Nhe*I-*Xho*I, *Nde*I-*Hind*III or *Nhe*I-*Hind*III).

5'-end primer tail:	<u>CGCGGATCCCATATG</u>	( <i>Bam</i> HI- <i>Nde</i> I)
	<u>CGCGGATCCGCTAGC</u>	( <i>Bam</i> HI- <i>Nhe</i> I)
	<u>CCGGAATTCTACATATG</u>	( <i>Eco</i> RI- <i>Nde</i> I)
	<u>CCGGAATTCTAGCTAGC</u>	( <i>Eco</i> RI- <i>Nhe</i> I)
3'-end primer tail:	<u>CCCGCTCGAG</u>	( <i>Xho</i> I)
	<u>CCCGCTCGAG</u>	( <i>Hind</i> III)

For cloning ORFs into the pGEX-His vector, the 5' and 3' primers contained only one restriction enzyme site (*Eco*RI, *Kpn*I or *Sal*I for the 5' primers and *Pst*I, *Xba*I, *Sph*I or *Sal*I for the 3' primers). Again restriction sites were chosen according to the particular restriction pattern of the gene (table 1).

5'-end primer tail:	(AAA) <u>AAAGAATTC</u>	( <i>Eco</i> RI)
	(AAA) <u>AAAGGTACC</u>	( <i>Kpn</i> I)
3'-end primer tail:	(AAA) <u>AAACTGCAG</u>	( <i>Pst</i> I)
	(AAA) <u>AAATCTAGA</u>	( <i>Xba</i> I)

5' or 3'-end primer tail:      AAAGCATGC      (*Sph*I)  
AAAAAAGTCGAC      (*Sal*I)

As well as containing the restriction enzyme recognition sequences, the primers included nucleotides which hybridized to the sequence to be amplified. The melting temperature depended on the number and type of hybridising nucleotides in the whole primer, and was determined for each primer using the formulae:

$$T_m = 4 (G+C) + 2 (A+T) \quad (\text{tail excluded})$$

$$T_m = 64.9 + 0.41 (\% \text{ GC}) - 600/N \quad (\text{whole primer})$$

The melting temperatures of the selected oligonucleotides were usually 65-70°C for the whole oligo and 50-55°C for the hybridising region alone.

Table 1 shows the forward and reverse primers used for each amplification. In certain cases, the sequence of the primer does not exactly match the sequence of the predicted ORF. This is because when initial amplifications were performed, the complete 5' and/or 3' sequences for some meningococcal B ORFs were not known. However the corresponding sequences had been identified in *Gonococcus* or in *Meningococcus A*. Hence, when the *Meningococcus B* sequence was incomplete or uncertain, *Gonococcal* or *Meningococcal A* sequences were used as the basis for primer design. These sequences were altered to take account of codon preference. It can be appreciated that, once the complete sequence is identified, this approach will no longer be necessary.

Oligonucleotides were synthesized using a Perkin Elmer 394 DNA/RNA Synthesizer, eluted from the columns in 2.0ml  $\text{NH}_4\text{OH}$ , and deprotected by 5 hours incubation at  $56^\circ\text{C}$ . The oligos were precipitated by addition of 0.3M Na-Acetate and 2 volumes ethanol. The samples were centrifuged and the pellets resuspended in either 100 $\mu\text{l}$  or 1.0ml of water. The  $\text{OD}_{260}$  was determined using a Perkin Elmer Lambda Bio spectrophotometer and the concentration adjusted to 2-10pmol/ $\mu\text{l}$ .

## Amplification

The standard PCR protocol was as follows: 50-200ng of genomic DNA was used as a template in the presence of 20-40μM of each oligonucleotide primer, 400-800μM dNTPs solution, 1x PCR buffer (including 1.5mM MgCl<sub>2</sub>), 2.5 units *TaqI* DNA polymerase (using



Perkin-Elmer AmpliTaq, GIBCO Platinum, Pwo DNA polymerase, or Tahara Shuzo Taq polymerase). In some cases, PCR was optimised by the addition of 10µl DMSO or 50µl 2M Betaine.

After a hot start (adding the polymerase during a preliminary 3 minute incubation of the whole mix at 95°C), each sample underwent a two-step amplification. The first 5 cycles were performed using the hybridization temperature that excluded the restriction enzyme tail of the primer (see above). This was followed by 30 cycles using the hybridization temperature calculated for the whole length oligos. The cycles were completed with a 10 minute extension step at 72°C. The standard cycles were as follows:

	Denaturation	Hybridisation	Elongation
First 5 cycles	30 seconds 95°C	30 seconds 50-55°C	30-60 seconds 72°C
Last 30 cycles	30 seconds 95°C	30 seconds 65-70°C	30-60 seconds 72°C

Elongation times varied according to the length of the ORF to be amplified. Amplifications were performed using either a 9600 or a 2400 Perkin Elmer GeneAmp PCR System. To check the results, 1/10 of the amplification volume was loaded onto a 1-1.5% (w/v) agarose gel and the size of each amplified fragment compared with a DNA molecular weight marker.

The amplified DNA was either loaded directly on a 1% agarose gel or first precipitated with ethanol and resuspended in a volume suitable to be loaded on a 1.0% agarose gel. The DNA fragment corresponding to the band of correct size was purified using the Qiagen Gel Extraction Kit, following the manufacturer's protocol. DNA fragments were eluted in a volume of 30µl or 50µl with either H<sub>2</sub>O or 10mM Tris, pH 8.5.

#### **Digestion of PCR fragments**

The purified DNA corresponding to the amplified fragment was doubly-digested with the appropriate restriction enzymes for; cloning into pET-21b+ and expressing the protein as a C-terminus His-tagged fusion, for cloning into pGEX-KG and expressing the protein as a N-

terminus GST-fusion, and for cloning into pGEX-His and expressing the protein as a N-terminus GST-His tagged fusion.

Each purified DNA fragment was incubated at 37°C for 3 hours to overnight with 20 units of appropriate restriction enzyme (New England Biolabs) in a volume of either 30 or 40 µl in the presence of suitable digestion buffer. Digested fragments were purified using the QIAquick PCR purification kit (following the manufacturer's instructions) and eluted in a volume of 30 µl or 50 µl with either H<sub>2</sub>O or 10mM Tris, pH 8.5. The DNA concentration was determined by quantitative agarose gel electrophoresis (1.0% gel) in the presence of a titrated molecular weight marker.

#### **Digestion of the cloning vectors (pET22B, pGEX-KG, pTRC-His A, pET21b+, pGEX-KG, and pGEX-His)**

The vector pGEX-His is a modified pGEX-2T vector carrying a region encoding six histidine residues upstream of the thrombin cleavage site and containing the multiple cloning site of the vector pTRC99 (Pharmacia). 10 µg plasmid was double-digested with 50 units of each restriction enzyme in 200 µl reaction volume in the presence of appropriate buffer by overnight incubation at 37°C. After loading the whole digestion on a 1% agarose gel, the band corresponding to the digested vector was purified from the gel using the Qiagen QIAquick Gel Extraction Kit and the DNA was eluted in 50 µl of 10 mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD<sub>260</sub> of the sample, and adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

10 µg of plasmid vector was doubly-digested with 50 units of each restriction enzyme in a volume of 200 µl with the appropriate buffer overnight at 37°C. The digest was loaded onto a 1.0% agarose gel and the band corresponding to the digested vector purified using the Qiagen QIAquick Gel Extraction Kit. DNA was eluted in 50 µl of 10mM Tris-HCl, pH 8.5. The DNA concentration was evaluated by measuring OD<sub>260nm</sub> and the concentration adjusted to 50 µg/µl. 1 µl of plasmid was used for each cloning procedure.

#### **Cloning**

For some ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated in both pET22b and pGEX-KG. In a final volume of 20 µl, a molar

ratio of 3:1 fragment/vector was ligated using 0.5 µl of NEB T4 DNA ligase (400 units/µl), in the presence of the buffer supplied by the manufacturer. The reaction was incubated at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit", following the manufacturer's instructions.

In order to introduce the recombinant plasmid in a suitable strain, 100 µl *E. coli* DH5 competent cells were incubated with the ligase reaction solution for 40 minutes on ice, then at 37°C for 3 minutes, then, after adding 800 µl LB broth, again at 37°C for 20 minutes. The cells were then centrifuged at maximum speed in an Eppendorf microfuge and resuspended in approximately 200 µl of the supernatant. The suspension was then plated on LB ampicillin (100 mg/ml ).

The screening of the recombinant clones was performed by growing 5 randomly-chosen colonies overnight at 37 °C in either 2 ml (pGEX or pTC clones) or 5ml (pET clones) LB broth + 100 µg/ml ampicillin. The cells were then pelleted and the DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions, to a final volume of 30 µl. 5 µl of each individual miniprep (approximately 1g ) were digested with either *NdeI/XhoI* or *BamHI/XhoI* and the whole digestion loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1Kb DNA Ladder, GIBCO). The screening of the positive clones was made on the base of the correct insert size.

For other ORFs, the fragments corresponding to each ORF, previously digested and purified, were ligated into both pET21b+ and pGEX-KG. A molar ratio of of 3:1 fragment/vector was used in a final volume of 20µl, that included 0.5µl T4 DNA ligase (400 units/µl, NEB) and ligation buffer supplied by the manufacturer. The reaction was performed at room temperature for 3 hours. In some experiments, ligation was performed using the Boehringer "Rapid Ligation Kit" and the manufacturer's protocol.

Recombinant plasmid was transformed into 100µl of competent *E. coli* DH5 or HB101 by incubating the ligase reaction solution and bacteria for 40 minutes on ice then at 37°C for 3 minutes. This was followed by the addition of 800µl LB broth and incubation at 37°C for 20 minutes. The cells were centrifuged at maximum speed in an Eppendorf microfuge, resuspended in approximately 200µl of the supernatant and plated onto LB ampicillin (100mg/ml ) agar.

Screening for recombinant clones was performed by growing 5 randomly selected colonies overnight at 37°C in either 2.0ml (pGEX-KG clones) or 5.0ml (pET clones) LB broth + 100µg/ml ampicillin. Cells were pelleted and plasmid DNA extracted using the Qiagen QIAprep Spin Miniprep Kit, following the manufacturer's instructions. Approximately 1µg of each individual miniprep was digested with the appropriate restriction enzymes and the digest loaded onto a 1-1.5% agarose gel (depending on the expected insert size), in parallel with the molecular weight marker (1kb DNA Ladder, GIBCO). Positive clones were selected on the basis of the size of insert.

ORFs were cloned into PGEX-His, by doubly-digesting the PCR product and ligating into similarly digested vector. After cloning, recombinant plasmids were transformed into the *E.coli* host W3110. Individual clones were grown overnight at 37°C in LB broth with 50µg/ml ampicillin.

Certain ORFs may be cloned into the pGEX-HIS vector using *EcoRI-PstI* cloning sites, or *EcoRI-SalI*, or *SalI-PstI*. After cloning, the recombinant plasmids may be introduced in the *E.coli* host W3110.

## Expression

Each ORF cloned into the expression vector may then be transformed into the strain suitable for expression of the recombinant protein product. 1 µl of each construct was used to transform 30 µl of *E.coli* BL21 (pGEX vector), *E.coli* TOP 10 (pTRC vector) or *E.coli* BL21-DE3 (pET vector), as described above. In the case of the pGEX-His vector, the same *E.coli* strain (W3110) was used for initial cloning and expression. Single recombinant colonies were inoculated into 2ml LB+Amp (100 µg/ml), incubated at 37°C overnight, then diluted 1:30 in 20 ml of LB+Amp (100 µg/ml) in 100 ml flasks, making sure that the OD<sub>600</sub> ranged between 0.1 and 0.15. The flasks were incubated at 30°C into gyratory water bath shakers until OD indicated exponential growth suitable for induction of expression (0.4-0.8 OD for pET and pTRC vectors; 0.8-1 OD for pGEX and pGEX-His vectors). For the pET, pTRC and pGEX-His vectors, the protein expression was induced by addition of 1mM IPTG, whereas in the case of pGEX system the final concentration of IPTG was 0.2 mM. After 3 hours incubation at 30°C, the final concentration of the sample was checked by OD. In order to check expression, 1ml of each sample was removed, centrifuged in a microfuge, the pellet

resuspended in PBS, and analysed by 12% SDS-PAGE with Coomassie Blue staining. The whole sample was centrifuged at 6000g and the pellet resuspended in PBS for further use.

#### **GST-fusion proteins large-scale purification.**

For some ORFs, a single colony was grown overnight at 37°C on LB+Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600 ml of fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD<sub>550</sub> 0.8-1. Protein expression was induced with 0.2mM IPTG followed by three hours incubation. The culture was centrifuged at 8000 rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml cold PBS. The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia) (previously washed with PBS) and incubated at room temperature for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold PBS for 10 minutes, resuspended in 1ml cold PBS, and loaded on a disposable column. The resin was washed twice with 2ml cold PBS until the flow-through reached OD<sub>280</sub> of 0.02-0.06. The GST-fusion protein was eluted by addition of 700µl cold Glutathione elution buffer 10mM reduced glutathione, 50mM Tris-HCl) and fractions collected until the OD<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel using either Biorad SDS-PAGE Molecular weight standard broad range (M1) (200, 116.25, 97.4, 66.2, 45, 31, 21.5, 14.4, 6.5 kDa) or Amersham Rainbow Marker (M<sup>r</sup>) (220, 66, 46, 30, 21.5, 14.3 kDa) as standards. As the MW of GST is 26kDa, this value must be added to the MW of each GST-fusion protein.

For other ORFs, for each clone to be purified as a GST-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp. (100µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD<sub>550nm</sub> reached 0.6-0.8. Recombinant protein expression was induced by addition of IPTG (final concentration 0.2mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml cold PBS. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and mixed with 150µl Glutathione-Sepharose 4B resin (Pharmacia), previously equilibrated with PBS, and incubated at room temperature with gentle agitation for 30 min. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batchwise) with 10ml cold PBS for 10 min, resuspended in 1ml cold PBS, and loaded onto a disposable column. The resin continued to be washed with cold PBS, until the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The GST-fusion protein was eluted by addition of 700µl cold glutathione elution buffer (10mM reduced glutathione, 50mM Tris-HCl pH 8.0) and fractions collected, until the OD<sub>280nm</sub> of the eluate indicated all the recombinant protein was obtained. 20µl aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. The molecular mass of the purified proteins was determined using either the Bio-Rad broad range molecular weight standard (M1) (200, 116, 97.4, 66.2, 45.0, 31.0, 21.5, 14.4, 6.5 kDa) or the Amersham Rainbow Marker (M2) (220, 66.2, 46.0, 30.0, 21.5, 14.3 kDa). The molecular weights of GST-fusion proteins are a combination of the 26 kDa GST protein and its fusion partner. Protein concentrations were estimated using the Bradford assay.

#### **His-fusion soluble proteins large-scale purification.**

For some ORFs, a single colony was grown overnight at 37°C on a LB + Amp agar plate. The bacteria were inoculated into 20ml of LB+Amp liquid culture and incubated overnight in a water bath shaker. Bacteria were diluted 1:30 into 600ml fresh medium and allowed to grow at the optimal temperature (20-37°C) to OD<sub>550</sub> 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000 rpm at 4°C, the supernatant was discarded and the bacterial pellet was resuspended in 7.5ml cold 10mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 10 mM imidazole, pH 8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed two times and centrifuged again. The supernatant was collected and mixed with 150µl Ni<sup>2+</sup>-resin (Pharmacia) (previously washed with 10mM imidazole buffer) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700g for 5 minutes at 4°C. The resin was washed twice with 10 ml cold 10mM imidazole buffer for 10 minutes,

resuspended in 1ml cold 10mM imidazole buffer and loaded on a disposable column. The resin was washed at 4°C with 2ml cold 10mM imidazole buffer until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The resin was washed with 2ml cold 20mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 20 mM imidazole, pH 8) until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl cold 250mM imidazole buffer (300 mM NaCl, 50 mM phosphate buffer, 250 mM imidazole, pH 8) and fractions collected until the O.D<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

#### **His-fusion insoluble proteins large-scale purification.**

A single colony was grown overnight at 37 °C on a LB + Amp agar plate. The bacteria were inoculated into 20 ml of LB+Amp liquid culture in a water bath shaker and grown overnight. Bacteria were diluted 1:30 into 600ml fresh medium and let to grow at the optimal temperature (37°C) to O.D<sub>550</sub> 0.6-0.8. Protein expression was induced by addition of 1 mM IPTG and the culture further incubated for three hours. The culture was centrifuged at 8000rpm at 4°C. The supernatant was discarded and the bacterial pellet was resuspended in 7.5 ml buffer B (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8). The cells were disrupted by sonication on ice for 30 sec at 40W using a Branson sonifier B-15, frozen and thawed twice and centrifuged again. The supernatant was stored at -20°C, while the pellets were resuspended in 2 ml guanidine buffer (6M guanidine hydrochloride, 100mM phosphate buffer, 10 mM Tris-HCl, pH 7.5) and treated in a homogenizer for 10 cycles. The product was centrifuged at 13000 rpm for 40 minutes. The supernatant was mixed with 150µl Ni<sup>2+</sup>-resin (Pharmacia) (previously washed with buffer B) and incubated at room temperature with gentle agitation for 30 minutes. The sample was centrifuged at 700 g for 5 minutes at 4°C. The resin was washed twice with 10 ml buffer B for 10 minutes, resuspended in 1ml buffer B, and loaded on a disposable column. The resin was washed at room temperature with 2ml buffer B until the flow-through reached the OD<sub>280</sub> of 0.02-0.06. The resin was washed with 2ml buffer C (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the flow-through reached the O.D<sub>280</sub> of 0.02-0.06. The His-fusion protein was eluted by addition of 700µl elution buffer (urea 8M, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions collected until the OD<sub>280</sub> was 0.1. 21µl of each fraction were loaded on a 12% SDS gel.

**Purification of His-fusion proteins.**

For each clone to be purified as a His-fusion, a single colony was streaked out and grown overnight at 37°C on a LB/Amp (100 µg/ml) agar plate. An isolated colony from this plate was inoculated into 20ml of LB/Amp (100 µg/ml) liquid medium and grown overnight at 37°C with shaking. The overnight culture was diluted 1:30 into 600ml LB/Amp (100 µg/ml) liquid medium and allowed to grow at the optimal temperature (20-37°C) until the OD<sub>550nm</sub> reached 0.6-0.8. Expression of recombinant protein was induced by addition of IPTG (final concentration 1.0mM) and the culture incubated for a further 3 hours. Bacteria were harvested by centrifugation at 8000xg for 15 min at 4°C.

The bacterial pellet was resuspended in 7.5ml of either (i) cold buffer A (300mM NaCl, 50mM phosphate buffer, 10mM imidazole, pH 8.0) for soluble proteins or (ii) buffer B (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 8.8) for insoluble proteins. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. For insoluble proteins, pellets were resuspended in 2.0 ml buffer C (6M guanidine hydrochloride, 100mM phosphate buffer, 10mM Tris-HCl, pH 7.5) and treated with a Dounce homogenizer for 10 cycles. The homogenate was centrifuged at 13 000xg for 40 min and the supernatant retained.

Supernatants for both soluble and insoluble preparations were mixed with 150µl Ni<sup>2+</sup>-resin (previously equilibrated with either buffer A or buffer B, as appropriate) and incubated at room temperature with gentle agitation for 30 min. The resin was Chelating Sepharose Fast Flow (Pharmacia), prepared according to manufacturers protocol. The batch-wise preparation was centrifuged at 700xg for 5 min at 4°C and the supernatant discarded. The resin was washed twice (batch-wise) with 10ml buffer A or B for 10 min, resuspended in 1.0 ml buffer A or B and loaded onto a disposable column. The resin continued to be washed with either (i) buffer A at 4°C or (ii) buffer B at room temperature, until the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The resin was further washed with either (i) cold buffer C (300mM NaCl, 50mM phosphate buffer, 20mM imidazole, pH 8.0) or (ii) buffer D (8M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 6.3) until the the OD<sub>280nm</sub> of the flow-through reached 0.02-0.01. The His-fusion protein was eluted by addition of 700µl of either (i) cold elution buffer A (300mM NaCl, 50mM phosphate buffer, 250mM imidazole, pH 8.0) or (ii) elution buffer B (8 M urea, 10mM Tris-HCl, 100mM phosphate buffer, pH 4.5) and fractions



collected until the  $O.D_{280nm}$  indicated all the recombinant protein was obtained. 20 $\mu$ l aliquots of each elution fraction were analyzed by SDS-PAGE using a 12% gel. Protein concentrations were estimated using the Bradford assay.

### **His-fusion proteins renaturation**

In the cases where denaturation was required to solubilize proteins, a renaturation step was employed prior to immunization. Glycerol was added to the denatured fractions obtained above to give a final concentration of 10%(v/v). The proteins were diluted to 200 $\mu$ g/ml using dialysis buffer I (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, 2.0M urea, pH 8.8) and dialysed against the same buffer for 12-14 hours at 4°C. Further dialysis was performed with buffer II (10% (v/v) glycerol, 0.5M arginine, 50mM phosphate buffer, 5.0mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Alternatively, 10% glycerol was added to the denatured proteins. The proteins were then diluted to 20 $\mu$ g/ml using dialysis buffer I (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, 2M urea, pH 8.8) and dialysed against the same buffer at 4°C for 12-14 hours. The protein was further dialysed against dialysis buffer II (10% glycerol, 0.5M arginine, 50mM phosphate buffer, 5mM reduced glutathione, 0.5mM oxidised glutathione, pH 8.8) for 12-14 hours at 4°C.

Protein concentration was evaluated using the formula:

$$\text{Protein (mg/ml)} = (1.55 \times OD_{280}) - (0.76 \times OD_{260})$$

### **Purification of proteins**

To analyse the solubility, pellets obtained from 3.0ml cultures were resuspended in 500 $\mu$ l buffer M1 (PBS pH 7.2). 25 $\mu$ l of lysozyme (10mg/ml) was added and the bacteria incubated for 15 min at 4°C. Cells were disrupted by sonication on ice four times for 30 sec at 40W using a Branson sonifier 450 and centrifuged at 13 000xg for 30 min at 4°C. The supernatant was collected and the pellet resuspended in buffer M2 [8M urea, 0.5M NaCl, 20mM imidazole and 0.1M  $NaH_2PO_4$ ] and incubated for 3 to 4 hours at 4°C. After centrifugation, the supernatant was collected and the pellet resuspended in buffer M3 [6M guanidinium-HCl, 0.5M NaCl, 20mM imidazole and 0.1M  $NaH_2PO_4$ ] overnight at 4°C. The

supernatants from all steps were analysed by SDS-PAGE. Some proteins were found to be soluble in PBS, others need urea or guanidium-HCl for solubilization.

For preparative scale purifications, 500ml cultures were induced and fusion proteins solubilized in either buffer M1, M2 or M3 using the procedure described above. Crude extracts were loaded onto a Ni-NTA superflow column (Quiagen) equilibrated with buffer M1, M2 or M3 depending on the solubilization buffer employed. Unbound material was eluted by washing the column with the same buffer. The recombinant fusion protein was eluted with the corresponding buffer containing 500mM imidazole then dialysed against the same buffer in the absence of imidazole.

### **Mice immunisations**

20µg of each purified protein are used to immunise mice intraperitoneally. In the case of some ORFs, Balb-C mice were immunised with Al(OH)<sub>3</sub> as adjuvant on days 1, 21 and 42, and immune response was monitored in samples taken on day 56. For other ORFs, CD1 mice could be immunised using the same protocol. For ORFs 25 and 40, CD1 mice were immunised using Freund's adjuvant, and the same immunisation protocol was used, except that the immune response was measured on day 42, rather than 56. Similarly, for still other ORFs, CD1 mice were immunised with Freund's adjuvant, but the immune response was measured on day 49. Alternatively, 20µg of each purified protein was mixed with Freund's adjuvant and used to immunise CD1 mice intraperitoneally. For many of the proteins, the immunization was performed on days 1, 21 and 35, and immune response was monitored in samples taken on days 34 and 49. For some proteins, the third immunization was performed on day 28, rather than 35, and the immune response was measured on days 20 and 42, rather than 34 and 49.

### **ELISA assay (sera analysis)**

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 7ml of Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10000 rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated

for 2 hours at room temperature and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200 µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200 µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN<sub>3</sub> in PBS) were added to each well and the plates incubated for 90 minutes at 37°C. Wells were washed three times with PBT. 100 µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100 µl of substrate buffer for HRP (25 ml of citrate buffer pH5, 10 mg of O-phenildiamine and 10 µl of H<sub>2</sub>O) were added to each well and the plates were left at room temperature for 20 minutes. 100 µl H<sub>2</sub>SO<sub>4</sub> was added to each well and OD<sub>490</sub> was followed. The ELISA was considered positive when OD<sub>490</sub> was 2.5 times the respective pre-immune sera.

Alternatively, The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into Mueller-Hinton Broth (Difco) containing 0.25% Glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.3-0.4. The culture was centrifuged for 10 minutes at 10 000rpm. The supernatant was discarded and bacteria were washed once with PBS, resuspended in PBS containing 0.025% formaldehyde, and incubated for 1 hour at 37°C and then overnight at 4°C with stirring. 100µl bacterial cells were added to each well of a 96 well Greiner plate and incubated overnight at 4°C. The wells were then washed three times with PBT washing buffer (0.1% Tween-20 in PBS). 200µl of saturation buffer (2.7% Polyvinylpyrrolidone 10 in water) was added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 200µl of diluted sera (Dilution buffer: 1% BSA, 0.1% Tween-20, 0.1% NaN<sub>3</sub> in PBS) were added to each well and the plates incubated for 2 hours at 37°C. Wells were washed three times with PBT. 100µl of HRP-conjugated rabbit anti-mouse (Dako) serum diluted 1:2000 in dilution buffer were added to each well and the plates were incubated for 90 minutes at 37°C. Wells were washed three times with PBT buffer. 100µl of substrate buffer for HRP (25ml of citrate buffer pH5, 10mg of O-

phenildiamine and 10 $\mu$ l of H<sub>2</sub>O<sub>2</sub>) were added to each well and the plates were left at room temperature for 20 minutes. 100 $\mu$ l of 12.5% H<sub>2</sub>SO<sub>4</sub> was added to each well and OD<sub>490</sub> was followed. The ELISA titers were calculated arbitrarily as the dilution of sera which gave an OD<sub>490</sub> value of 0.4 above the level of preimmune sera. The ELISA was considered positive when the dilution of sera with OD<sub>490</sub> of 0.4 was higher than 1:400.

#### **FACScan bacteria Binding Assay procedure.**

The acapsulated MenB M7 strain was plated on chocolate agar plates and incubated overnight at 37°C. Bacterial colonies were collected from the agar plates using a sterile dracon swab and inoculated into 4 tubes containing 8ml each Mueller-Hinton Broth (Difco) containing 0.25% glucose. Bacterial growth was monitored every 30 minutes by following OD<sub>620</sub>. The bacteria were let to grow until the OD reached the value of 0.35-0.5. The culture was centrifuged for 10 minutes at 4000rpm. The supernatant was discarded and the pellet was resuspended in blocking buffer (1% BSA in PBS, 0.4% NaN<sub>3</sub>) and centrifuged for 5 minutes at 4000rpm. Cells were resuspended in blocking buffer to reach OD<sub>620</sub> of 0.07. 100 $\mu$ l bacterial cells were added to each well of a Costar 96 well plate. 100 $\mu$ l of diluted (1:100, 1:200, 1:400) sera (in blocking buffer) were added to each well and plates incubated for 2 hours at 4°C. Cells were centrifuged for 5 minutes at 4000rpm, the supernatant aspirated and cells washed by addition of 200 $\mu$ l/well of blocking buffer in each well. 100 $\mu$ l of R-Phicoerytrin conjugated F(ab)<sub>2</sub> goat anti-mouse, diluted 1:100, was added to each well and plates incubated for 1 hour at 4°C. Cells were spun down by centrifugation at 4000rpm for 5 minutes and washed by addition of 200 $\mu$ l/well of blocking buffer. The supernatant was aspirated and cells resuspended in 200 $\mu$ l/well of PBS, 0.25% formaldehyde. Samples were transferred to FACScan tubes and read. The condition for FACScan (Laser Power 15mW) setting were: FL2 on; FSC-H threshold:92; FSC PMT Voltage: E 01; SSC PMT: 474; Amp. Gains 6.1; FL-2 PMT: 586; compensation values: 0.

#### **OMV preparations**

Bacteria were grown overnight on 5 GC plates, harvested with a loop and resuspended in 10 ml 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30 minutes and the bacteria disrupted by sonication for 10' on ice ( 50% duty cycle, 50% output ). Unbroken cells were removed by centrifugation at 5000g for 10 minutes and the total cell envelope

fraction recovered by centrifugation at 50000g at 4°C for 75 minutes. To extract cytoplasmic membrane proteins from the crude outer membranes, the whole fraction was resuspended in 2% sarkosyl (Sigma) and incubated at room temperature for 20 minutes. The suspension was centrifuged at 10000g for 10 minutes to remove aggregates, and the supernatant further ultracentrifuged at 50000g for 75 minutes to pellet the outer membranes. The outer membranes were resuspended in 10mM Tris-HCl, pH8 and the protein concentration measured by the Bio-Rad Protein assay, using BSA as a standard.

### **Whole Extracts preparation**

Bacteria were grown overnight on a GC plate, harvested with a loop and resuspended in 1ml of 20mM Tris-HCl. Heat inactivation was performed at 56°C for 30' minutes.

### **Western blotting**

Purified proteins (500ng/lane), outer membrane vesicles (5µg) and total cell extracts (25µg) derived from MenB strain 2996 were loaded onto a 12% SDS-polyacrylamide gel and transferred to a nitrocellulose membrane. The transfer was performed for 2 hours at 150mA at 4°C, using transfer buffer (0.3 % Tris base, 1.44 % glycine, 20% (v/v) methanol). The membrane was saturated by overnight incubation at 4°C in saturation buffer (10% skimmed milk, 0.1% Triton X100 in PBS). The membrane was washed twice with washing buffer (3% skimmed milk, 0.1% Triton X100 in PBS) and incubated for 2 hours at 37°C with mice sera diluted 1:200 in washing buffer. The membrane was washed twice and incubated for 90 minutes with a 1:2000 dilution of horseradish peroxidase labelled anti-mouse Ig. The membrane was washed twice with 0.1% Triton X100 in PBS and developed with the Opti-4CN Substrate Kit (Bio-Rad). The reaction was stopped by adding water.

### **Bactericidal assay**

MC58 and 2996 strains were grown overnight at 37°C on chocolate agar plates. 5-7 colonies were collected and used to inoculate 7ml Mueller-Hinton broth. The suspension was incubated at 37°C on a nutator and let to grow until OD<sub>620</sub> was in between 0.5-0.8. The culture was aliquoted into sterile 1.5ml Eppendorf tubes and centrifuged for 20 minutes at maximum speed in a microfuge. The pellet was washed once in Gey's buffer (Gibco) and resuspended in the same buffer to an OD<sub>620</sub> of 0.5, diluted 1:20000 in Gey's buffer and stored at 25°C.

50µl of Gey's buffer/1% BSA was added to each well of a 96-well tissue culture plate. 25µl of diluted (1:100) mice sera (dilution buffer: Gey's buffer/0.2% BSA) were added to each well and the plate incubated at 4°C. 25µl of the previously described bacterial suspension were added to each well. 25µl of either heat-inactivated (56°C waterbath for 30 minutes) or normal baby rabbit complement were added to each well. Immediately after the addition of the baby rabbit complement, 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 0). The 96-well plate was incubated for 1 hour at 37°C with rotation and then 22µl of each sample/well were plated on Mueller-Hinton agar plates (time 1). After overnight incubation the colonies corresponding to time 0 and time 1h were counted.

### Gene Variability

The *ORF4* and *919* genes were amplified by PCR on chromosomal DNA extracted from various *Neisseria* strains (see list of strains). The following oligonucleotides used as PCR primers were designed in the upstream and downstream regions of the genes:

orf 4.1	(forward)	CGAATCCGGACGGCAGGACTC
orf 4.3	(reverse)	GGCAGGGAATGGCGGATTAAAG
919.1	(forward)	AAAATGCCTCTCCACGGCTG or CTGCGCCCTGTGTTAAAATCCCCT
919.6	(reverse)	CAAATAAGAAAGGAATTTTG or GGTATCGCAAACTTCGCCTTAATGCG

The PCR cycling conditions were:

1 cycle	2 min. at 94°
30 cycles	30 sec. at 94°
	30 sec. at ~ 54° or ~ 60° ( in according to T <sub>m</sub> of the primers)
	40 sec. at 72°
1 cycle	7 min. at 72°

The PCR products were purified from 1 % agarose gel and sequenced using the following primers:

orf 4.1 (forward)	CGAATCCGGACGGCAGGACTC
orf 4.2 (forward)	CGACCGCGCCTTTGGGACTG
orf 4.3 (reverse)	GGCAGGGAATGGCGGATTAAAG
orf 4.4 (reverse)	TCTTTGAGTTTGATCCAACC

- 919.1 (forward) AAAATGCCTCTCCACGGCTG or  
CTGCGCCCTGTGTTAAAATCCCCCT
- 919.2 (forward) ATCCTTCCGCTCGGCTGCG
- 919.3 (forward) AAAACAGCGGCACAATCGAC
- 919.4 (forward) ATAAGGGCTACCTCAAATC
- 919.5 (forward) GCGCGTGGATTATTTTGGG
- 919.6 (reverse) CAAATAAGAAAGGAATTTTG or  
GGTATCGCAAACTTCGCCTTAATGCG
- 919.7 (reverse) CCCAAGGTAATGTAGTGCCG
- 919.8 (reverse) TAAAAAAAGTTCGACAGGG
- 919.9 (reverse) CCGTCCGCCTGTCGTCGCCC
- 919.10 (reverse) TCGTTCGCGCGGGGTCGGGG

All documents cited herein are incorporated by reference in their entireties.

The following Examples are presented to illustrate, not limit, the invention

#### EXAMPLE 1

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

**Table 1: Oligonucleotides used for PCR for Examples 2-10**

ORF	Primer	Sequence	Restriction sites
279	Forward	CGCGGATCCCATATG-TTGCCTGCAATCACGATT <SEQ ID 3021>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA <SEQ ID 3022>	XhoI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA <SEQ ID 3023>	BamHI-NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC <SEQ ID 3024>	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT <SEQ ID 3025>	BamHI-NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC <SEQ ID 3026>	XhoI
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC <SEQ ID 3027>	BamHI-NdeI
	Reverse	CCCGCTCGAG-CGGGCGGTATTCGGG <SEQ ID 3028>	XhoI
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT <SEQ ID 3029>	BamHI-NdeI

128	Reverse	CCCGCTCGAG-ATAATAATATCCGCGCCC <SEQ ID 3030>	XhoI
	Forward	CGCGGATCCCATATG-ACTGACAACGCACT <SEQ ID 3031>	BamHI-NdeI
206	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA <SEQ ID 3032>	XhoI
	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA <SEQ ID 3033>	BamHI-NdeI
287	Reverse	CCCGCTCGAG-TTCTGTAAAAAAGTATGTGC <SEQ ID 3034>	XhoI
	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG <SEQ ID 3035>	EcoRI-NheI
406	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTGCC <SEQ ID 3036>	XhoI
	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG <SEQ ID 3037>	BamHI-NdeI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG <SEQ ID 3038>	XhoI

### Localization of the ORFs

The following DNA and amino acid sequences are identified by titles of the following form: [g, m, or a] [#].[seq or pep], where "g" means a sequence from *N. gonorrhoeae*, "m" means a sequence from *N. meningitidis B*, and "a" means a sequence from *N. meningitidis A*; "#" means the number of the sequence; "seq" means a DNA sequence, and "pep" means an amino acid sequence. For example, "g001.seq" refers to an *N. gonorrhoeae* DNA sequence, number 1. The presence of the suffix "-1" to these sequences indicates an additional sequence found for the same ORF, thus, data for an ORF having both an unsuffixed and a suffixed sequence designation applies to both such designated sequences. Further, open reading frames are identified as ORF #, where "#" means the number of the ORF, corresponding to the number of the sequence which encodes the ORF, and the ORF designations may be suffixed with ".ng" or ".a", indicating that the ORF corresponds to a *N. gonorrhoeae* sequence or a *N. meningitidis A* sequence, respectively. The word "partial" before a sequence indicates that the sequence may be a partial or a complete ORF. Computer analysis was performed for the comparisons that follow between "g", "m", and "a" peptide sequences; and therein the "pep" suffix is implied where not expressly stated. Further, in the event of a conflict between the text immediately preceding and describing which sequences are being compared, and the



designated sequences being compared, the designated sequence controls and is the actual sequence being compared.

ORF: contig:

279 gnm4.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3039>:

m279.seq

```

1   ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGGCGCGT TTGGCACC GG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCCCTGCA ATCACGATTT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGCAAAAT TCAATGCGCC GGCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGCGCG CAGGCGTTTT GCCGCCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 3040; ORF 279>:

m279.pep

```

1   ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAOMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3041>:

g279.seq

```

1   atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcggggt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcggcggc gttgcctgca atcacgactt gtccggcgca
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattt tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggaacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgcccatc
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 3042; ORF 279.ng>:

g279.pep

```

1   MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKNSASAAT SAVYSPRLCP ATAAGVLPPA
151 SK*

```

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:     : :     :     :     :     :     :     :     :     :					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60

a279.seq

```
1 ATGACNCNGA TTTGCGGCTG CTTGATTTC ACGGTTTNNNA GGGCTTCGGC
51 GAGTTTGTCTG GCGGCGGGTT TCATGAGGCT GCAATGGGAA GGTACNGACA
101 CNGGCAGCGG CAGGGCGCGT TTTGGCGCCG CTTCTTTTGGC GGCAAGCATA
151 GCGCGCTTGA CGGCGGCGGC ATTGCCTGCA ATCACGACTT GTCCGGGCGCA
201 GTTGAAGTTA ACGGCTTCAA CCACCTCATC CTGTGCGGAT TCGCGCAAA
251 TTTGTTTTAC CTGTTTCTCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA NGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT CCAATGCGCC GCGGCGCAACN AGTGGCGTGT
401 ATTCGCCGAN GCTGTGTCCG GCAACGGCGG CAGGCGTTTT GCCGCCGCT
451 TCCGAATAG
```

```
a279.pcp.
1  MTXICGCLIS TVXKRASASLS AAGFMRLQWE GTDGSGRAR LAPASLAASI
51 ARSTAAALPA IITCPGELKL TASTTSSCAD SAQICFTCSS SKPRIAAIAP
101 TPCGTADCIS SARXRTSLTA SAKSNAPEAT SAVYSPXLCP ATAAGVLPFA
151 SE*
```

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRRARLAPASLAAMARPTAAALPA :          :          :          :          :					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTFCGTADCISSARRRSTLTA                     :					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTFCGTADCISSARXRSTLTA					
	70	80	90	100	110	120
	130	140	150			
m279.pep	SAKFNAPAATSAVYSPRLCFATAAGVLPPASKX                     :					
a279	SAKSNAPAATSAVYSPXLCFATAAGVLPPASEX					
	130	140	150			

m519.seq	(partial)	1	51	101	151	201
1	..TCCGTTATCG	GGCGTATGGA	GTTGGACAAA	ACGTTTGAAG	AACGCGACGA	
51	AATCAACAGT	ACTGTTGTG	CGGCTTTGGA	CGAGGCGGCC	GGGgCTTgGG	
101	GTGTGAAGGT	TTTGC GTTAT	GAGATTAAG	ACTTGGTCC	GCCGC AAGAA	
151	ATCCTTCGCT	CAATGCAGCG	GCAAATTACT	GCTTAACCGC	AAAAACGGCA	
201	CCGTATCGCC	GAATCCGAAG	GTCGTAAAT	CGAACAAATC	AACCTTGCCC	

```

251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
351 AGGTGAAGCG GAATCCTTGC GCCTTGTTGC CGAAGCCAAT GCCGAAGCCA
401 TCCGTCAAAT TGCCGCGGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTGCGCGAC ATCGGCAGCC
551 TGATTTCTGC CCGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3046; ORF 519>:

```

m519.pep (partial)
  1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
  51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLLISAGMK IIDSSKTAK*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3047>:

```

g519.seq
  1 atggaatttt tcattatctt gttggcagcc gtcgccgttt tcggcttcaa
  51 atcctttgtc gtcattcccc agcaggaagt ccacgttgtc gaaaggctcg
 101 ggcgtttcca tcgcgccctg acggccggtt tgaatatctt gattcccttt
 151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc cttagacgt
 201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
 251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
 301 agcaactaca ttatggcaat taccagctt gccaaacga cgtgcttc
 351 cggtatcggt cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
 401 tcaacagtac cgtcgtctcc gccctcgatg aagccgccgg ggcttggggg
 451 gtgaaagtcc tccgttacga aatcaaggat ttggttcgcg cgcaagaaat
 501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
 551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
 601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctcaggctgc
 651 ggtcaatgcg tccaatgccg agaaaatcgc cgcattcaac cgcgcaaaag
 701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
 751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcgggtcaa
 801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
 851 aagacaatac gcggattaag cccgccaagg ttgccgaaat cgggaaccct
 901 aattttcggc ggcatgaaaa attttcgccg gaagcaaaaa cggccaaata
 951 a

```

This corresponds to the amino acid sequence <SEQ ID 3048; ORF 519.ng>:

```

g519.pep
  1 MEFFIILLAA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
  51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEN
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFKN LAKEDNTRIK PAKVAEIGNP
 301 NFRHEKFSF EAKTAK*

```

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

```

m519.pep          10      20      30
                  SVIGRMELDKTFEERDEINSTVVAALDEAA
g519              YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
                  90      100     110     120     130     140
m519.pep          40      50      60      70      80      90
                  GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE

```

```

g519      |||||:|||||
          GAWGVKVLRYEIKDLVPPQEIILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
          150      160      170      180      190      200

m519.pep  100      110      120      130      140      150
          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
          |||||:|||||
g519      210      220      230      240      250      260
          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQSGADAV

m519.pep  160      170      180      190      200
          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK
          |||||:|||||
g519      270      280      290      300      310
          NLKIAGQYVTAFAKLNKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3049>:

```

a519.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGTTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCGTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGCTCTC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCGCG CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCATGCGC TCAATGCGC AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTTGCGC AAGCCAATGC CGAAGCCATC
751 CGTCAAAATG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3050; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGEKFSV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 ORFs 519 and 519.a showed a 99.5% identity in 199 aa overlap

```

m519.pep 10 20 30
          SVIGRMELDKTFEERDEINSTVVAALDEAA
          |||||:|||||
a519      90 100 110 120 130 140
          YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA

m519.pep 40 50 60 70 80 90
          GAWGVKVLRYEIKDLVPPQEIILSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
          |||||:|||||
a519      150 160 170 180 190 200
          GAWGVKVLRYEIKDLVPPQEIILSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE

          100 110 120 130 140 150

```

```

m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a519          IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
                210      220      230      240      250      260

                160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                ||||||||||||||||||||||||||||||||||||||||||||||||||
a519          NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
                270      280      290      300      310

```

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3051>:

```

m519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
101 GGCCTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ATCCAGCCAG GTCTGCATCA CGCGCGACA TACGCAGCTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC TGTGTTGCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGC AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3052; ORF 519-1>:

```

m519-1.
1  MEFFIILLVA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51 IDRWAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3053>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51 ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCCTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ATCCAGCCAG GTCTGCATCA CGCGCGATA TACGCAATG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GGCGGGGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG

```

851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
 901 ATTTCTGCCG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 3054; ORF 519-1.ng>:

g519-1.pep  
 1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF  
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGLIYFQV TDPKLASYGS  
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGEAQA AVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI  
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
 301 ISAGMKIIDS SKTAK\*

m519-1/g519-1 ORFs 519-1 and 519-1.ng showed a 99.0% identity in 315 aa overlap

g519-1.pep	10	20	30	40	50	60
	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGLIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGLIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
g519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep	250	260	270	280	290	300
	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANA EAI RQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
g519-1.pep	310					
	ISAGMKIIDS SKTAKX					
m519-1	ISAGMKIIDS SKTAKX					
	310					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3055>:

a519-1.seq  
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA  
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG  
 101 GCGGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT  
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG  
 251 GTATCATCTA TTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCG  
 301 AGCAACTACA TTATGGCGAT TACCAGCTT GCCCAAACGA CGCTGCGTTC  
 351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAA

```

401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCAA GCGGTTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 3056; ORF 519-1.a>:

a519-1.pep.

```

1  MEFFIILLAA VVVFGEKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKCLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEGRKIEQINLAS
201 GQREAEIQQS EGEEAQAANA SNAEKIARIN RAKGEAESLR LVAEANAIAEI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 ORFs 519-1 and 519-1.a showed a 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
a519-1.pep	MEFFIILLAAVVVFGEKSFVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGEKSFVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
a519-1.pep	70	80	90	100	110	120
	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKCLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKCLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
a519-1.pep	130	140	150	160	170	180
	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
a519-1.pep	190	200	210	220	230	240
	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAANASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAANASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
a519-1.pep	250	260	270	280	290	300
	LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
m519-1	LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL					
	250	260	270	280	290	300
a519-1.pep	310					
	ISAGMKIIDSSKTAKX					
m519-1	ISAGMKIIDSSKTAKX					
	310					

576 and 576-1 gnm22.seq

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3057>:

```
m576.seq.. (partial)
1   ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
51  GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
151 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
351 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451 GTGATTCCGG GTTGGACCGA AGCGTACAG CTTCTGAAAG AAGGCGGCGA
501 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551 GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651 CATCAAAAAA GTAAATTAA
```

This corresponds to the amino acid sequence <SEQ ID 3058; ORF 576>:

```
m576.pep.. (partial)
1   ..MQQASYAMGV DIGRSLKOMK EQGAEIDLKV FTEAMQAVYD GKEIKMTTEEQ
51  AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3059>:

```
g576.seq.. (partial)
1   ..atggcgctgg acatcgagcg ctccttgaaa caaatgaagg aacaggggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcttcgagg agcagcaggg taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccc
251 aagacggcgt gaagaccact gcttcgggtc tgcagtacaa aatcaccaaa
301 cagggtgaag gcaaacagcc gacaaaagac gacatcggtt ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtagcgc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcgggcg acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa
```

This corresponds to the amino acid sequence <SEQ ID 3060; ORF 576.ng>:

```
g576.pep.. (partial)
1   ..MGVDIGRSLK QMKEQGAIED LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGAEFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 ORFs 576 and 576.ng showed a 97.2% identity in 215 aa overlap

```

          10      20      30      40      50      60
m576.pep  MQQASYAMGV DIGRSLKOMKEQGAIEDLKV FTEAMQAVYD GKEIKMTTEEQAQEVMMKFLQ
          |||

```



```

g576          MGVDIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAQEVMMKFLQ
                10      20      30      40      50

                70      80      90      100     110     120
m576.pep      EQQAKAVEKHKADAKANKEKGEAFLKENAAKDGVKTASGLQYKITKQEGEGKQPTKDDIV
                |||||
g576          EQQAKAVEKHKADAKANKEKGEAFLKENAAEDGVKTASGLQYKITKQEGEGKQPTKDDIV
                60      70      80      90      100     110

                130     140     150     160     170     180
m576.pep      TVEYEGRLIDGTVFDSSKANGGPVTFPLSQVIPGWTEGVQLLKEGGEATFYIPSNLAYRE
                |||||
g576          TVEYEGRLIDGTVFDSSKANGGPATFPLSQVIPGWTEGVRLLEKGEATFYIPSNLAYRE
                120     130     140     150     160     170

                190     200     210     220
m576.pep      QGAGDKIGPNATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN
                |||||
g576          QGAGEKIGPNATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN
                180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3061>:

```

a576.seq
1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCG CCGCTTTGGC
51  ACTTTCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCG TTCTTCGCG CAGGGCGACA CCTCTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 3062; ORF 576.a>:

```

a576.pep
1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

m576/a576 ORFs 576 and 576.a showed a 99.5% identity in 222 aa overlap

```

                10      20      30
m576.pep      MQQASYAMGV DIGRSLKQMKEQGAEIDLKV
                |||||
a576          CGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV DIGRSLKQMKEQGAEIDLKV
                30      40      50      60      70      80

                40      50      60      70      80      90
m576.pep      FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                |||||
a576          FTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKHKADAKANKEKGEAFLKENAA
                90      100     110     120     130     140

```

	100	110	120	130	140	150
m576.pep	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
a576	KDGVKTTASGLQYKITKQEGGKQPTKDDIVTVEYEGRLIDGTVFDSSKANGGPVTFPLSQ					
	150	160	170	180	190	200
m576.pep	VIPGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
a576	VILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPNATLVFDVKLVKIGAPENAPA					
	210	220	230	240	250	260
m576.pep	KQPAQVDIKKVN					
a576	KQPAQVDIKKVN					
	270					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3063>:

m576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTTCCGCG	CAGGGCGACA	CCTCTTCGAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	GATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	GCAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGAAG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCTCAGGAAG	TCATGATGAA	ATTCTTCAG	GAACAACAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGACG	CGAAGGCCAA	TAAAGAAAAA	GGCGAAGCCT
401	TTCTGAAAGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGC
451	CTGCAATACA	AAATCACCAA	ACAGGGCGAA	GGCAAACAGC	CGACCAAGA
501	CGACATCGTT	ACCGTGGAA	ACGAAGGCCG	CCTGATTGAC	GGTACGGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	TCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACAG	CTTCTGAAAG	AAGGCGGCCA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG
701	GCGACAAAAT	CGGTCGGAAC	GCCACTTTGG	TATTTGATGT	GAAACTGGTC
751	AAAATCGGCG	CACCCGAAAA	CGCGCCCGCC	AAGCAGCCGG	CTCAAGTCGA
801	CATCAAAAAA	GTAAATTAA			

This corresponds to the amino acid sequence <SEQ ID 3064; ORF 576-1>:

m576-1.pep

1	MNTIFKISAL	TLSAALALSA	CGKKEAAPAS	ASEPAAASSA	QGDTSIGST
51	MQQASYAMGV	DIGRSLQMK	EQGAEIDLKV	FTEAMQAVYD	GKEIKMTEEQ
101	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK	GEAFLKENAA	KDGVKTTASG
151	LQYKITKQGE	GKQPTKDDIV	TVEYEGRLID	GTVFDSSKAN	GGPVTFFLSQ
201	VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
251	KIGAPENAPA	KQPAQVDIKK	VN*		

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3065>:

g576-1.seq

1	ATGAACACCA	TTTTCAAAAT	CAGCGCACTG	ACCCTTTCCG	CCGCTTTGGC
51	ACTTTCCGCC	TGCGGCAAAA	AAGAAGCCGC	CCCCGCATCT	GCATCCGAAC
101	CTGCCGCCGC	TTCTGCCGCG	CAGGGCGACA	CCTCTTCAAT	CGGCAGCACG
151	ATGCAGCAGG	CAAGCTATGC	AATGGGCGTG	GACATCGGAC	GCTCCCTGAA
201	ACAAATGAAG	GAACAGGGCG	CGGAAATCGA	TTTGAAAGTC	TTTACCGATG
251	CCATGCAGGC	AGTGTATGAC	GGCAAAGAAA	TCAAAATGAC	CGAAGAGCAG
301	GCCCAGGAAG	TGATGATGAA	ATTCTGCAG	GAGCAGCAGG	CTAAAGCCGT
351	AGAAAAACAC	AAGGCGGATG	CGAAGGCCAA	CAAAGAAAAA	GGCGAAGCCT
401	TCCTGAAGGA	AAATGCCGCC	AAAGACGGCG	TGAAGACCAC	TGCTTCCGGT
451	CTGCAGTACA	AAATCACCAA	ACAGGGTGAA	GGCAAACAGC	CGACAAAAGA
501	CGACATCGTT	ACCGTGGAA	ACGAAGGCCG	CCTGATTGAC	GGTACCGTAT
551	TCGACAGCAG	CAAAGCCAAC	GGCGGCCCGG	CCACCTTCCC	TTTGAGCCAA
601	GTGATTCCGG	GTTGGACCGA	AGGCGTACGG	CTTCTGAAAG	AAGGCGGCCA
651	AGCCACGTTT	TACATCCCGT	CCAACCTTGC	CTACCGCGAA	CAGGGTGCGG

701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3066; ORF 576-1.ng>:

g576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ  
 101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ  
 201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPDQVDIKK VN\*

g576-1/m576-1 ORFs 576-1 and 576-1.ng showed a 97.8% identity in 272 aa overlap

g576-1.pep	10	20	30	40	50	60
	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTDAMQAVYDGKEIKMTEEQAEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPATFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGEKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVIPGWTEGVRLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	250	260	270			
	ATLVFDVKLVKIGAPENAPAKQPDQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3067>:

a576-1.seq

1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC  
 51 ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCC GCATCT GCATCCGAAC  
 101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCAGC  
 151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA  
 201 GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG  
 251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG  
 301 GCTCAGGAAG TCATGATGAA ATTCTTCAG GAACAACAGG CTAAAGCCGT  
 351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT  
 401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC  
 451 CTGCAATACA AAATCACCAC ACAGGGCGAA GGCAACAGC CGACCAAGA  
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATGAC GGTACGGTAT  
 551 TCGACAGCAG CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTGAGCCAA  
 601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCCA  
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG

701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 3068; ORF 576-1.a>:

a576-1.pep

1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

a576-1/m576-1 ORFs: 576-1 and 576-1.a showed a 99.6% identity in 272 aa overlap

a576-1.pep	10	20	30	40	50	60
	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	70	80	90	100	110	120
	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	130	140	150	160	170	180
	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	190	200	210	220	230	240
	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	250	260	270			
	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

919 gnm43.seq

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3069>:

m919.seq

1 ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TACGGCATCG CGCCCGCCAT  
 51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA  
 101 CATCCGTCAT CAACGCGCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC  
 151 GGAACGACGG TCGGCGCGCG CGGGGCCGTC TATACCGTTG TACCGCACCT  
 201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT  
 251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG  
 301 TCGGCCCAAG CCTTTCAAAC CCCCCTCCAT TCCTTTCAGG CAAAACAGTT  
 351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG  
 401 CCGGTACGGT TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGACAGG

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451 CGGACGGCAC AAGCCCGCTT CCGGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCGTCCTCC CTGCCTGCGG GTTTCGCGAG CGGAAAAGCC CTTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCcG ATTCCCATC ACCGCGCGCA CAACAGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCTTG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCyTA CGTTTCCATC GGACGCTATA TGGCGGATAA GGGCTACCTC
901 AAACCTCGGAC AAACCTCCAT GCAGGGCATT AAGTCTTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGGAAG AGCAATGACG GCCCTGTCCG CGCACTGGGC
1051 ACGCCGCTGA TGGGGGAATA TGCCGCGCGA GTCGACCGGC ACTACATTAC
1101 CTTGGGTGCG CCCTTATTTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTC CTACCCAACG
1301 GTATGAAGCC CGAATACCGc CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3070; ORF 919>:

m919.pep

```

1 MKKYLFRAL YGIAAAILAA COSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFOAQQFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGGDR
151 RTAQARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSRFPI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KSYMQRNPQR LAEVLGQNPS YIFFRELAGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 3071>:

g919.seq

```

1 ATGAAAAAAC ACCTGCTCCG CTCGCCCTG TACGGcatCG CCGCCgccAT
51 CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGCGCG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTCAT TCCTTTcAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACGC cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtacggt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCGGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCGTCCTCC CTGCCTGCGG GTTTCGCGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACCGCCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTTGAaggAA GCCGCTTCCT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGGCgcgcTT GACGGCAAag cccCATCCT CggttacgcC
751 GAagaccCcg tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCCT
801 GAAAACCCcg tccggcaaat acatCCGCAT cggaTacgcc gacAAAAACG
851 AACAtccgTa tgtttccatc ggACGctata TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGcatc aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GCGCAGGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 3072; ORF 919.ng>:

g919.pep  
 1 MKKHLRLRSAL YGIAAAAILAA CQSRSIQTFF QPDTSVINGP DRPAGIPDPA  
 51 GTTVAGGGAV YTVVPHLSMP HWAQDFAKS LQSFRLGCAN LKNRQGWQDV  
 101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR  
 151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIRQTGKN SGTIDNAGGT  
 201 HTADLSRFPI TARTTAIKGR FEGRSFLPYH TRNQINGGAL DGKAPILGYA  
 251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL  
 301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAYS GNEGPVGALG  
 351 TPLMGEYAGA IDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG  
 401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P\*

ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF 919.ng) from *N. gonorrhoeae*:

m919/g919

m919.pep	10	20	30	40	50	60
	MKKYLFRAALYGIAAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV					
g919	MKKHLRLRSALYGIAAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	10	20	30	40	50	60
m919.pep	70	80	90	100	110	120
	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER					
g919	YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER					
	70	80	90	100	110	120
m919.pep	130	140	150	160	170	180
	YFTPWQVAGNSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNSLAGTVTGYEYEPVLKGDGRRTERARFPIYGI PDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
m919.pep	190	200	210	220	230	240
	LVRIRQTGKN SGTIDNTGGTHTADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
g919	LVRIRQTGKN SGTIDNAGGTHADLSRFPI TARTTAIKGRFEGRSFLPYHTRNQINGGAL					
	190	200	210	220	230	240
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
g919	DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL					
	250	260	270	280	290	300
m919.pep	310	320	330	340	350	360
	KLGQTSMQGIKSYMQRNPQR LAEVLGQNPSYI FFFRELAYSNDGPVGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQR LAEVLGQNPSYI FFFRELAYSNDGPVGALGTPLMGEYAGA					
	310	320	330	340	350	360
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPL FVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
g919	IDRHYITLGAPL FVATAHPVTRKALNRLIM AQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420

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                430      440
m919.pep      QKTTGYVWQLLPNGMKPEYRPX
                |||||
g919          QKTTGYVWQLLPNGMKPEYRPX
                430      440

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 3073>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TCGGGCATCG CCGCCGCCAT
51 CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCGG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGGCGGCGG .CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TCGGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTTCAGG CAAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCC CTGCCTGCCG GTTTGCGGAG CGGAAAAGCC CTGTCCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACGCCCG ACCTCTCCCA ATTCCCCATC ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAACCCCG TCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTT ACCCGCAAAG
1151 CCCTCAACCG CTTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC
1201 CGGCTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGCGCAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG
1301 GTATGAAGCC CGAATACCGC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 3074; ORF 919.a>:

```

a919.pep
1  MKKYLFRAL CGIAAAILAA CQSKSIQTFP QPDTSVINGP DRPVGIPDPA
51 GTTVGGGGAV YTVVPHLSLP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SVQAKQFFER YFTPQVAGN GSLAGVTGY YEPVLKGDDR
151 RTAARFPIY GIPDDFISVP LPAGLRSGKA LVRIRQTGKN SGTIDNTGGT
201 HTADLSQFFI TARTTAIKGR FEGRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMQQNPR LAEVLGQNPS YIFFRELTGS SNDGPVGALG
351 TPLMGEYAGA VDRHYITLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

```

m919/a919 ORFs 919 and 919.a showed a 98.6% identity in 441 aa overlap

```

                10      20      30      40      50      60
m919.pep      MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
                |||||
a919          MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
                10      20      30      40      50      60

                70      80      90      100     110     120
m919.pep      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
                |||||
a919          YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHVSQAKQFFER
                70      80      90      100     110     120

```

m919.pep	130	140	150	160	170	180
	YFTPWQVAGNGSLAGTVTGYE	PVLKGD	DRRTAQARFPIYGIPDDFISV	FLPAGLRSGKA		
a919	YFTPWQVAGNGSLAGTVTGYE	PVLKGD	DRRTAQARFPIYGIPDDFISV	FLPAGLRSGKA		
m919.pep	190	200	210	220	230	240
	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
a919	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
m919.pep	250	260	270	280	290	300
	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
a919	DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
m919.pep	310	320	330	340	350	360
	KLQQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA			
a919	KLQQTSMQGIKSYMQRNPQRLAEVLGQNPSYIFFREL	AGSSNDGPV	GALGTPLMGEYAGA			
m919.pep	370	380	390	400	410	420
	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
a919	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK					
m919.pep	430	440				
	QKTTGYVWQLLPNGMKPEYRPX					
a919	QKTTGYVWQLLPNGMKPEYRPX					

121 and 121-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3075>:

m121.seq

```

1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGCGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxCAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGC GA CGCGTCTCA CACGACGGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA

```



This corresponds to the amino acid sequence <SEQ ID 3076; ORF 121>:

```

1 METQLYIGIM SGTSMDGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRQL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSQNLAPS DITALGCHGQ
101 TVRHAPENGY SIQLADLPLL Axxxxxxxxxxx xxxxxxxxxxxx
151 xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx xxxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLRSF TAQTVCDAVS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

q121.seq

1	ATGGAACAC	AGCTTTACAT	CGGCATTATG	TCGGGAACCA	GTATGGACGG
51	GGCGGATGCC	GTGCTGGTAC	GGATGGACGG	CGGCAATATG	CTGGGCGCGG
101	AAGGGCAGC	CTTTACCCCC	TACCTGACG	GGTTGCGCCG	CAAAATTGCTG
151	GATTTGCAG	ACACAGGCAC	AGACGAATG	CACCGCAGCA	GGATGTTGTC
201	GCAAGAACTC	AGCGCGCTGT	ACCGCGAAAC	CGCCGCGGAA	TGCTGTGTCGA
251	GTCAAAACCT	CGCTCCGTGC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTtac	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	CGGGAAGTga	cgcggatttt	TACCGTCgcg	cacttcCGCA
401	GCCGCGACCT	TGCTGCCGCG	GGacaAGGTG	CGCCGCTGCT	GCCGCTCTTT
451	CACGAAGCCC	TGTTCCGCGA	TGACAGGGAA	ACACGCGTGG	TACTGAACAT
501	CGCGGGGATT	GCCAAACATCA	GCGTACTCCC	CCCCGCGGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGGCCGGGC	AATATGCTGA	TGGAcgcgctg	gacgcagggca
601	cacTGGcagc	TGCTTTACGA	CAAAAacggt	gcAAAGcgcg	cacAAGGCAA
651	catatTGCcg	CAACTGCTCG	cgagcgtTGT	CGCCcaccCG	TATTTCTCAC
701	AACCCcacc	aaAAAGCACG	GGgcGCGaac	TgtttgcccT	AAattggctc
751	gaaacctAcc	ttgacgcgcg	cgaaaaaccga	tacgacgtat	tgcgcagcgt
801	ttcccgattc	accgcgcaaa	cctTttggga	cgccgtctca	CACGCAGCGT
851	CAGATGCCCG	TCAAATGTAC	ATTTGCGCG	CGGGCATCCG	CAATCTGTTT
901	TTAATGGCGG	ATTTGGCAGA	ATGTTTCGGC	ACACGCGTTT	CCCTGCACAG
951	CACCGCGGAA	CTGAACCTCG	ATCCTCAATG	GGTGGAGGCG	gccgCATTtg
1001	cgtggttgG	GGCGTGTtGG	ATTAACGCA	TTCCCGGTAG	TCCGCACAAA
1051	GCGACCGGCG	CATCCAAACC	GTGTATTCTG	GCGCGGGAT	ATTATTATTG
1101	A				

**g121.pgp**

1	METQLYIGIM	SGTSMGDGADA	VLVRMDGGKW	LGAEGHAFTP	YPDRLRRKLL
51	DLQDTGTDEL	HRSRMLSQEL	SRLYAQTAAE	LLCSQNLAPE	DITAGLCHGQ
101	TVRHAPEHYG	SIQLADLPLL	AELTRIFTVP	DFSRDLAAG	GQAGLVPFAF
151	HEALFRDDRE	TRVVNLIGGI	ANISVLPPGA	PAFGFDITGPG	NMLMDAWTQA
201	HWQLPYDKNG	AKAAQGNILP	QLLGRLLAHP	YFSQPHPKST	GRELFALNWL
251	ETYLDGGENR	YDVLRTLRSF	TAQTVWDAYS	HAAADARQMY	ICGGGIRNPV
301	LMADLAEFCF	TRVSLHSTAE	LNLDQPWVEA	AAFAWLAAACW	INRIPGSPHK
351	ATGASKPCIL	GAGSY*			

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSM	DGADAVLIRMDG	GKWLGAEGHAFT	PYPGR	LRRLDLDQ	TGADEL
g121	METQLYIGIMSGTSM	DGADAVLVRMDG	GKWLGAEGHAFT	PYPDL	RRLKLLDLDQ	TGTDEL
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSR	LYAQTAELLCSQ	NLAPSDITALG	CHGQTVRHA	PEHGYSIQ	LADLP

```

g121      HRSRMLSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL
           70      80      90      100      110      120
           130     140     150     160     170     180
m121.pep  AXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
           | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      AELTRIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRVVLNIGGIANISVLPPGA
           130     140     150     160     170     180
           190     200     210     220     230     240
m121.pep  XXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST
           : : : : : : : : : : : : : : : : : : : : : : : : : : : :
g121      PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
           190     200     210     220     230     240
           250     260     270     280     290     300
m121.pep  GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDASHAAADARQMYICDGGIRNPV
           | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
g121      GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDASHAAADARQMYICGGGIRNPV
           250     260     270     280     290     300
           310     320     330     340     350     360
m121.pep  LMADLAECFGTRVSLHSTADLNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           | | | | | | | | | | | | | | | | | | | | | | | | | |
g121      LMADLAECFGTRVSLHSTAE LNLDPOWVEAAFAWLAACWINRIPGSPHKATGASKPCIL
           310     320     330     340     350     360

m121.pep  XAGYYYYX
           | | | |
g121      GAGYYYYX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3079>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCAGCG CTTTACCCCC TACCCCGGCA GGTACGCGG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTGAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCGGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCGCTCGT CCGCGCTTTT
451 CACGAAGCCC TGTTCGCGCA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGACCGGCG AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCGG TATTTGCGAC
701 AACCCACCCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TCGGACGCT
801 TTCCCGATTG ACCGCGCAA CCGTTTTCGA CGCCGTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCC
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCAAACC GTGTATTCTG GGCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3080; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAEL LLCSQNLAPS DITALGCHGQ
101 TVRHAPEHSY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWMOA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV

```

301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AFAWMAACW VNRIPGSPHK  
 351 ATGASKPCIL GAGYYY\*

m121/a121 ORFs 121 and 121.a showed a 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
a121	METQLYIGIMSGTSMDGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPEHGYSIQLADLPPL					
a121	HRSRMLSQELSRLYAQTAELCSQNLAPSDITALGCHGQTVRHAPEHSYSVOLADLPPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	XX					
a121	AERTQIFTVGDFRSRDLAAGGQAPLVPAPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	PAFGFDTPGPNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVSHAAADARQMYICDGGIRNPV					
a121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVFVDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	LMADLAECFGTRVSLHSTAE LNLDPQWVEA AFAWMAACWVNRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYY					
a121	GAGYYYY					

Further work revealed the DNA sequence identified in *N. meningitidis* <SEQ ID 3081>:

m121-1.seq

1	ATGGAAACAC	AGCTTTACAT	CGGCATCATG	TCGGGAACCA	GCATGGACGG
51	GGCGGATGCC	GTACTGATAC	GGATGGACGG	CGGCAAATGG	CTGGGCGCGG
101	AAGGGCACGC	CTTTACCCCC	TACCCCGGCA	GGTTACGCCG	CCAATTGCTG
151	GATTTGCAGG	ACACAGGCGC	AGACGAACTG	CACCGCAGCA	GGATTTTGTC
201	GCAAGAACTC	AGCCGCCTAT	ATGCGCAAAC	CGCCGCCGAA	CTGCTGTGCA
251	GTCAAAACCT	CGCACCGTCC	GACATTACCG	CCCTCGGCTG	CCACGGGCAA
301	ACCGTCCGAC	ACGCGCCGGA	ACACGGTTAC	AGCATACAGC	TTGCCGATTT
351	GCCGCTGCTG	GCGGAACGGA	CGCGGATTTT	TACCGTCGGC	GACTTCCGCA
401	GCCGCGACCT	TGCGGCCGGC	GGACAAGGCG	CGCCACTCGT	CCCCGCCTTT
451	CACGAAGCCC	TGTTCCGCGA	CAACAGGGAA	ACACGCGCGG	TACTGAACAT
501	CGGCGGGATT	GCCAACATCA	GCGTACTCCC	CCCCGACGCA	CCCGCCTTCG
551	GCTTCGACAC	AGGCGCGGGC	AATATGCTGA	TGGACGCGTG	GACGCAGGCA
601	CACTGGCAGC	TTCTTACGA	CAAAAACGGT	GCAAAGGCGG	CACAAGGCAA
651	CATATTGCCG	CAACTGCTCG	ACAGGCTGCT	CGCCCACCCG	TATTTGCGAC
701	AACCCACCC	TAAAAGCACG	GGGCGCGAAC	TGTTTGCCCT	AAATTGGCTC
751	GAAACCTACC	TTGACGGCGG	CGAAAACCGA	TACGACGTAT	TGCGGACGCT
801	TTCCCGTTTT	ACGCGCAAA	CCGTTTGCGA	CGCCGTCTCA	CACGCAGCGG

```

851 CAGATGCCCC TCAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GGCCTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3082; ORF 121-1>:

m121-1.pep

```

1 METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPHEGY SIQLADLPLL AERTRIFTVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPPDA PAFGFDTGPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRLTSRF TAQTVCDAYS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 ORFs 121-1 and 121.ng showed a 95.6% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKWLGAEGHAFTYPGRLLRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGADAVLVRMDGGKWLGAEGHAFTYPDRLLRKLDDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
g121	HRSRILSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDNRETRAVLNIGGIANISVLPPDA					
g121	AELTRIFTVGDFRSRDLAAGGQAPLVPAFHEALFRDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121-1.pep	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRLTSRFTAQTVCDAYS HAAADARQMYICGGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRLTSRFTAQTVWDAYS HAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLDPQWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAELNLDPQWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
	XAGYYYX					
m121-1.pep						
g121	GAGYYYX					

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3083>:

a121-1.seq

```

1 ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG

```

```

51  GCGGGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCCG CAAATTGCTG
151 GATTTGCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTGAGAC ACGCGCCGGA ACACAGTTAC AGCGTACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TCGGCGCGGC GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCCGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCCGAC
701 AACCCACCC TAAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGACGGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 3084; ORF 121-1.a>:

a121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRSF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121-1/a121-1 ORFs 121-1 and 121-1.a showed a 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSMGADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
a121-1	METQLYIGIMSGTSMGADAVLIRMDGGKW LGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
	10	20	30	40	50	60
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
a121-1	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEGYSIQLADLPLL					
	70	80	90	100	110	120
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	AERTRIFTVGDFRSRDLAAGGQAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA					
a121-1	AERTQIFTVGDFRSRDLAAGGQAPLVPFHEALFRDDRETRAVLNIGGIANISVLPPDA					
	130	140	150	160	170	180
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
a121-1	PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	190	200	210	220	230	240
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLRSFTAQTVCDVASHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLRSFTAQTVFVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300
m121-1.pep	GRELFALNWLETYLDGGENRYDVLRTLRSFTAQTVCDVASHAAADARQMYICGGGIRNPV					
a121-1	GRELFALNWLETYLDGGENRYDVLRTLRSFTAQTVFVASHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

	310	320	330	340	350	360
m121-1.pep	LMADLAECFGTRVSLHSTADLNLD	PQWVEAAXFAWLAACWINRIPG	SPHKATGASKPCIL			
a121	LMADLAECFGTRVSLHSTAE	NLDLPQWVEAAAFWMAACWVNRI	PGSPHKATGASKPCIL			
	310	320	330	340	350	360

m121-1.pep	XAGYYYY
a121	GAGYYYY

## 128 and 128-1

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3085>:

m128.seq (partial)

```

1 ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCAC
1 TACGCCAGCG AAAAATGCG CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51 wGTCAAAAAA TAYTTCCCYG TCGGCAAwGT ATTAACCGA CTGTTCGCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCGTC
151 TGGCACAAG ACGTGCCTA TtkTGAATTG CAACAAAACG GCGAaMCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CCGCTACCT CGTCTGCAAC TTCGCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKa ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAT TTCGTTTGGG AATACAATGT CTTGGCACA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCGCCAAAA ACTTCCAAsG CGGCATGTT yTsGTCCGGC AAwTGGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTGCGCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCGGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCGAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 3086; ORF 128>:

m128.pep (partial)

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRIWGV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQTKL NH
//
1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTVPV
51 WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSDGTL
101 QLPTAYLVCN FAPPVGGREA RLSHDEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELXDKXL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQVQL DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT
301 GKRFWQEILA VGXSRSGAES FKAFRGREPS IDALLRHS GF DNAV*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3087>:

```

g128.seq
1  atgattgaca acgCactgct ccacttgggc gaagaaccCC GTTTaatca
51  aatccaaacc gaagACatca AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTTGCA ACGCTTTCCT CCGCACAAAA AACCAAGCTC GATCACGACC
401 TCGCGGATTT CGTATTGAGC GCGCGCGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTTAC TTTGACGATG
551 CCGCACCGCT TGCCGCGCATT CCCGAAGACG CGCTCGCCAT GTTTGCGCGC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTTC AAACGACGGC
751 AAATTCGACA ACACCGCAA CATCGACCGC ACCTCGAAA ACGCATTGAA
801 AACCGccaaa CTGCTCGGCT TAAAAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGCG GGACACGCCC GAACAGGTTT TAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCAGCCG TGGGACTTGA
1001 GTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTTCG
1101 CCAAATCAAA AAACCTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCC
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CCGCAAAACC
1201 ATCGGCGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGCGCG
1251 CGCGTGGATG AACGActaca AAGGCCGCG CGCTTTGCC GACGgcacGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AacCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGTCCGGCAT CAacggcgta GAATGGGACG CGGTGGAAT GCCCAGCCAG
1501 TTTATGGAAA ACTTCGTTTG GGAATACAAT GTATTGGCAC AAATGTCCCG
1551 CCACGAAGAA AccgGCGAGC CCTGCCGAA AGAACTCTTC GACAAAAATG
1601 TcgcCGCCAA AAACCTCCAG CGCGGTATGT TCCTCGTCCG GCAAATGGAG
1651 TCGCCCTCT TCGATATGAT GATTTACAGT GAAAGCGACG AATGCCGTCT
1701 GAAAAACTGG CAGCAGGTTT TAGACAGCGT GCGCAAAGAA GTcGCCGTCA
1751 TCCAACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCacatctTC
1801 GCcggcGGCT ATTCGCGAGG CTATTACAGC TACGCATGGG CCGAAGTCCt
1851 cAGCACCGAT GCCTACGCCG CTTTGAAGA AAGcGCGac gtcGCCGCA
1901 CAGGCAAACG CTTCTGGCAA GAAAtccttg ccgtcggcgg ctCCGCGAC
1951 gcgGCGGAAT CCTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTGCTGCGC CAaagcggtT TCGACAACGC gGcttgA

```

This corresponds to the amino acid sequence <SEQ ID 3088; ORF 128.ng>:

```

g128.pep
1  MIDNALLHLG EEPRFNQIQT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRWGVV SHLNSVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQ WDSL YAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLLQLPTAY LVCNFAPFVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRWFQ EILAVGGSRS

```

651 AAESFKAERG REPSIDALLR QSGFDNAA\*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng)  
from *N. gonorrhoeae*:

m128/g128

g128.pep	10	20	30	40	50	60
	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIAKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
g128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
g128.pep	130	140	150	160	170	180
	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130	//				
g128.pep				340	350	360
				YAGEKLREAKYAFSETEVKKYFPVGKVLG		
m128				YASEKLREAKYAFSETXVKKYFPVGXVLNG		
				10	20	30
g128.pep	370	380	390	400	410	420
	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
g128.pep	430	440	450	460	470	480
	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
g128.pep	490	500	510	520	530	540
	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKMLAAKNFQXGMF					
	160	170	180	190	200	210
g128.pep	550	560	570	580	590	600
	LVRQMEFALFDMMIYSESDCRLKNWQQVLDVSRKEVAVIQPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDEGRKNWQQVLDVSRKKVAVIQPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
g128.pep	610	620	630	640	650	660
	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAERGREGS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRGAESFKAERGREGS					
	280	290	300	310	320	330



```

          670      679
g128.pep  IDALLRQSGFDNAX
          |||||:|||||:
m128      IDALLRHSGFDNAVX
          340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3089>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTACG CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCAAGATC
401 TCGCGGATTT CGTCCTCAGC GCGCGGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 CGCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAATA CGCCGAATTG TCGCTGGCAA
851 CCAAAATGCG GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCGCG CCAAACCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GTTACGCCGG CGAAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTTCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGGCGCG
1251 CCGTGGATG AACGACTACA AAGGCCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTACCCCC GCCCGTCCGG
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAAGTGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAATCTTTC GACAAAATGC
1601 TCGCGGCCAA AAATCTCAA CGCGGAATGT TCCTCGTCCG CCAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGCTCG
1751 TCCGACCGCC CGAATACAAC CGCTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CTTTGAAGA AAGCGACGAT GTCGCGCCA
1901 CAGGCAAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTCAAAGC CTTCCGCGGA CGCGAACC GAATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3090; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51  NTVPELTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDAAAPLAGI PEDALAMFAA
201 AAQSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKFQ RGMFLVRQME

```

551 FALFDMMIYS EDDEGRKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF  
 601 AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS  
 651 AAESFKAFRG REPSIDALLR HSGFDNAA\*

m128/a128 ORFs 128 and 128.a showed a 66.0% identity in 677 aa overlap

m128.pep	10	20	30	40	50	60
	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAQAQHTGWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAQAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
m128.pep	70	80	90	100	110	120
	ERVGRIWGVVSHLNCVADTFELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
a128	ERVGRIWGVVSHLNSVTDTFELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
m128.pep	130					
	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLLENALQTAKLIGFKNYAELSLATKMDTPEQVLNFLHDL					
	250	260	270	280	290	300
m128.pep						140
						YASEKLREAKYAFSETXVKKYFPVGX
a128						ARRAKPYAEKDIAEVKAFARESGLADLQFWDLGYAGEKLREAKYAFSETEVKKYFPVGK
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQKKLYGIGFTEKTPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAFPVGGREARLSHDEILILFHETGHGLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGRKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600

m128-1.seq

This corresponds to the amino acid sequence <SEO ID 3092: ORF 128-1>:

m128-1.pep.

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTGWA  
51 NTVEPLTGIT ERVGRIGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI

```

101  GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151  ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201  AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251  KFDNTANIDR TLANALQTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301  ARRAKPYAEK DLAEVKAFAR ESINLADLQP WDLGYASEKL REAKYAFSET
351  EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401  IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFAPPVG
451  GREARLSHDE ILILFHETGH GLHLLTQVD ELGVSGINGV EWDAVELPSQ
501  FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551  FALFDMMIYS EDDEGRLLKNW QQVLDLVRK VAVIQPPEYN RFALSFGHIF
601  AGGYSAGYYS YAWAEVLSAD AYAAFEESDD VAATGKRFWQ EILAVGGSRS
651  AAESFKAFRG REPSIDALLR HSGFDNAV*

```

The following DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3093>:

g128-1.seq (partial)

```

1    ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51   AATCAAAACC GAAGACATCA AATCCGCGCT CCAAACCGCC ATCGCCGAAG
101  CGCGCGGACA AATCGCGGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151  AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201  GGGCGTCGTG TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACTGCGCG
251  CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301  GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351  CGAATTGCA ACCTTTTCCC CCGCACAAAA AACCAAGCTC GATCAGGACC
401  TGCGCGATTT CGTATTGAGC GGCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451  GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501  CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551  CCGCACCGCT TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCC
601  GCCGCGCAAA GCGAAGGCAA AACAGGTTAC AAAATCGGCT TGCAGATTCC
651  GCACTACCTT GCCGTTATCC AATACGCCGG CAACCGCGAA CTGCGCGAAC
701  AAATCTACCG CGCCTACGTT ACCCGTGCCA GCGAACTTC AAACGACGGC
751  AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGATTGAA
801  AACC GCCCAA CTGCTCGGCT TAAAAATTA CGCCGAATTG TCCTGGCAA
851  CCAAATGGC GGACACGCCG GAACAGGTTT TAAACTTCCT GCACGACCTC
901  GCCGCGCGCG CCAAACCTTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951  CTTCGCCCCG GAACACCTCG GTCTCGCCGA CCCGCGCCG TGGGACTTGA
1001 GCTACGCCCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTTCTGGCAG GCCTGTTCCG
1101 CCAAATCAAA AAATCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCCG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCCGC
1351 GGCAAAGAAG CGCGTTTAAG CCACGACGAA ATCTCACC TCTTCCACGA
1401 AACC GGCCAC GGAATGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TGCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 3094; ORF 128-1.ng>:

g128-1.pep (partial)

```

1    MIDNALLHLG EEPFRNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGTWA
51   NTVERLTGIT ERVGRINGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101  GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151  ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201  AAQSEKTYGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251  KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNLFHDL
301  ARRAKPYAEK DLAEVKAFAR EHLGLADPOP WDLGYASEKL REAKYAFSET
351  EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVWHKDVR YFELQONGKT
401  IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLQLPTAY LVCNFAPPVG
451  GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

m128-1/g128-1 ORFs 128-1 and 128-1.ng showed a 94.5% identity in 491 aa overlap

10 20 30 40 50 60

100

g128-1.pep	MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQHTGTWANTVERLTGIT
m128-1	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGTWANTVEPLTGIT
	10 20 30 40 50 60
g128-1.pep	ERVGRIWGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1	ERVGRIWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
	70 80 90 100 110 120
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSESKTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV
	190 200 210 220 230 240
g128-1.pep	TRASELSNDGKFDNTANIDRTLLENALKTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
g128-1.pep	ARRAKPYAEKDLAEVKAFAREHLGLADPQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
g128-1.pep	VLAGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHLHLLTQVD
	430 440 450 460 470 480
g128-1.pep	ELGVSGINGVK
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540

The following DNA sequence was identified in *N. meningitidis* <SEQ ID 3095>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGCG GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTGC AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CCGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACACGATC
401 TGC GCGATT CGTCTCAGC GCGCGGAAC TGCCGCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTCCG CCAAATCTC

```

```

501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCCTG TGCCGGCATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTATCC AATACGCCGA CAACCGCAA CTGCGCGAAC
701 AAATCTACCG CGCCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAAAC TAACCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACCCCG GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCGCGCGCG CCAAACCCCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCCG GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAATCAAAA AAATCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTGTACGCA CGCGAAGGCA AACGCGCGCG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTTAC CTCTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAGAAG CCCGCTTGA CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCA
1501 TTTATGGAAT ATTTCTGTTG GGAATACAAT GTCTTGGCGC AAATGTCCCG
1551 CCACGAAGAA ACCGCGGTTT CCTGCGCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAATCTCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGTCCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGC CCTTTGAAGA AAGCGACGAT GTCGCGGCCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CTTCAAAGC CTTCCGCGGA CGCGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 3096; ORF 128-1.a>:

a128-1.pep

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51 NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GDIELYNRF KTIKNSPEFD TLSHAQTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTA LLGFKNYAE SLATKMDATP EQVLNLFHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLPQ WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTQLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV EWDDELPSQ
501 FMENFWEYN VLAQMSAHEE TGVPLPKELF DKMLAANKNFQ RGMFLVRQME
551 FALFDMMIYS EDEGRLLKNW QQVLDVSRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAFAEESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*

```

m128-1/a128-1 ORFs 128-1 and 128-1.a showed a 97.8% identity in 677 aa overlap

```

          10      20      30      40      50      60
a128-1.pep MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          |||
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
a128-1.pep ERVGRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m128-1      ERVGRWGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

          130     140     150     160     170     180

```

a128-1.pep	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY
	130 140 150 160 170 180
a128-1.pep	190 200 210 220 230 240
	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLRREQIYRAYV
m128-1	FDDAAPLAGIPEDALAMFAAAQSEKGTGYKIGLQIPHYLAVIQYADNRKLRREQIYRAYV
	190 200 210 220 230 240
a128-1.pep	250 260 270 280 290 300
	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
m128-1	TRASELSDDGKFDNTANIDRTLLENALQTAKLLGFKNYAELSLATKMADTPEQVLNFLHDL
	250 260 270 280 290 300
a128-1.pep	310 320 330 340 350 360
	ARRAKPYAEKDLAEVKAFARESLGLADLQPWDLGYAGEKLREAKYAFSETEVKKYFPVGK
m128-1	ARRAKPYAEKDLAEVKAFARESLNLADLQPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	370 380 390 400 410 420
	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQQNETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	430 440 450 460 470 480
	NDYKGRRRFSDGTLQLPTAYLVCNFTFPVGGKEARLSHDEILTLFHETGHGLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAFPVGGREARLSHDEILILFHETGHGLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	490 500 510 520 530 540
	ELGVSGINGVEWDAVELPSQFMENFWWEYNVLAQMSAHEETGVPLPKE LFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFWWEYNVLAQMSAHEETGVPLPKE LFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	550 560 570 580 590 600
	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQVLDVSRKEVAVVRPPE YNRFANSFGHIF
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRKKNWQVLDVSRKKVAVIQPPE YNRFALSFGHIF
	550 560 570 580 590 600
a128-1.pep	610 620 630 640 650 660
	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGS RSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGS RSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	670 679
	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670

```

1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GGCAGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAT AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCCCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCCGAcA GCCGcYTCAA
351 GGCCGGCGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAAACCA TCAAACCGA AAAACTCTCC ACACCGTTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 3098; ORF 206>:

m206.pep..

```

1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRT
101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3099>:

g206.seq

```

1  atgttttccc cgcacaaaac ctttttcctc tgtctcggcg cactgctcct
51  cgcctcatgc ggcacgacct ccggcaaaca ccgccaaccg aaacccaaac
101 agacagtccg gcaaatccaa gccgtccgca tcagccacat cggcgcgaca
151 caaggctcgc aggaactcat gctccacagc ctcggactca tcggcacgcc
201 ctacaaatgg ggcggcagca gcaccgcaac cggcttcgac tgcagcggca
251 tgattcaatt ggttacaaa aacgccctca acgtcaagct gccgcgcacc
301 gcccgcgaca tggcggcggc aagccgcaaa atccccgaca gccgctcaa
351 ggccggcgac atcgtattct tcaacaccgg cggcgcacac cgctactcac
401 acgtcggact ctacatcggc aacggcgaat tcatccatgc ccccggcagc
451 ggcaaaaacca taaaaccga aaaactctcc acaccgtttt acgccaaaaa
501 ctaccttggg ggcatacgt tttttacaga atga

```

This corresponds to the amino acid sequence <SEQ ID 3100; ORF 206.ng>:

g206.pep

```

1  MFSPDKTLFL CLGALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIGRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPRT
101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*

```

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC					
g206	MFSPDKTLFLCLGALLLASC					
	10	20	30	40	50	60
	CGTTS					
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSSTATGFD					
g206	LGLIGTPYKWGGSSSTATGFD					
	70	80	90	100	110	120
	CSGMIQFVYKNALNVKLPRT					
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLS					
g206	IVFFNTGGAHRYSHVGLYIGNGEFIHAPSGKTIKTEKLS					



130 140 150 160 170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3101>:

```
a206.seq
1  ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT
51  CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC
101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA
151 CAAGGCTCGC AGGAACTCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC
201 CTACAAATGG GCGGCAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA
251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC
301 GCGCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCCGACA GCCGCGCTTAA
351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC
401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC
451 GGCAAACCA TCAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA
501 CTACCTCGGC GCACATACTT TCTTACAGA ATGA
```

This corresponds to the amino acid sequence <SEQ ID 3102; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR
101 ARDMAAASRK IPDSRLKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TPFYAKNYLG AHTFFTE*
```

m206/a206 ORFs 206 and 206.a showed a 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKT IKTEKLS TPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKT IKTEKLS TPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

287

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3103>:

```
m287.seq
1  ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTTC CCCTTTCAGC
51  CTGCGGGGGC GCGGGTGGCG GATCGCCCGA TGTCAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTCTCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCGC CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CGGTTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAC AGCGGATAAT CCCAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CGGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCGG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGGCA GCGGGGCAA ATGCCGGCAA
501 TACGGCTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTGAGATCC CATCCCCGCG TCAAACCCTG CACCTGCGAA TGGCGGTAGC
```

```

601 AATTTTGAA GGGTTGATT GGCTAATGGC GTTTGTATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGA TGAAGAAGTA CAGCTAAAT CAGAATTTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 GTTCGGTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTCAGC CTGACGGGGC
1001 ATTCCGGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCGG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAAG
1201 TTGCGCGCAA AAGTCGATTT CGGCAGCAAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGGAT GATTTCGATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAAACGG CTTTAAGGGG ACTTGGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGAAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCGG GAAAATACAG
1401 CTATCGCCC ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTGCGCGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 3104; ORF 287>:

m287.pep

```

1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMAANA
151 DGMQGGDDPSA GGQNAAGTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFRVRLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRSLPAE MPLIPVNOAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPFGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTKQKFK AALDNGGFKG TWTENGSGDV
451 SGKFGYPAGE EVAGKYSYRP TDAEKGFGV FAGKKEQD*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3105>:

g287.seq

```

1 atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51 ctgtgggggc ggcgggtgcg gatcgcccga tgtcaagtcg gcggacacgc
101 cgtcaaaacc ggccgcccc gttgttgctg aaaatgccgg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgcgcgaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttccgacaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaa atgccgcgca
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaacctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 attgaccac tgtaaaggcg attcttgtaa tgggtgataat ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaacc acctactcgt tctgcacggt cgaggaggtc gttccgggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgctga ttgtggatgg
801 ggaagcggtc agcctgacgg ggcattccgg caatatcttc gcgccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcgatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttggttg
951 cacggccgtg tacaacggcg aagtgtgca tttccatag gaaaacggcc
1001 gtccgtaccc gtccggaggc aggtttgccg caaaagtcga ttccggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgcca tcgatgaaa cggctttaag gggacttggg
1151 cggaatgg cggggggat gttccggaa ggttttacgg ccggcgccg
1201 gaggaagtgg cggaataa cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 3106; ORF 287.ng>:

g287.pep

```

1 MFKRSVIAMA CIFPLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV

```

```

51 LPKEKKDEEA AGGAPQADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAQND MPQNAESAN QTGNNQPAGS SDSAPASNPA PANGGSDFGFR
151 TNVGNVSVVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARSRRSLPA
251 EIPLIPVNQA DTLIVDGEAV SLTGHSNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRFPYPSGG RFAAKVDFGS
351 KSVDDGIIDSG DDLHMGTKF KAAIDGNGFK GTWTENGGGD VSGRFYGPAG
401 EEVAGKYSYR PTDAEKGFGF VFAGKKDRD*

```

m287/g287 ORFs 287 and 287.ng showed a 70.1% identity in 499 aa overlap

```

m287.pep      10      20      30      40      49
               MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSE-----KETEA
g287          10      20      30      40      50      60
               MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLFPKEKKDEEA

m287.pep      50      60      70      80      90      100      109
               KEDAPQAGSQGQAPSQAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
g287          70      80      90      100      110
               AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQNMPQNAA--

m287.pep      110     120     130     140     150     160     169
               DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQDDPSAGGQNAGNTA
g287          -----

m287.pep      170     180     190     200     210     220     229
               AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFRVLDLANGVLIDGPSQNTLTHCKGDS
g287          120     130     140     150     160     170
               -ESANQTGNNQPAGSSDSAPASNPAPANGGSDFGRTNVGNVSVVIDGPSQNTLTHCKGDS

m287.pep      230     240     250     260     270     280     289
               CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP
g287          180     190     200     210     220     230
               CNGDNLLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVKKDGTNKYIIFYTD

m287.pep      290     300     310     320     330     340     349
               KPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT
g287          240     250     260     270     280     290
               KPPT-----RSARSRRSLPAEIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLT

m287.pep      350     360     370     380     390     400     409
               YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGS
g287          300     310     320     330     340     350
               YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFPAKVDGFS

m287.pep      410     420     430     440     450     460     469
               KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGGSDVSGKFYGPAGEEVAGKYSYR
g287          360     370     380     390     400     410
               KSVDDGIIDSGDDLHMGTKFKAAIDGNGFKGTWTENGGSDVSGRFYGPAGEEVAGKYSYR

m287.pep      470     480     489
               PTDAEKGFGFVFAGKKEQDX

```

g287

|||||:|  
PTDAEKGFGVFAGKKDRDX  
420 430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3107>:

a287.seq

```

1 ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51 CTGTGGGGGC GGCGGTGGCG GATCGCCGA TGTAAAGTCG GCGGACACGC
101 TGTCAAAACC TGCCGCCCTT GTTGTACTG AAGATGTCGG GGAAGAGGTG
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CCGTCAAGAT ATGGCGGCAG
251 TTTCGGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATCCC
301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGGCG ACAACCGGCA
451 AACCAACCGG ATATGGCAA TCGGCGGAC GGAATGCAGG GGGACGATCC
501 GTCGGCAGGG GAAATGCCG GCAATACGGC AGATCAAGCT GCAAATCAAG
551 CTGAAACAA TCAAGTCGGC GGCTCTCAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAAGT ATGCGATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTG AAAAATTAAG TGATGAAGAA AAAATTAATA AATATAAAAA
801 AGACGAGCAA CGAGAGAATT TTGTGGTTT GGTGCTGAC AGGGTAGAAA
851 AGAATGGAAC TAACAAATAT GTCATCATT ATAAAGACAA GTCCGCTTCA
901 TCTTCATCTG CCGGATTCAG GCGTCTGCA CCGTCGAGGC GGTGCGTTCC
951 GGCCGAGATG CCGCTGATTC CCGTCAATCA GCGCGATACG CTGATTGTCG
1001 ATGGGGAAGC GGTACGCTG ACGGGGCAAT CCGGCAATAT CTTCGCGCCC
1051 GAAGGGAATT ACCGGTATCT GACTTACGGG GCGGAAAAAT TGTCCGCGCG
1101 ATCGTATGCC CTCAGTGTGC AAGGCGAACC GGCAAAAGGC GAAATGCTTG
1151 CGGGCACGGC CGTGACAAAC GGCGAAGTGC TGCATTTCCTA TATGAAAAC
1201 GGCCGTCCGT CCGGTCCCG AGGCAGGTTT GCCGCAAAAG TCGATTTCGG
1251 GACCAAATCT GTGGACGGCA TTATCGACAG CGGCGATGAT TTGCATATGG
1301 GTACGCAAAA ATTCAAAGCC GTTATCGATG GAAACGGCTT TAAGGGGACT
1351 TGGACGAAA ATGGCGGCGG GGATGTTTCC GGAAGGTTT ACGGCCCGGC
1401 CGGCGAAGAA GTGGCGGGA AATACAGCTA TCGCCCGACA GATGCGGAAA
1451 AGGGCGGATT CCGCGTGTTC GCCGCAAAA AAGAGCAGGA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 3108; ORF 287.a>:

a287.pep

```

1 MFKRSVIAMA CIVALSAACGG GGGGSPDVKS ADTLSKPAAP VVTEDVGEEV
51 LPKEKKDEEA VSGAPQADTQ DATAGKGGQD MAAVSAENTG NGGAATTDNP
101 ENKDEGPOND MPQNAADTDS STPNHTPAPN MPTRDMGNOA PDAGESAQPA
151 NOPDMANAD GMQDDPSAG ENAGNTADQA ANQAEENQVG GSQNPASSTN
201 PNATNGGSDF GRINVANGIK LDSGSENVTL THCKDKVCDR DFLDEEAPPK
251 SEFEKLSDEE KINKYKKDEQ RENFVGLVAD RVEKNGTNKY VIIYKDKSAS
301 SSSARFRRSA RSRRSLPAEM PLIPVNQADT LIVDGEAVSL TGHSGNIFAP
351 EGNRYRLTYG AEKLSGGSYA LSVQGEPAKG EMLAGTAVYN GEVLHFHMFEN
401 GRPSPSGGRF AAKVDFGSKS VDGIIIDSGD LHMGTQKFKF VIDGNGFKGT
451 WTENGGGDVS GRFYGPAGEE VAGKYSYRPT DAEKGGFGVF AGKKEQD*

```

m287/a287 ORFs 287 and 287.a showed a 77.2% identity in 501 aa overlap

```

10 20 30 40 49
m287.pep MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETE
|||||:|
a287 MFKRSVIAMACIVALSAACGGGGGGSPDVKSADTLSKPAAPVVTEDVGEEVLPKEKKDEEA
10 20 30 40 50 60

50 60 70 80 90 100 109
m287.pep KEDAPQAGSQGQAPSQAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNMPQNAAGT
||||:| |:::||||| |||||:|:|:|:| |||||
a287 VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATTDNPNENKDEGPONDMPQNAADT
70 80 90 100 110

```

	110	120	130	140	150	160	169
m287.pep	DSSTPNHTPDNMLAGNMENQATDAGESSQPANQPDMANAADGMQGDPSAGGQNAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADGMQGDPSAG-ENAGNTA						
	120	130	140	150	160	170	
	170	180	190	200	210	220	229
m287.pep	AQQANQAGNNQAAGSSDPIPASNPAPANGGSNFGVRDLANGVLIDGPSQINITLTHCKGDS						
a287	DQAANQAENNOVGGSQNPASSTNPNATNGGSDFGRINVANGIKLDSGSENVTLTHCKDKV						
	180	190	200	210	220	230	
	230	240	250	260	270	280	289
m287.pep	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVIYKD						
	240	250	260	270	280	290	
	290	300	310	320	330	340	
m287.pep	KP--TSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
a287	KSASSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRY						
	300	310	320	330	340	350	
	350	360	370	380	390	400	
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRFPYPTRGRFAAKVDF						
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF						
	360	370	380	390	400	410	
	410	420	430	440	450	460	
m287.pep	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS						
a287	GSKSVDGIIDSGDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFGYPAGEEVAGKYS						
	420	430	440	450	460	470	
	470	480	489				
m287.pep	YRPTDAEKGFGVFAGKKEQDX						
a287	YRPTDAEKGFGVFAGKKEQDX						
	480	490					

406

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3109>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGCGGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGTGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA

```

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701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGGAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3110; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGP *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3111>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTGCA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGCGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCGCGG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3112; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTSLSTLNA PALSRQSDG SGSSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACG	TLTGIPSHGGGKRFVEQEL	VAASARA	AVK	DMDLQALHGR	
m406	MQARLLIPILFSVFILSACG	TLTGIPSHGGGKRFVEQEL	VAASARA	AVK	DMDLQALHGR	

110

	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGGLTG					
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMPYKVSCKGKPTGLMVDPSDIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMPYKVSCKGKPTGLMVDPSDIRPYGNHTGNSAPSVEADN					
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGQPX					
m406	SHEGYGYSDEVVRQHRQGQPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3113>:

```

a406.seq
1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGGAC GACATAGACA
951 AGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 3114; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAQV
51  DMDLQALHGR KVALYIATMG DQSGSGLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRSETT AETTSGGLTG LTTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRNTNKKLL IKPKTNAFEA

```

251 AYKENYALWM GPYKVSKEGK PTEGLMVDFS DIQPYGNHMG NSAPSVEADN  
 301 SHEGYGYSDE AVRRHRQGQP \*

m406/a406 ORFs 406 and 406.a showed a 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
a406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m406.pep	LTTSLSLTNAPALSRTQSDGSGSKSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTTSLSLTNAPALSRTQSDGSGSKSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m406.pep	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVSANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m406.pep	IKPKTNAFEAAYKENYALWMGPYKVSKEGK PTEGLMVDFS DIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAYKENYALWMGPYKVSKEGK PTEGLMVDFS DIQPYGNHMGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
m406.pep	SHEGYGYSDEVVRQHRQGQPX					
a406	SHEGYGYSDEAVRRHRQGQPX					
	310	320				

## EXAMPLE 2

### Expression of ORF 919

The primer described in Table 1 for ORF 919 was used to locate and clone ORF 919. The predicted gene 919 was cloned in pET vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 919-His fusion protein purification. Mice were immunized with the purified 919-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; PP, purified protein, TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm



that 919 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 919 are provided in Figure 10. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 3

#### Expression of ORF 279

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 11. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 4

#### Expression of ORF 576 and 576-1

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera

were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).. These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 576 are provided in Figure 12. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

#### EXAMPLE 5

##### Expression of ORF 519 and 519-1

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. The predicted gene 519 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 13. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 6

Expression of ORF 121 and 121-1

The primer described in Table 1 for ORF 121 was used to locate and clone ORF 121. The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 121 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 121 are provided in Figure 14. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 121 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 7

Expression of ORF 128 and 128-1

The primer described in Table 1 for ORF 128 was used to locate and clone ORF 128. The predicted gene *128* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 128 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 128 are provided in Figure 15. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J.*

*Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 128 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 8

### Expression of ORF 206

The primer described in Table 1 for ORF 206 was used to locate and clone ORF 206. The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worthnoting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a recative band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C is shown the FACS analysis, in panel D the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 206 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 16. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 206 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 9

Expression of ORF 287

The primer described in Table 1 for ORF 287 was used to locate and clone ORF 287. The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A). These experiments confirm that 287 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 287 are provided in Figure 17. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 287 and the amino acid sequence encoded thereby is provided in Example 1.

## EXAMPLE 10

Expression of ORF 406

The primer described in Table 1 for ORF 406 was used to locate and clone ORF 406. The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B). These experiments confirm that 406 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 406 are provided in Figure 18. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 406 and the amino acid sequence encoded thereby is provided in Example 1.

### EXAMPLE 11

Table 2 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 225 among different strains.

**Table 2**

225 gene variability: List of used <i>Neisseria</i> strains		
Identification Strains number		Source / reference
Group B		
zo01_225	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo02_225	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zo03_225	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zo04_225	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zo05_225	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zo06_225	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zo07_225	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zo08_225	528	R. Moxon / Seiler <i>et al.</i> , 1996
zo09_225	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zo10_225	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zo11_225	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zo12_225	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zo13_225	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zo14_225	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zo15_225	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zo16_225	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zo17_225	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zo18_225	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zo19_225	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zo20_225	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zo21_225	MC58	R. Moxon
zo96_225	2996	Our collection
Group A		
zo22_225	205900	R. Moxon
zo23_225	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998
Group C		
zo24_225	90/18311	R. Moxon
zo25_225	93/4286	R. Moxon

**Others**

zo26\_225 A22 (group W) R. Moxon / Maiden *et al.*, 1998  
 zo27\_225 E26 (group X) R. Moxon / Maiden *et al.*, 1998  
 zo28\_225 860800 (group Y) R. Moxon / Maiden *et al.*, 1998  
 zo29\_225 E32 (group Z) R. Moxon / Maiden *et al.*, 1998

**Gonococcus**

zo32\_225 Ng F62 R. Moxon / Maiden *et al.*, 1998  
 zo33\_225 Ng SN4 R. Moxon

fa1090 FA1090 R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

>FA1090 <SEQ ID 3115>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS  
 GFMQHIFKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
 RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z2491 <SEQ ID 3116>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRVPARRAGNA  
 DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF  
 MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
 IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z001\_225 <SEQ ID 3117>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z002\_225 <SEQ ID 3118>  
 MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z003\_225 <SEQ ID 3119>  
 MDSFFKPAVWAVLWLMFAVRLADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDSRFLN\*

Z004\_225 &lt;SEQ ID 3120&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z005\_225 &lt;SEQ ID 3121&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z006\_225 &lt;SEQ ID 3122&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z007\_225 &lt;SEQ ID 3123&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z008\_225 &lt;SEQ ID 3124&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGSAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z009\_225 &lt;SEQ ID 3125&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z010\_225 &lt;SEQ ID 3126&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z011\_225 &lt;SEQ ID 3127&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF  
MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDSRFLN\*

Z012\_225 &lt;SEQ ID 3128&gt;

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDSRFLN\*

Z013\_225 &lt;SEQ ID 3129&gt;



MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z014\_225 <SEQ ID 3130>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z015\_225 <SEQ ID 3131>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIKFRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z016\_225 <SEQ ID 3132>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z017\_225 <SEQ ID 3133>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z018\_225 <SEQ ID 3134>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z019\_225 <SEQ ID 3135>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z020\_225 <SEQ ID 3136>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLNEQPVLVFNRAFPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF  
MQHIKFRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF  
IAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDP SRFLN\*

Z021\_225 <SEQ ID 3137>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKNDP SRFLN\*

Z022\_225 <SEQ ID 3138>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLVFNRAFPARRAG  
NADELIGSAMGLNEQPVLVFNRAFPARRAGNADELIGSAMGLNEQPVLVFNRAFPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKFRAMGINLPRTSAEQARMGTPVAR

SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z023\_225 <SEQ ID 3139>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z024\_225 <SEQ ID 3140>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z025\_225 <SEQ ID 3141>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z026\_225 <SEQ ID 3142>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSISTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z027\_225 <SEQ ID 3143>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z028\_225 <SEQ ID 3144>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z029\_225 <SEQ ID 3145>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIKRAMGINLPRTSAEQARMGTPVAR  
SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
VKKN DPSRFLN\*

Z032\_225 <SEQ ID 3146>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN\*

Z033\_225 <SEQ ID 3147>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG  
NADELIGSAMGLNEQPVLPVNRAPARRAGNADELIGSAMGLLGIAYRYGGTSVSTGFDCS  
GFMQHIKRAMGINLPRTSAEQARMGAPVARSELQPGDMVFFRTLGGSRISHVGLYIGNN  
RFIHAPRTGKNIEITSLSHKYWSGKYAFARRVKKN DPSRFLN\*

Z096\_225 <SEQ ID 3148>

MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG  
 NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA  
 DELIGNAMGLLGIAYRYGGTSISTGFDSCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR  
 SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR  
 VKKNDPSRFLN\*

Figure 19 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 225, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 12

Table 3 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 235 among different strains.

**Table 3**

#### **235 gene variability: List of used *Neisseria* strains**

<b>Identification Strains number</b>	<b>Reference</b>
<b>Group B</b>	
gnmzq01 NG6/88	Seiler <i>et al.</i> , 1996
gnmzq02 BZ198	Seiler <i>et al.</i> , 1996
gnmzq03 NG3/88	Seiler <i>et al.</i> , 1996
gnmzq04 1000	Seiler <i>et al.</i> , 1996
gnmzq05 1000	Seiler <i>et al.</i> , 1996
gnmzq07 BZ169	Seiler <i>et al.</i> , 1996
gnmzq08 528	Seiler <i>et al.</i> , 1996
gnmzq09 NGP165	Seiler <i>et al.</i> , 1996
gnmzq10 BZ133	Seiler <i>et al.</i> , 1996
gnmzq11 NGE31	Seiler <i>et al.</i> , 1996
gnmzq13 NGE28	Seiler <i>et al.</i> , 1996
gnmzq14 NGH38	Seiler <i>et al.</i> , 1996
gnmzq15 SWZ107	Seiler <i>et al.</i> , 1996
gnmzq16 NGH15	Seiler <i>et al.</i> , 1996
gnmzq17 NGH36	Seiler <i>et al.</i> , 1996
gnmzq18 BZ232	Seiler <i>et al.</i> , 1996
gnmzq19 BZ83	Seiler <i>et al.</i> , 1996
gnmzq21 MC58	Virji <i>et al.</i> , 1992
<b>Group A</b>	
gnmzq22 205900	Our collection

gnmzq23 F6124 Our collection  
 z2491 Z2491 Maiden *et al.*, 1998

### Group C

gnmzq24 90/18311 Our collection  
 gnmzq25 93/4286 Our collection

### Others

gnmzq26 A22 (group W) Maiden *et al.*, 1998  
 gnmzq27 E26 (group X) Maiden *et al.*, 1998  
 gnmzq28 860800 (group Y) Maiden *et al.*, 1998  
 gnmzq29 E32 (group Z) Maiden *et al.*, 1998  
 gnmzq31 *N. lactamica* Our collection

### Gonococcus

gnmzq32 Ng F62 Maiden *et al.*, 1998  
 gnmzq33 Ng SN4 Our collection

fa1090 FA1090 Dempsey *et al.* 1991

### References:

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.  
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279  
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

FA1090 <SEQ ID 3149>

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

GNMZQ01 <SEQ ID 3150>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANNL  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ02 <SEQ ID 3151>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
 YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ03 <SEQ ID 3152>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST

AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ04 <SEQ ID 3153>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ05 <SEQ ID 3154>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ07 <SEQ ID 3155>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ08 <SEQ ID 3156>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ09 <SEQ ID 3157>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ10 <SEQ ID 3158>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ11 <SEQ ID 3159>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ13 <SEQ ID 3160>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ14 <SEQ ID 3161>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ15 <SEQ ID 3162>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILD SVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ16 <SEQ ID 3163>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ17 <SEQ ID 3164>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ18 <SEQ ID 3165>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ19 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ21 <SEQ ID 3166>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ22 <SEQ ID 3167>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ23 <SEQ ID 3168>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ24 <SEQ ID 3169>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ25 <SEQ ID 3170>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ26 <SEQ ID 3171>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ27 <SEQ ID 3172>

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS  
YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT  
DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ28 &lt;SEQ ID 3173&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ29 &lt;SEQ ID 3174&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ31 &lt;SEQ ID 3175&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTA FKESKPASILVVPPLNESPDVNGTWGMLAST  
 AEPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITITEYGTS  
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKTAAAYDLLSPYSHNGILKGPRFVEEQPK\*

GNMZQ32 &lt;SEQ ID 3176&gt;

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

GNMZQ33 &lt;SEQ ID 3177&gt;

MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST  
 AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVGAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPK\*

Z2491 &lt;SEQ ID 3178&gt;

MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST  
 AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDVLYITVTEYGTS  
 YQILDsvTTVSAKARLVDSRNGKELWSGSASIREGSNNNSGLLGALVSAVVNQIANSLT  
 DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPK\*

Figure 20 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 235, further confirming its utility as an antigen for both vaccines and diagnostics.

### EXAMPLE 13

Table 4 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 287 among different strains.

Table 4

#### 287 gene variability: List of used *Neisseria* strains

Identification Strains number	Reference
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**Group B**

287_2	BZ198	Seiler <i>et al.</i> , 1996
287_9	NGP165	Seiler <i>et al.</i> , 1996
287_14	NGH38	Seiler <i>et al.</i> , 1996
287_21	MC58	Virji <i>et al.</i> , 1992

**Group A**

z2491	Z2491	Maiden <i>et al.</i> , 1998
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**Gonococcus**

fa1090	FA1090	Dempsey <i>et al.</i> 1991
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**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden R. *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.  
 Virji M. *et al.*, Mol. Microbiol., 1992, 6:1271-1279  
 Dempsey J.F. *et al.*, J. Bacteriol., 1991, 173:5476-5486

The amino acid sequences for each listed strain are as follows:

## 287\_14 &lt;SEQ ID 3179&gt;

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG  
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADTDSLTPNHTPAS  
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ  
 TAGSQNPASSTNPSATNSGGDFGRNTVGNSSVVIDGPSQNTLTHCKGDCSCGNNFLDEEV  
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTS FAR  
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP  
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGII  
 DSGDGLHMTQKFKAAIDGNGFKGTWTENGGDVSCKFYGPAGEEVAGKYSYRPTDAEKG  
 GFGVFAGKKEQD\*

## 287\_2 &lt;SEQ ID 3180&gt;

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG  
 QGAPSAQGGQDMAAVSEENTGNGGAAATDKPKNEDEGAQNDMPQNAADTDSLTPNHTPAS  
 NMPAGNMENQAPDAGESEQPANQPDMAANTADGMQGGDDPSAGGENAGNTAAQGTNQAENNQ  
 TAGSQNPASSTNPSATNSGGDFGRNTVGNSSVVIDGPSQNTLTHCKGDCSCGNNFLDEEV  
 QLKSEFEKLSADAKISNYKKDGKNDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTS FAR  
 FRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEGNYRYLTYGAEKLP  
 GGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPSRGRFAAKVDFGSKSVDGII  
 DSGDGLHMTQKFKAAIDGNGFKGTWTENGGDVSCKFYGPAGEEVAGKYSYRPTDAEKG  
 GFGVFAGKKEQD\*

## 287\_21. &lt;SEQ ID 3181&gt;

MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVVSEKETEAKEDAPQAGSQG  
 QGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQNDMPQNAAGTDSSTPNHTPDP  
 NMLAGNMENQATDAGESSQPANQPDMAANTADGMQGGDDPSAGGQNAAGNTAAQGANQAGNNQ  
 AAGSSDPIPASNPAPANGGSNFRVLDLNGVLIDGPSQNTLTHCKGDCSCGNNFLDEEV  
 QLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYIIIFYKPKPTS FARFRRS



ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY  
 ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD  
 DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGV  
 FAGKKEQD\*

287\_9 <SEQ ID 3182>

MFKRSVIAMACIVALSACGGGGGSPDVKSADTLSPKPAAPVVTEDVGEEVLPKEKKDEEA  
 VSGAPQADTQDATAGKGGQDMAAVSAENTGNNGAATTNPNKDEGPQNDMPQNAADTDS  
 STPNHTPAPNMPTRDMGNQAPDAGESAQPANQPDMANAADMGGDDPSAGENAGNTADQA  
 ANQAEENNQVGGSQNPASSTNPNATNGGSDFGRIINVANGIKLDSGSENVTLTHCKDKVCDR  
 DFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNYVITYKDKSAS  
 SSSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYG  
 AEKLSGGSYALSQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDFGSKS  
 VDGIIDSGDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPT  
 DAEKGGFGVFAGKKEQD\*

FA1090 <SEQ ID 3183>

MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEVLPKEKKDEEA  
 AGGAPQADTQDATAGEGSDMAAVSAENTGNNGAATTNPNKEDAGAQNMPQNAAESAN  
 QTGNNQAPAGSSSAPASNPAPANGGSDFGRTNVGNSVVDGFSQNTLTHCKGDSNGDN  
 LLDEEAPSKSEFEKLSDEEKIKRYKKDEQRENFVGLVADRVEKNGTNYVITYKDKPPT  
 SARRRSLPAEIPLIPIVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGS  
 YALRVQGEPAKGEMLVGTAVYNGEVLHFHMENGRPYPSGGRFAAKVDFGSKSVVDGIIDSG  
 DDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYSYRPTDAEKGGFG  
 VFAGKKDRD\*

Z2491 <SEQ ID 3184>

MFKRSVIAMACIFALSACGGGGGSPDVKSADTLSPKPAAPVSEKETEAKEDAPQAGSQG  
 QGAPSAQGSQDMAAVSEENTGNNGAVTADNPKNEDEVAQNMPQNAAGTDSSTPNHTPDP  
 NMLAGNMENQATDAGESSQPANQPDMANAADMGGDDPSAGGQAGNTAAQGANQAGNNQ  
 AAGSSDPIPASNPAPANGGNSFRVLDLAVGLIDGFSQNTLTHCKGDSGNNFLDEEV  
 QLKSEFEKLSADKISNYKKDGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFARFRRS  
 ARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYLTYGAEKLPGGSY  
 ALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDFGSKSVVDGIIDSGD  
 DLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGV  
 FAGKKEQD\*

Figure 21 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 287, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 14

Table 5 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 519 among different strains.

Table 5

#### 519 gene variability: List of used *Neisseria* strains

Identification Strains	Source / reference
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**number****Group B**

zv01_519	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv02_519	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zv03_519ass	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zv04_519	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zv05_519	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zv06_519ass	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zv07_519	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zv11_519	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zv12_519	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zv18_519	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zv19_519	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zv20_519ass	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zv21_519ass	MC58	R. Moxon
zv96_519	2996	Our collection

**Group A**

zv22_519ass	205900	R. Moxon
z2491_519	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

**Others**

zv26_519	A22	(group W) R. Moxon / Maiden <i>et al.</i> , 1998
zv27_519	E26	(group X) R. Moxon / Maiden <i>et al.</i> , 1998
zv28_519	860800	(group Y) R. Moxon / Maiden <i>et al.</i> , 1998
zv29_519ass	E32	(group Z) R. Moxon / Maiden <i>et al.</i> , 1998

**Gonococcus**

zv32_519	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
fa1090_519	FA1090	R. Moxon

**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
Maiden *et al.*, Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

FA1090\_519 <SEQ ID 3185>  
MEFFII~~LL~~AAVAVFGFKSFVVI~~PQ~~QEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTV~~DI~~YFQVTDPKLASYGSSNYIMAITQLAQTTLR~~SV~~IG  
RMELDKTFFERDEINSTVVSALDEAAGAWGV~~KL~~RYEIKDLVPPQEILRAMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANA~~E~~AI~~R~~QIAAALQTQGGADAVNLKIAEQYVA~~AF~~NNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

Z2491\_519 &lt;SEQ ID 3186&gt;

MEFFIILLAAVVVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV01\_519 &lt;SEQ ID 3187&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV02\_519 &lt;SEQ ID 3188&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV03\_519 &lt;SEQ ID 3189&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV04\_519 &lt;SEQ ID 3190&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV05\_519 &lt;SEQ ID 3191&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV06\_519ASS &lt;SEQ ID 3192&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERK  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV07\_519 &lt;SEQ ID 3193&gt;

MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV11\_519 &lt;SEQ ID 3194&gt;

MEFFIILLAAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV12\_519 &lt;SEQ ID 3195&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV18\_519 &lt;SEQ ID 3196&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV19\_519 &lt;SEQ ID 3197&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV20\_519ASS &lt;SEQ ID 3198&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSM  
ISAGMKIIDSSKTAK\*

ZV21\_519ASS &lt;SEQ ID 3199&gt;

MEFFIILLVAVAVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV22\_519ASS &lt;SEQ ID 3200&gt;

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV26\_519 &lt;SEQ ID 3201&gt;

MEFFIILLAAVVVFGFKSFVVI PQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTD PKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR  
LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV27\_519 &lt;SEQ ID 3202&gt;

MEFFI ILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV28\_519 <SEQ ID 3203>

MEFFI ILLA AVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV29\_519ASS <SEQ ID 3204>

MEFFI ILLA AVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV32\_519 <SEQ ID 3205>

MEFFI ILLA AVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

ZV96\_519 <SEQ ID 3206>

MEFFI ILLA AVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL  
KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG  
RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE  
KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQA AVNASNAEKIARINRAKGEAESLR  
LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL  
ISAGMKIIDSSKTAK\*

Figure 22 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 519, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 15

Table 6 lists several *Neisseria* strains which were used to assess the conservation of the sequence of ORF 919 among different strains.

**Table 6**

#### **919 gene variability: List of used *Neisseria* strains**

Identification Strains	Source / reference
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**number****Group B**

zm01	NG6/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm02	BZ198	R. Moxon / Seiler <i>et al.</i> , 1996
zm03	NG3/88	R. Moxon / Seiler <i>et al.</i> , 1996
zm04	297-0	R. Moxon / Seiler <i>et al.</i> , 1996
zm05	1000	R. Moxon / Seiler <i>et al.</i> , 1996
zm06	BZ147	R. Moxon / Seiler <i>et al.</i> , 1996
zm07	BZ169	R. Moxon / Seiler <i>et al.</i> , 1996
zm08n	528	R. Moxon / Seiler <i>et al.</i> , 1996
zm09	NGP165	R. Moxon / Seiler <i>et al.</i> , 1996
zm10	BZ133	R. Moxon / Seiler <i>et al.</i> , 1996
zm11asbc	NGE31	R. Moxon / Seiler <i>et al.</i> , 1996
zm12	NGF26	R. Moxon / Seiler <i>et al.</i> , 1996
zm13	NGE28	R. Moxon / Seiler <i>et al.</i> , 1996
zm14	NGH38	R. Moxon / Seiler <i>et al.</i> , 1996
zm15	SWZ107	R. Moxon / Seiler <i>et al.</i> , 1996
zm16	NGH15	R. Moxon / Seiler <i>et al.</i> , 1996
zm17	NGH36	R. Moxon / Seiler <i>et al.</i> , 1996
zm18	BZ232	R. Moxon / Seiler <i>et al.</i> , 1996
zm19	BZ83	R. Moxon / Seiler <i>et al.</i> , 1996
zm20	44/76	R. Moxon / Seiler <i>et al.</i> , 1996
zm21	MC58	R. Moxon
zm96	2996	Our collection

**Group A**

zm22	205900	R. Moxon
zm23asbc	F6124	R. Moxon
z2491	Z2491	R. Moxon / Maiden <i>et al.</i> , 1998

**Group C**

zm24	90/18311	R. Moxon
zm25	93/4286	R. Moxon

**Others**

zm26	A22 (group W)	R. Moxon / Maiden <i>et al.</i> , 1998
zm27bc	E26 (group X)	R. Moxon / Maiden <i>et al.</i> , 1998
zm28	860800 (group Y)	R. Moxon / Maiden <i>et al.</i> , 1998
zm29asbc	E32 (group Z)	R. Moxon / Maiden <i>et al.</i> , 1998
zm31asbc	<i>N. lactamica</i>	R. Moxon

**Gonococcus**

zm32asbc	Ng F62	R. Moxon / Maiden <i>et al.</i> , 1998
zm33asbc	Ng SN4	R. Moxon

fa1090	FA1090	R. Moxon
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**References:**

Seiler A. *et al.*, Mol. Microbiol., 1996, 19(4):841-856.  
 Maiden et al., Proc. Natl. Acad. Sci. USA, 1998, 95:3140-3145.

The amino acid sequences for each listed strain are as follows:

**FA1090 <SEQ ID 3207>**

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYFVLKGDGRRTARFPIYGI PDDFISVPLPAGLRSGKN  
 LVRI RQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPI LGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNEGVPVAGLGTPLMGEYAGA  
 IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

**Z2491 <SEQ ID 3208>**

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSVQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYFVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRI RQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPI LGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

**ZM01 <SEQ ID 3209>**

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYFVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPI LGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

**ZM02 <SEQ ID 3210>**

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYFVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPI LGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

**ZM03 <SEQ ID 3211>**

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYFVLKGDGRRTAQARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRI RQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPI LGYAEDPVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPGVAGLGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

**ZM04 <SEQ ID 3212>**

MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMQNPORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM05 <SEQ ID 3213>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM06 <SEQ ID 3214>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM07 <SEQ ID 3215>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM08N <SEQ ID 3216>

MKKYLFRALYGIAAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM09 <SEQ ID 3217>

MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM10 <SEQ ID 3218>

MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYYEPVLKGDDRRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQGTGKNSGTIDNTGGTHADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL



KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM11ASBC <SEQ ID 3219>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEPEVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM12 <SEQ ID 3220>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEPEVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM13 <SEQ ID 3221>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEPEVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM14 <SEQ ID 3222>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEPEVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM15 <SEQ ID 3223>

MKKYLFRAALYGI AAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDLAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEPEVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGGHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM16 <SEQ ID 3224>

MKKYLFRAALCGIAAAILAACQSKSIQTFPQPDTSVINGPGRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTGTGYEPEVLKGDRTTAQARFPIYGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGGHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPI LGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLGTSMQGIKSYMRQNPQRLAEVLGQNPSYIFFRELTSNGDGPVGALGTPLMGEYAGA  
VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM17 <SEQ ID 3225>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM18 <SEQ ID 3226>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM19 <SEQ ID 3227>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM20 <SEQ ID 3228>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM21 <SEQ ID 3229>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKSYMRQNPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM22 <SEQ ID 3230>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMQONPORLAEVLGQNPSYIFFRELTSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM23ASBC <SEQ ID 3231>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDRTAQAARFPIYGI PDDFISVPLPAGLRSGKA  
 LVRIQRTGKNSGTIDNAGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL

KLGQTSMQGIKSYMRQNPQRLAEVLGQNPYSIIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGETAGK  
MKEPGYVWQLLPNGMKPEYRP\*

ZM24 <SEQ ID 3232>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGGDDRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPYSIIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM25 <SEQ ID 3233>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPAPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGGDDRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGKYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPYSIIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM26 <SEQ ID 3234>

MKKYLFRAALYGIASAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGGDDRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKAYMQNPQRLAEVLGQNPYSIIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM27BC <SEQ ID 3235>

MKKYLFRAALYGISAILAACQSKSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGGDDRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNAGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPYSIIFFRELTGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGETAGK  
MKEPGYVWQLLPNGMKPEYRP\*

ZM28 <SEQ ID 3236>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGGDDRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKAYMRQNPQRLAEVLGQNPYSIIFFRELAGSSNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM29ASBC <SEQ ID 3237>

MKKYLFRAALCGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
YFTPWQVAGNGSLAGTVTGYEYEPVLKGGDDRTAQARFPIYIGIPDDFISVPLPAGLRSGKA  
LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
KLQTSMQGIKSYMRQNPQRLAEVLGQNPYSIIFFRELTGSGNDGPVGALGTPLMGEYAGA  
VDRHYITLGAFLFVATTHPTRKALNRLIMAQDTGSAIKGAVRVDFWGYGDEAGELAGK  
QKTTGYVWQLLPNGMKPEYRP\*

ZM31ASBC <SEQ ID 3238>

MKKHLFRAALYGIAAAILAACQSKSIQTFFQPDTSIKGPDRPAGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM32ASBC <SEQ ID 3239>

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKA  
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGGNDGPVGALGTPLMGEYAGA  
 IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM33ASBC <SEQ ID 3240>

MKKHLLRSALYGIAAAILAACQSRSIQTFFQPDTSVINGPDRPAGIPDPAGTTVAGGGAV  
 YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKRFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN  
 LVRIRQTGKNSGTIDNAGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSGNEGPVGALGTPLMGEYAGA  
 IDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

ZM96 <SEQ ID 3241>

MKKYLFRAALYGIAAAILAACQSKSIQTFFQPDTSVINGPDRPVGIPDPAGTTVGGGGAV  
 YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCAQAFQTPVHSFQAKQFFER  
 YFTPWQVAGNGSLAGTVTGYEYEPVLKGDGRRRTAQARFPIYGIPDDFISVPLPAGLRSGKA  
 LVRIRQTGKNSGTIDNTGGTHADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL  
 DGKAPILGYAEDPVELFFMHIOGSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL  
 KLGQTSMQGIKAYMRQNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA  
 VDRHYITLGAPLFFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK  
 QKTTGYVWQLLPNGMKPEYRP\*

Figure 23 shows the results of aligning the sequences of each of these strains. Dark shading indicates regions of homology, and gray shading indicates the conservation of amino acids with similar characteristics. As is readily discernible, there is significant conservation among the various strains of ORF 919, further confirming its utility as an antigen for both vaccines and diagnostics.

#### EXAMPLE 16

Using the above-described procedures, the following oligonucleotide primers were employed in the polymerase chain reaction (PCR) assay in order to clone the ORFs as indicated:

Table 7: Oligonucleotides used for PCR to amplify complete or partial ORFs

ORF	primer	Sequence	Restriction sites
001	Forward	CGCGGATCCCATATG-TGGATGGTGCTGGTCAT	BamHI-
	Reverse	CCCGCTCGAG-TGCCGTCTTGTCCAC	NdeI
003	Forward	CGCGGATCCCATATG-GTCGTATTCGTGGC	XhoI
	Reverse	CCCGCTCGAG-AAAATCATGAACACGCGC	BamHI-
005	Forward	CGCGGATCCCATATG-GACAATATTGACATGT	NdeI
	Reverse	CCCGCTCGAG-CATCACATCCGCCCG	XhoI
006	Forward	CGCGGATCCCATATG-CTGCTGGTGCTGG	BamHI-
	Reverse	CCCGCTCGAG-AGTTCCGGCTTTGATGT	NdeI
007	Forward	CGCGGATCCCATATG-GCCGACAACAGCATCAT	XhoI
	Reverse	CCCGCTCGAG-AAGGCGTTCATGATATAAG	BamHI-
008	Forward	CGCGGATCCCATATG-AACAACAGACATTTTG	NdeI
	Reverse	CCCGCTCGAG-CCTGTCCGGTAAAAGAC	XhoI
009	Forward	CGCGGATCCCATATG-CCCCGCGCTGCT	BamHI-
	Reverse	CCCGCTCGAG-TGGCTTTTGCCACGTTTT	NdeI
011	Forward	CGCGGATCCCATATG-AAGACACACCGCAAG	XhoI
	Reverse	CCCGCTCGAG-GGCGGTCAGTACGGT	BamHI-
012	Forward	CGCGGATCCCATATG-CTCGCCCGTTGCC	NdeI
	Reverse	CCCGCTCGAG-AGCGGGGAAGAGGCAC	XhoI
013	Forward	CGCGGATCCCATATG-CCTTTGACCATGCT	BamHI-
	Reverse	CCCGCTCGAG-CTGATTCGGCAAAAAAATCT	NdeI
018	Forward	CGCGGATCCCATATG-CAGCAGAGGCAGTT	XhoI
	Reverse	CCCGCTCGAG-GACGAGGCGAACGCC	BamHI-
019	Forward	AAAGAATTC-CTGCCAGCCGGCAAGACCCCGGC	NdeI
	Reverse	AAACTGCAG-TCAGCGGGCGGGGACAATGCCCAT	XhoI
023	Forward	AAAGAATTC-AAAGAATATTCGGCATGGCAGGC	Eco RI
	Reverse	AAACTGCAG-TTACCCCCAAATCACTTTAACTGA	Pst I
025	Forward	AAAGAATTC-TGCGCCACCCAACAGCCTGCTCC	Eco RI
	Reverse	AAACTGCAG-TCAGAACGCGATATAGCTGTTCGG	Pst I
031	Forward	CGCGGATCCCATATG-GTCTCCCTTCGCTT	BamHI-
	Reverse	CCCGCTCGAG-ATGTAAGACGGGGACAAC	NdeI
032	Forward	CGCGGATCCCATATG-CGGCGAAACGTGC	XhoI
			BamHI-

	Reverse	CCCGCTCGAG-CTGGTTTTTTGATATTTGTG	NdeI
033	Forward	CGCGGATCCCATATG-GCGGCGGCAGACA	XhoI
	Reverse	CCCGCTCGAG-ATTTGCCGCATCCCGAT	BamHI-
034	Forward	CGCGGATCCCATATG-GCCGAAAACAGCTACGG	NdeI
	Reverse	CCCGCTCGAG-TTTGACGATTTGGTTCAATT	XhoI
036	Forward	CGCGGATCCCATATG-CTGAAGCCGTGCG	BamHI-
	Reverse	CCCGCTCGAG-CCGGACTGCGTATCGG	NdeI
038	Forward	CGCGGATCCCATATG-ACCGATTTCGCCA	XhoI
	Reverse	CCCGCTCGAG-TTCTACGCCGTACTGCC	BamHI-
039	Forward	CGCGGATCCCATATG-CCGTCCGAACCGC	NdeI
	Reverse	CCCGCTCGAG-TAGGATGACGAGGTAGG	XhoI
041	Forward	CGCGGATCCCATATG-TTCGTGCGCGAACCGC	BamHI-
	Reverse	CCCGCTCGAG-GCCCAAAAACCTCTTTCAA	NdeI
042	Forward	CGCGGATCCCATATG-ACGATGATTGCTTGC	XhoI
	Reverse	CCCGCTCGAG-TTTGCAGCCTGCATTTGAC	BamHI-
043	Forward	AAAAAAGGTACC-ATGGTTGTTCAAATCAAATATC	NdeI
	Reverse	AAACTGCAG-TTATTGCGCTTCACCTCCGCCGC	XhoI
043a	Forward	AAAAAAGGTACC-GCAAAGTGCATGGCGGCTTGGACGGTGC	Kpn I
	Reverse	AAAAAACTGCAG-TTAATCCTGCAACACGAATTCGCCCGTCCG	Pst I
044	Forward	CGCGGATCCCATATG-CCGTCCGACTAGAG	Kpn I
	Reverse	CCCGCTCGAG-ATGCGCTACGGTAGCCA	Pst I
046	Forward	AAAGAATTC-ATGTCGGCAATGCTCCCGACAAG	BamHI-
	Reverse	AAACTGCAG-TCACTCGGCGACCCACACCGTGAA	NdeI
047	Forward	CGCGGATCCCATATG-GTCATCATAACAGGCG	XhoI
	Reverse	CCCGCTCGAG-TCCGAAAAAGCCCATTTTG	Eco RI
048	Forward	AAAGAATTC-ATGCTCAACAAAGGCGAAGAATTGCC	XhoI
	Reverse	AAACTGCAG-TCAAGATTGACGGGGATGATGCC	Eco RI
049	Forward	AAAGAATTC-ATGCGGGCGCAGGCGTTTGATCAGCC	Pst I
	Reverse	AAACTGCAG-AAGGCGTATCTGAAAAAATGGCAG	Eco RI
050	Forward	CGCGGATCCCATATG-GGCGCGGGCTGG	Pst I
	Reverse	CCCGCTCGAG-AATCGGGCCATCTTCGA	BamHI-
052	Forward	AAAAAAGAATTC-ATGGCTTTGGTGGCGGAGGAAAC	NdeI
	Reverse	AAAAAAGTTCGAC-TCAGGCGGCGTTCCTTCACCTTCCT	XhoI
052a	Forward	AAAAAAGAATTC-GTGGCGGAGGAAACGGAAATATCCGC	Sal I
			Eco RI

	Reverse	AAAAAACTGCAG-TTAGCTGTTTTTGGAAACGCCGTCCAACCC	Pst I
073	Forward	CGCGGATCCCATATG-TGTATGCCATATAAGAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACCGGATTGTCCGAC	XhoI
075	Forward	CGCGGATCCCATATG-CCGTCTTACTTCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCACCAATGCCGATTATTT	XhoI
077a	Forward	AAAAAAGAATTC-GGCGGCATTTTCATCGACACCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGAACATCTGCACAAACGCAAT	Pst I
080	Forward	AAAGAATTC-GCGTCCGGGCTGGTTTGGTTTACAATTC	Eco RI
	Reverse	AAACTGCAG-CTATTCTTCGGATTCTTTTTCGGG	Pst I
081	Forward	AAAGAATTC-ATGAAACCACTGGACCTAAATTCATCTG	Eco RI
	Reverse	AAACTGCAG-TCACTTATCCTCCAATGCCTC	Pst I
082	Forward	AAAGAATTC-ATGTGGTTGTTGAAGTTGCCTGC	Eco RI
	Reverse	AAACTGCAG-TTACGCGGATTCGGCAGTTGG	Pst I
084	Forward	AAAGAATTC-TATCACCAGAATATGAATACGGCTACCG	Eco RI
	Reverse	AAACTGCAG-TTATACTTGGGCGCAACATGA	Pst I
085	Forward	CGCGGATCCCATATG-GGTAAAGGGCAGGACT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAAGCCTTAAACGCTTCG	XhoI
086	Forward	AAAAAAGGTACC-TATTTGGCATCAAAAGAAGGCGG	Kpn I
	Reverse	AAACTGCAG-TTACTCCACCCGATAACCGCG	Pst I
087	Forward	AAAGAATTC-ATGGGCGGTAAAACCTTTATGC	Eco RI
	Reverse	AAACTGCAG-TTACGCCGCACACGCAATCGC	Pst I
087a	Forward	AAAAAAGAATTC-AAGCTATTAGGCGTGCCGATTGTGATTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCTGCAAGATGCCAGCTTGCC	Pst I
088	Forward	AAAAAAGAATTC-ATGTTTTTATGGCTCGCACATTTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAGCGGATTTTGAGGGTACTCAAACC	Pst I
089	Forward	CGCGGATCCCATATG-CCGCCAAAATCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCGCATACCAAAGCCA	XhoI
090	Forward	CGCGGATCCCATATG-CGCATAGTCGAGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAAAACGGCGGTACG	XhoI
091	Forward	AAAGAATTC-ATGGAAATACCCGTACCGCCGAGTCC	Eco RI
	Reverse	AAACTGCAG-TCAGCGCAGGGGGTAGCCCAAGCC	Pst I
092	Forward	AAAGAATTC-ATGTTTTTTATTTCAATCCG	Eco RI
	Reverse	AAACTGCAG-TCAAATCTGTTTCGACAATGC	Pst I
093	Forward	AAAGAATTC-ATGCAGAATTTTGGCAAAGTGGC	Eco RI
	Reverse	AAACTGCAG-CTATGGCTCGTCATACCGGGC	Pst I
094	Forward	AAAGAATTC-ATGCCGTCACGGAAGCGCATCAACTC	Eco RI
	Reverse	AAACTGCAG-TTATCCCGGCCATACCGCCGAACA	Pst I
095	Forward	AAAGAATTC-ATGTCTTTTCATTTGAACATGGACGG	Eco RI
	Reverse	AAACTGCAG-TCAACGCCGCAGGCACTAACGCCC	Pst I
096	Forward	AAAGAATTC-ATGGCTCGTCATACCGGGCAGGG	Eco RI

	Reverse	AAACTGCAG-TCAAAGGAAAAGGCCGTCTGAAAAGCG	Pst I
097	Forward	AAAGAATTC-ATGGACACTTCAAAACAAACACTGTTG	Eco RI
	Reverse	AAACTGCAG-TCAGCCCAAATACCAGAATTCAG	Pst I
098	Forward	AAAGAATTC-GATGAACGCAGCCAGCATGGATACG	Eco RI
	Reverse	AAACTGCAG-TTACGACATTCTGATTTGGCA	Pst I
102	Forward	AAAAAAGAATTC-GGCCTGATGATTTTGGAAGTCAACAC	Eco RI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Pst I
105	Forward	CGCGGATCCCATATG-TCCGCAAACGAATACG	BamHI-
	Reverse	CCCGCTCGAG-GTGTTCTGCCAGTTTCAG	NdeI
107	Forward	AAAAAAGAATTC- CTGATGATTTTGGAAAGTCAACACCCATTATCC	XhoI
	Reverse	AAAAAACTGCAG-TTATCCTTTAAATACGGGGACGAGTTC	Eco RI
107b	Forward	AAAAAAGAATTC- GATACCCAAGCCCCCGCCGGCACAACTACTG	Pst I
	Reverse	AAAAAACTGCAG- TTACGCGTCGCCTTTAAAGTATTTGAGCAGGCTGGAGAC	Eco RI
108	Forward	AAAGAATTC-ATGTTGCCGGGCTTCAACCG	Pst I
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Eco RI
108a	Forward	AAAAAAGAATTC-GGTAACACATTTCGGCAGCTTAGACGGTGG	Pst I
	Reverse	AAACTGCAG-TTAGCGGTACAGGTGTTTGAAGCA	Eco RI
109	Forward	AAAGAATTC-ATGTATTATCGCCGGGTATGGG	Pst I
	Reverse	AAACTGCAG-CTAGCCCAAAGATTTGAAGTGTC	Eco RI
111	Forward	CGCGGATCCCATATG-TGTTCTGGAACAAACCGC	Pst I
	Reverse	CCCGCTCGAG-GCGGAGCAGTTTTTCAA	BamHI-
114	Forward	CGCGGATCCCATATG-GCTTCCATCACTTCGC	NdeI
	Reverse	CCCGCTCGAG-CATCCGCGAAATCGTC	XhoI
117	Forward	AAAAAAGGTACC-ATGGTCGAAGAACTGGAAGTCTG	Kpn I
	Reverse	AAACTGCAG-TTAAAGCCGGGTAACGCTCAATAC	Pst I
118	Forward	AAAGTCGACATGTGTGAGTTCAAGGATATTATAAG	Sal I
	Reverse	AAAGCATGC-CTATTTTTTGTGTAATAATCAAATC	Sph I
121	Forward	CGCGGATCCCATATG-GAAACACAGCTTTACAT	BamHI-
	Reverse	CCCGCTCGAG-ATAATAATATCCCGCGCCC	NdeI
122	Forward	CGCGGATCCCATATG-GTCATGATTAATCCGCA	XhoI
	Reverse	CCCGCTCGAG-AATCTTGGTAGATTGGATTT	BamHI-
125	Forward	AAAGAATTC-ATGTCGGGCAATGCCTCCTCTCC	NdeI
	Reverse	AAACTGCAG-TCACGCCGTTTCAAGACG	XhoI
125a	Forward	AAAAAAGAATTC-ACGGCAGGCAGCACCGCCGCACAGGTTTC	Eco RI
	Reverse	AAAAAACTGCAG- TTATTTTGCCACGTCGGTTTCTCCGGTGAACAACGC	Pst I
126	Forward	CGCGGATCCCATATG-CCGTCTGAAACCC	BamHI-



	Reverse	CCCGCTCGAG-ATATTCCGCCGAATGCC	NdeI
127	Forward	AAAGAATTC-ATGGAAATATGGAATATGTTGGACACTTG	XhoI
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Eco RI
127a	Forward	AAAAAAGAATTC-AAGGAACTGATTATGTGTCTGTCGGG	Pst I
	Reverse	AAACTGCAG-TTAAAGTGTTTCGGAGCCGGC	Eco RI
128	Forward	CGCGGATCCCATATG-ACTGACAACGCACT	Pst I
	Reverse	CCCGCTCGAG-GACCGCGTTGTCGAAA	BamHI-
130	Forward	CGCGGATCCCATATG-AAACAACCTCCGCGA	NdeI
	Reverse	CCCGCTCGAG-GAATTTTGCACCGGATTG	XhoI
132	Forward	AAAGAATTC-ATGGAACCTTCAAAACCTTAATTTG	XhoI
	Reverse	AAAAAACTGCAG-TCACCATGTCGGCATTGAAAAAC	Eco RI
134	Forward	CGCGGATCCCATATG-TCCCAAGAAATCCTC	Pst I
	Reverse	CCCGCTCGAG-CAGTTTGACCGAATGTTC	BamHI-
135	Forward	CGCGGATCCCATATG-AAATACAAAAGAATCGTATT	NdeI
	Reverse	CCCGCTCGAG-AAATTCGGTCAGAAGCAGG	XhoI
137	Forward	AAAAAAGGTACC-ATGATTACCCATCCCCAATTCGATCC	Kpn I
	Reverse	AAAAAACTGCAG-TCAGTGCTGTTTTTTCATGCCGAA	Pst I
137a	Forward	AAAAAAGAATTC-GGCCGCAAACACGGCATCGGCTTCCT	Eco RI
	Reverse	AAAAAACTGCAG-TTAAGCGGGATGACGCGGCAGCATACC	Pst I
138	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTGGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Xba I
141	Forward	AAAGAATTC-ATGAGCTTCAAAACCGATGCCGAAATCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAACAAGCCGTGAATCACGCC	Pst I
142	Forward	CGCGGATCCCATATG-CGTGCCGATTTCATG	BamHI-
	Reverse	CCCGCTCGAG-AAACTGCTGCACATGGG	NdeI
143	Forward	AAAAAAGAATTC- ATGCTCAGTTTCGGCTTTCTCGGCGTTCAGAC	XhoI
	Reverse	AAAAAACTGCAG-TCAAACCCCGCCGTGTGTTTCTTTAAT	Eco RI
144	Forward	AAAAAAGAATTC-GGTCTGATCGACGGGCGTGCCGTAAC	Pst I
	Reverse	AAAAAATCTAGA-TCGGCATCGGCCGGCATATGTCCG	Eco RI
146	Forward	AAAAAAGAATTC- CGCCAAGTCGTCATTGACCACGACAAAGTC	Xba I
	Reverse	AAAAAACTGCAG-TTAGGCATCGGCAAATAGGAAACTGGG	Eco RI
147	Forward	AAAAAAGAATTC-ACTGAGCAATCGGTGGATTTGGAAAC	Pst I
	Reverse	AAAAAATCTAGA-TTAGGTAAAGCTGCGGCCCATTTGCGG	Eco RI
148	Forward	AAAAAAGAATTC- ATGGCGTTAAAAACATCAAACCTGGAACACGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGCCCTTCATACAGCCTTCGTTTTG	Eco RI
149	Forward	CGCGGATCCCATATG-CTGCTTGACAACAAAGT	Xba I
			BamHI-

	Reverse	CCCGCTCGAG-AACTTCACGTTACGCC	NdeI
150	Forward	CGCGGATCCCATATG-CAGAACACAAATCCG	XhoI
	Reverse	CCCGCTCGAG-ATAAACATCACGCTGATAGC	BamHI-
151	Forward	AAAAAAGAATTC- ATGAAACAAATCCGCAACATCGCCATCATCGC	NdeI
	Reverse	AAAAAACTGCAG-TCAATCCAGCTTTTAAAGTGGCGGCG	XhoI
152	Forward	AAAAAAGAATTC- ATGAAAAACAAAACCAAAGTCTGGGACCTCCC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGGACAGGAGCAGGATGGCGGC	Pst I
153	Forward	AAAAAAGAATTC-ATGGCGTTTGCTTACGGTATGAC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTCATGTTTTCCGTTTCATT	Pst I
153a	Forward	AAAAAAGAATTC-CGGACTTCGGTATCGGTTCCCCAGCATTG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGCCGACGAAATACTCAGACTTTTCGG	Pst I
154	Forward	CGCGGATCCCATATG-ACTGACAACAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TCGGCTTCCTTTTCGGG	NdeI
155	Forward	AAAAAAGAATTC-ATGAAAATCGGTATCCCACGCGAGTC	XhoI
	Reverse	AAAAAACTGCAG-TTACCCTTTCTTAAACATATTCAGCAT	Eco RI
156	Forward	AAAAAAGAATTC-GCACAGCAAAACGGTTTTGAAGC	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCAGCCGCGACAAACAGCCC	Eco RI
157	Forward	CGCGGATCCCATATG-AGGAACGAGGAAAAAC	Pst I
	Reverse	CCCGCTCGAG-AAACACAAATATCCCCGC	BamHI-
158	Forward	AAAAAAGAATTC-GCGGAGCAGTTGGCGATGGCAAATTCTGC	NdeI
	Reverse	AAAAAATCTAGA-TTATCCACAGAGATTGTTTCCAGTTC	XhoI
160	Forward	CGCGGATCCCATATG-GACATTCTGGACAAAC	Eco RI
	Reverse	CCCGCTCGAG-TTTTGGCCGCCTTCTTT	Xba I
163	Forward	AAAAAAGGTACC-ACCGTGCCGGATCAGGTGCAGATGTG	Kpn I
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
163a	Forward	AAAAAAGAATTC-CGGCTGGTGACAGATAATGAGCCAGAC	Eco RI
	Reverse	AAAAAATCTAGA-TTACTCTGCCAATTCCACCTGCTCGTG	Xba I
164	Forward	CGCGGATCCCATATG-AACCGGACTTATGCC	BamHI-
	Reverse	CCCGCTCGAG-TTTGTTTCCGTCAAACCTGC	NdeI
165	Forward	CGCGGATCCGCTAGC-GCTGAAGCGACAGACG	XhoI
	Reverse	CCCGCTCGAG-AATATCCAATACTTTCGCG	BamHI-
206	Forward	CGCGGATCCCATATG-AAACACCGCCAACCGA	NdeI
	Reverse	CCCGCTCGAG-TTCTGTAAAAAAAGTATGTGC	XhoI
209	Forward	CGCGGATCCCATATG-CTGCGGCATTTAGGA	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-TACCCCTGAAGGCAAC	XhoI
211	Forward	AAAAAAGAATTC-ATGTTGCGGGTTGCTGCTGC	Eco RI
	Reverse	AAAAAACTGCAG-CTATCCTGCGGATTGGCATTGAAA	Pst I
212	Forward	CGCGGATCCCATATG-GACAATCTCGTATGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGGGTTAGATCCTTCC	XhoI
215	Forward	CGCGGATCCCATATG-GCATGGTTGGGTCTGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATATCTTTTGTATCATAAATC	XhoI
216	Forward	CGCGGATCCCATATG-GCAATGGCAGAAAACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TACAATCCGTGCCGCC	XhoI
217	Forward	CGCGGATCCCATATG-GCGGATGACGGTGTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACCCCGAATATCGAATCC	XhoI
218	Forward	CGCGGATCCCATATG-GTCGCGGTCTGATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TAACTCATAGAATCCTGC	XhoI
219	Forward	CGCGGATCCGCTAGC-ACGGCAAGGTTAAG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTAAACCATCTCCTCAAAAC	XhoI
223	Forward	CGCGGATCCCATATG-GAATTCAGGCACCAAGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTCCCGCGTGTC	XhoI
225	Forward	CGCGGATCCCATATG-GACGAGTTGACCAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTTCAGAAAGCGGGAC	XhoI
226	Forward	AAAGAATTC-CTTGCGATTATCGTGCGCACGCG	Eco RI
	Reverse	AAACTGCAG-TCAAAATCCCAAACGGGGAT	Pst I
228	Forward	CGCGGATCCCATATG-TCGCAAGAAGCCAAACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI
229	Forward	CGCGGATCCCATATG-CAAGAGGTTTGTCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACACAATATAGCGGATGAAC	XhoI
230	Forward	CGCGGATCCCATATG-CATCCGGGTGCCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAGTTTGGCGGCTTCGG	XhoI
232	Forward	AAAAAAGAATTC-ATGTACGCTAAAAAAGGCGGTTTGGG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAGGTTTTTTCCTGATTGCCGCCGC	Pst I
232a	Forward	AAAAAAGAATTC-GCCAAGGCTGCCGATACACAAATTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACATTGTCGTTGCCGCCAGATG	Pst I
233	Forward	CGCGGATCCCATATG-GCGGACAAACCCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGCATTGAGCAG	XhoI
234	Forward	CGCGGATCCCATATG-GCCGTTTCACTGACCG	BamHI-

	Reverse	GCCCAAGCTT-ACGGTTGGATTGCCATG	NdeI
235	Forward	CGCGGATCCCATATG-GCCTGCCAAGTTCAAA	Hind III
	Reverse	CCCGCTCGAG-TTTGGGCTGCTCTTC	BamHI-
236	Forward	CGCGGATCCCATATG-GCGCGTTTCGCCTT	NdeI
	Reverse	CCCGCTCGAG-ATGGGTCGCGCGCCGT	XhoI
238	Forward	CGCGGATCCGCTAGC-AACGGTTTGGATGCCCCG	BamHI-
	Reverse	CCCGCTCGAG-TTTGTCTAAGTTCCTGATATG	NdeI
239	Forward	CCGGAATTCTACATATG-CTCCACCATAAAGGTATTG	XhoI
	Reverse	CCCGCTCGAG-TGGTGAAGAGCGGTTTAG	EcoRI-
240	Forward	CGCGGATCCCATATG-GACGTTGGACGATTTC	NdeI
	Reverse	CCCGCTCGAG-AAACGCCATTACCCGATG	XhoI
241	Forward	CCGGAATTCTACATATG-CCAACACGTCCAAC	BamHI-
	Reverse	CCCGCTCGAG-GAATGCGCCTGTAATTAATC	NdeI
242	Forward	CGCGGATCCCATATG-ATCGGCAAACCTTGTTG	XhoI
	Reverse	GCCCAAGCTT-ACCGATACGGTCGCAG	BamHI-
243	Forward	CGCGGATCCCATATG-ACGATTTTTTCGATGCTGC	NdeI
	Reverse	CCCGCTCGAG-CGACTTGGTTACCGCG	XhoI
244	Forward	CGCGGATCCCATATG-CCGTCTGAAGCCC	BamHI-
	Reverse	CCCGCTCGAG-TTTTTTCGGTAGGGGATTT	NdeI
246	Forward	CGCGGATCCCATATG-GACATCGGCAGTGC	XhoI
	Reverse	CCCGCTCGAG-CCCGCGCTGCTGGAG	BamHI-
247	Forward	CGCGGATCCCATATG-GTCGGATCGAGTTAC	NdeI
	Reverse	CCCGCTCGAG-AAGTGTTCTGTTTGCGCA	XhoI
248	Forward	CGCGGATCCCATATG-CGCAAACAGAACACT	BamHI-
	Reverse	CCCGCTCGAG-CTCATCATTATTGCTAACA	NdeI
249	Forward	CGCGGATCCCATATG-AAGAATAATGATTGCTTC	XhoI
	Reverse	CCCGCTCGAG-TTCCCGACCTCCGAC	BamHI-
251	Forward	CGCGGATCCCATATG-CGTGCTGCGGTAGT	NdeI
	Reverse	CCCGCTCGAG-TACGAAAGCCGGTCGTG	XhoI
253	Forward	AAAAAAGAAATTC-ATGATTGACAGGAACCGTATGCTGCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I

253a	Forward	AAAAAAGAATTC-AAAATCCTTTTGAAAACAAGCGAAAACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTATTGGTCTTTCAAACGCCCTTCCTG	Pst I
254	Forward	AAAAAAGAATTC-ATGTATACAGGCGAACGCTTCAATAC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATTACGTAACCGTACACGCTGAC	Xba I
255	Forward	CGCGGATCCCATATG-GCCGCGTTGCGTTAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCGCAATACCGACCAG	XhoI
256	Forward	CGCGGATCCGCTAGC-TTTTAACACCGCCGGAC	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGCCTGTTTGTGCGG	XhoI
257	Forward	CGCGGATCCCATATG-GCGGTTTCTTTCCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCGTGAATATCGCG	XhoI
258	Forward	AAAAAAGAATTC-GATTATTTCTGGTGGATTGTTGCGTTCAG	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
258a	Forward	AAAAAAGAATTC-GCGAAGGCGGTGGCGCAAGGCGA	Eco RI
	Reverse	AAAAAACTGCAG-CTACGCATAAGTTTTTACCGTTTTTGG	Pst I
259	Forward	CGCGGATCCCATATG-GAAGAGCTGCCTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCTTTTCCGGCGTTT	XhoI
260	Forward	CGCGGATCCCATATG-GGTGCGGGTATGGT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACAGGGCGACACCCT	XhoI
261	Forward	AAAAAAGAATTC-CAAGATACAGCTCGGGCATTTCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAAACCAACAAGCCTTGGTCACT	Pst I
263	Forward	CGCGGATCCCATATG-GCACGTTTAACCGTA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGTAAGCCTGCAATT	XhoI
264	Forward	AAAAAAGGTACC-GCCGACGCAGTGGTCAAGGCAGAA	Kpn I
	Reverse	AAACTGCAG-TCAGCCGGCGGTCAATACCGCCCG	Pst I
265	Forward	AAAAAAGAATTC-GCGGAGGTCAAGAGAAGGTGTTTG	Eco RI
	Reverse	AAAAAACTGCAG-TTACGAATACGTCGTCAAATGCG	Pst I
266	Forward	AAAGAATTC-CTCATCTTTGCCAACGCCCCCTTC	Eco RI
	Reverse	AAACTGCAG-CTATTCCCTGTTGCGCGTGTGCCA	Pst I
267	Forward	AAAGAATTC-TTCTTCCGATTGATGTTAATCG	Eco RI
	Reverse	AAACTGCAG-TTAGTAAAAACCTTTCTGCTTGGC	Pst I
269	Forward	AAAGAATTC-TGCAAACCTTGCGCCACGTGCCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
269a	Forward	AAAAAAGAATTC-GACTTTATCCAAAACACGGCTTCGCC	Eco RI
	Reverse	AAACTGCAG-TTACGAAGACCGCAACGAAAGGCAGAG	Pst I
270	Forward	AAAGAATTC-GCCGTCAAGCTCGTTTTGTTGCAATG	Eco RI
	Reverse	AAACTGCAG-TTATTCGGCGGTAAATGCCGTCTG	Pst I
271	Forward	CGCGGATCCCATATG-CCTGTGTGCAGCTCGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCCCAGCCCCGTGGAG	XhoI

272	Forward	AAAGAATTC-ATGACCGCAAAGGAAGAACTGTTCGC	Eco RI
	Reverse	AAACTGCAG-TCAGAGCAGTTCCAAATCGGGGCT	Pst I
273	Forward	AAAGAATTC-ATGAGTCTTCAGGCGGTATTTATATACCC	Eco RI
	Reverse	AAACTGCAG-TTACGCGTAAGAAAAAACTGC	Pst I
274	Forward	CGCGGATCCCATATG-ACAGATTTGGTTACGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTTGCTTTTCACTATTATTGAA	NdeI
276	Forward	AAAAAAGAATTC- ATGATTTTGCCGTCGTCCATCACGATGATGCG	XhoI
	Reverse	AAAAAACTGCAG-CTACACCACCATCGGCGAATTTATGGC	Eco RI
277	Forward	AAAAAAGAATTC-ATGCCCCGCTTTGAGGACAAGCTCGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
277a	Forward	AAAAAAGAATTC-GGGGCGGCGGCTGGGTTGGACGTAGG	Pst I
	Reverse	AAAAAACTGCAG-TCATAAGCCATGCTTACCTTCCAACAA	Eco RI
278	Forward	AAAAAAGGTACC-GTCAAAGTTGTATTAATCGGGCCTTTGCC	Pst I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Kpn I
278a	Forward	AAAAAAGAATTC-AAAACTCTCCTAATTCGTCATAGTCG	Pst I
	Reverse	AAAAAACTGCAG-TCATTCAACCATATCAAATCTGCC	Eco RI
279	Forward	CGCGGATCCCATATG-TTGCTGCAATCACGATT	Pst I
	Reverse	CCCGCTCGAG-TTTAGAAGCGGGCGGCAA	BamHI-
280	Forward	AAAAAAGGTACC-GCCCCCTGCCGGTTGTAACCAG	NdeI
	Reverse	AAAAAACTGCAG-TTATTGCTTCATCGCGTTGGTCAAGGC	XhoI
281	Forward	AAAAAAGAATTC-GCACCCGTCGGCGTATTCCTCGTCATGCG	Kpn I
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Pst I
281a	Forward	AAAAAAGAATTC-TCCTACCACATCGAAATTCCTTCCGG	Eco RI
	Reverse	AAAAAATCTAGA-GGTCAGAATGCCGCCTTCTTTGCCGAG	Xba I
282	Forward	AAAAAAGAATTC-CTTTACCTTGACCTGACCAACGGGCACAG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACCTGCCAGTTGCGGGAATATCGT	Eco RI
283	Forward	CGCGGATCCCATATG-GCCGTCTTTACTTGGAAG	Pst I
	Reverse	CCCGCTCGAG-ACGGCAGTATTTGTTTACG	BamHI-
284	Forward	CGCGGATCCCATATG-TTGCCTGCAAAAGAATCG	NdeI
	Reverse	CCCGCTCGAG-CCGACTTTGCAAAAACCTG	XhoI
286	Forward	CGCGGATCCCATATG-GCCGACCTTTCGAAAA	XhoI
	Reverse	CCCGCTCGAG-GAAGCGCGTTCCCAAG	BamHI-
287	Forward	CCGGAATTCTAGCTAGC-CTTTCAGCCTGCGGG	NdeI
	Reverse	CCCGCTCGAG-ATCCTGCTCTTTTTTGCC	XhoI
288	Forward	CGCGGATCCCATATG-CACACCGGACAGG	EcoRI-
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	NheI
290	Forward	CGCGGATCCCATATG-GCGGTTTGGGGCGGA	XhoI
	Reverse	CCCGCTCGAG-CGTATCAAAGACTTGCGT	BamHI-

	Reverse	CCCGCTCGAG-TCGGCGCGGCGGGC	NdeI
292	Forward	CGCGGATCCCATATG-TGCGGGCAAACGCCC	XhoI
	Reverse	CCCGCTCGAG-TTGATTTTTCGGGATGATT	BamHI-
294	Forward	AAAAAAGAATTC-GTCTGGTCGATTCGGGTGTCAGAAC	NdeI
	Reverse	AAAAAACTGCAG-TTACCAGCTGATATAAAACATCGCTTT	XhoI
295	Forward	CGCGGATCCCATATG-AACCGGCCGGCCTCC	Eco RI
	Reverse	CCCGCTCGAG-CGATATTTGATTCCGTTGC	Pst I
297	Forward	AAAAAAGAATTC-GCATAATTGCTTCGACAGAGAG	BamHI-
	Reverse	AAAAAACTGCAG-TCAATCCGATTGCGACACGGT	NdeI
298	Forward	AAAAAAGAATTC-CTGATTGCCGTGTGGTTCAGCCAAAACCC	XhoI
	Reverse	AAAAAACTGCAG-TCATGGCTGTGTACTTGATGGTTGCGT	Eco RI
299	Forward	CGCGGATCCGCTAGC-CTACCTGTGCGCTCCG	Pst I
	Reverse	CCCGCTCGAG-TTGCCTGATTGCAGCGG	BamHI-
302	Forward	AAAAAAGAATTC-ATGAGTCAAACCGATACGCAACG	NheI
	Reverse	AAAAAACTGCAG-TTAAGGTGCGGGATAGAATGTGGGCGC	XhoI
305	Forward	AAAAAAGGTACC-GAATTTTACCGATTTCAGCACCGGA	Eco RI
	Reverse	AAAAAACTGCAG-TCATTCCCAACTTATCCAGCCTGACAG	Pst I
305a	Forward	AAAAAAGGTACC-TCCCGTTCGGGCAGTACGATTATGGG	Kpn I
	Reverse	AAAAAACTGCAG-TTACAAACCGACATCATGCAGGGTGAA	Pst I
306	Forward	CGCGGATCCCATATG-TTATGAACAAATTTTCCC	Kpn I
	Reverse	CCCGCTCGAG-CCGCATCGGCAGAC	Pst I
308	Forward	CGCGGATCCCATATG-TTAAATCGGGTATTTTATC	BamHI-
	Reverse	CCCGCTCGAG-ATCCGCCATTCCCTGC	NdeI
311	Forward	AAAAAAGGTACC-ATGTTCAATTTTGGCTGGGTGTTT	XhoI
	Reverse	AAACTGCAG-ATGTTCAATTTTGGCTGGGTGTTT	Kpn I
312	Forward	AAAAAAGGTACC-ATGAGTATCCCATCCGGCGAAATT	Pst I
	Reverse	AAACTGCAG-TCAGTTTTTCATCGATTGAACCGG	Kpn I
313	Forward	AAAAAAGAATTC-ATGGACGACCCGCGCACCTACGGATC	Pst I
	Reverse	AAAAAACTGCAG-TCAGCGGCTGCCGCCGATTTTGCT	Eco RI
401	Forward	CGCGGATCCCATATG-AAGGCGGCAACACAGC	Pst I
	Reverse	CCCGCTCGAG-CCTTACGTTTTTCAAAGCC	BamHI-
402	Forward	AAAAAAGAATTC-GTGCCTCAGGCATTTTCATTTACCCTTGC	NdeI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	XhoI
402a	Forward	AAAAAAGAATTC-AGGCTGATTGAAAACAAACACGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAAATCCCTCTGCCGTATTTGTATTC	Xba I
406	Forward	CGCGGATCCCATATG-TGCGGGACACTGACAG	Eco RI
	Reverse	CCCGCTCGAG-AGGTTGTCCTTGTCTATG	Xba I
			BamHI-
			NdeI
			XhoI

501	Forward	CGCGGATCCCATATG-GCAGGCGGAGATGGC	BamHI-
	Reverse	CCCGCTCGAG-GGTGTGATGTTACCC	NdeI
502	Forward	CGCGGATCCCATATG-GTAGACGCGCTTAAGCA	XhoI
	Reverse	CCCGCTCGAG-AGCTGCATGGCGGCG	BamHI-
503	Forward	CGCGGATCCCATATG-TGTTGCGGGAAAGGCG	NdeI
	Reverse	CCCGCTCGAG-CCGCGCATTCCTCGCA	XhoI
504	Forward	CGCGGATCCCATATG-AGCGATATTGAAGTGACG	BamHI-
	Reverse	GCCCAAGCTT-TGATTCAAGTCCTTGCCG	NdeI
505	Forward	CGCGGATCCCATATG-TTTCGTTTACAATTCAGG	HindIII
	Reverse	CCCGCTCGAG-CGGCGTTTTATAGCGG	BamHI-
510	Forward	CGCGGATCCCATATG-CCTTCGCGGACAC	NdeI
	Reverse	CCCGCTCGAG-GCGCACTGGCAGCG	XhoI
512	Forward	CGCGGATCCCATATG-GGACATGAAGTAACGGT	BamHI-
	Reverse	CCCGCTCGAG-AGGAATAGCCTTTGACG	NdeI
515	Forward	CGCGGATCCCATATG-GAGGAAATAGCCTTCGA	XhoI
	Reverse	CCCGCTCGAG-AAATGCCGCAAAGCATC	BamHI-
516	Forward	CGCGGATCCCATATG-TGTACGTTGATGTTGTGG	NdeI
	Reverse	CCCGCTCGAG-TTTGCGGGCGGCATC	XhoI
517	Forward	CGCGGATCCCATATG-GGTAAAGGTGTGGAAATA	BamHI-
	Reverse	CCCGCTCGAG-GTGCGCCCAGCCGT	NdeI
518	Forward	AAAGAATTC-GCTTTTTTACTGCTCCGACCGGAAGG	XhoI
	Reverse	AAACTGCAG-TCAAATTCAGACTCTGCCAC	Eco RI
519	Forward	CGCGGATCCCATATG-TTCAAATCCTTTGTCGTCA	Pst I
	Reverse	CCCGCTCGAG-TTTGGCGGTTTTGCTGC	BamHI-
520	Forward	CGCGGATCCCATATG-CCTGCGCTTCTTTCA	NdeI
	Reverse	CCCGCTCGAG-ATATTTACATTTCAGTCGGC	XhoI
521	Forward	CGCGGATCCCATATG-GCCAAAATCTATACCTGC	BamHI-
	Reverse	CCCGCTCGAG-CATACGCCCCAGTTCC	NdeI
522	Forward	CGCGGATCCCATATG-ACTGAGCCGAAACAC	XhoI
	Reverse	GCCCAAGCTT-TTCTGATTTCAAATCGGCA	BamHI-
523	Forward	CGCGGATCCCATATG-GCTCTGCTTTCCGCG	NdeI
	Reverse		HindIII



	Reverse	CCCGCTCGAG-AGGGTGTGTGATAATAAGAAG	XhoI
525	Forward	CGCGGATCCCATATG-GCCGAAATGGTTCAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCCGTGCATATCATAAA	XhoI
527	Forward	AAAGAATTC-TTCCCTCAATGTTGCCGTTTTCG	Eco RI
	Reverse	AAACTGCAG-TTATGCTAAACTCGAAACAAATTC	Pst I
529	Forward	CGCGGATCCGCTAGC-TGCTCCGGCAGCAAAAC	BamHI- NheI
	Reverse	GCCCAAGCTT-ACGCAGTTCGGAATGGAG	HindIII
530	Forward	CGCGGATCCCATATG-AGTGCGAGCGCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGACCGACTGATTCCG	XhoI
531	Forward	AAAAAAGAATTC-TATGCCGCCGCTACCAAATCTACGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAAACAGCGCCGTGCCGACGACAAG	Pst I
532	Forward	AAAAAAGAATTC-ATGAGCGGTCAGTTGGGCAAAGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
532a	Forward	AAAAAAGAATTC-TTGGGTGTCGCGTTTGAGCCGGAAGT	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTGTTCCAAGTGGTCGGTATCAAA	Pst I
535	Forward	AAAGAATTC-ATGCCCTTTCCCGTTTTTCAGAC	Eco RI
	Reverse	AAACTGCAG-TCAGACGACCCCGCCTTCCCC	Pst I
537	Forward	CGCGGATCCCATATG-CATACCCAAAACCAATCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCCTGCAAATAAAGGGTT	XhoI
538	Forward	CGCGGATCCCATATG-GTCGAGCTGGTCAAAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGGCATTTCGGTTTCGTC	XhoI
539	Forward	CGCGGATCCGCTAGC-GAGGATTTCAGGAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TACCAATGTCGGCAAATC	XhoI
542	Forward	AAAGAATTC-ATGCCGTCTGAAACCGTGTC	Eco RI
	Reverse	AAACTGCAG-TTACCGCGAACCGGTCAGGAT	Pst I
543	Forward	AAAAAAGAATTC-GCCTTCGATGGCGACGTTGTAGGTAC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
543a	Forward	AAAAAAGAATTC-GGCAAAACTCGTCATGAATTTGC	Eco RI
	Reverse	AAAAAATCTAGA- TTAATGAAGAAGAACATATTGGAATTTTGG	Xba I
544	Forward	AAAGAATTC-GCGCCCGCCTTCTCCCTGCCCGACCTGCACGG	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
544a	Forward	AAAAAAGAATTC- GCAATGACTATAAAAAACAAAACTTCCAAGTACTTGC	Eco RI
	Reverse	AAACTGCAG-CTATTGCGCCACGCGCGTATCGAT	Pst I
547	Forward	AAAGAATTC-ATGTTTCGTAGATAACGGATTTAATAAAAC	Eco RI
	Reverse	AAACTGCAG-TTAACAACAAAAACAAACCGCTT	Pst I
548	Forward	AAAGAATTC-GCCTGCAACCTCAAGACAACAGTGCGGC	Eco RI

	Reverse	AAACTGCAG-TCAGAGCAGGGTCCTTACATCGGC	Pst I
550	Forward	AAAAAAGTCGAC- ATGATAACGGACAGGTTTCATCTCTTTTCATTTTCC	Sal I
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
550a	Forward	AAAAAAGAATTC-GTAAATCACGCCTTTGGAGTCGCAAACGG	Eco RI
	Reverse	AAACTGCAG-TTACGCAAACGCTGCAAATCCCC	Pst I
552	Forward	AAAAAAGAATTC-TTGGCGCGTTGGCTGGATAC	Eco RI
	Reverse	AAACTGCAG-TTATTTCTGATGCCTTTTCCCAAC	Pst I
554	Forward	CGCGGATCCCATATG-TCGCCCCGCGCCCAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCCCTGTCAGACAC	XhoI
556	Forward	AAAGAATTC-GCGGGCGGTTTTGTTTGGACATCCCG	Eco RI
	Reverse	AAACTGCAG-TTAACGGTGCGGACGTTTCTGACC	Pst I
557	Forward	CGCGGATCCCATATG-TGCGGTTTCCACCTGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCCGCCTTCAGAAAGG	XhoI
558	Forward	AAAGAATTC-GAGCTTTATATGTTTCAACAGGGGACGGC	Eco RI
	Reverse	AAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
558a	Forward	AAAAAAGAATTC-ATTAGATTCTATCGCCATAAACAGACGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAAACAATGCCGTCTGAAAGTGGAGA	Pst I
560	Forward	AAAAAAGAATTC- TCGCCTTTCCGGGACGGGGCGCACAAGATGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATGCGGTTTCAGACGGCATTTTGGC	Pst I
561	Forward	CCGGAATTCTACATATG-ATACTGCCAGCCCGT	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCTTTCTTCAGATG	XhoI
562	Forward	CGCGGATCCCATATG-GCAAGCCCGTCGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGACCAACTCCAACCTCGT	XhoI
565	Forward	CGCGGATCCCATATG-AAGTCGAGCGCGAAATAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCATTGATCGGCGGC	XhoI
566	Forward	CGCGGATCCCATATG-GTCGGTGGCGAAGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCATGGGCGAAGTCA	XhoI
567	Forward	CCGGAATTCTACATATG-AGTGCGAACATCCTTG	EcoRI- NdeI
	Reverse	CCCGCTCGAG-TTTCCCCGACACCCTCG	XhoI
568	Forward	CGCGGATCCCATATG-CTCAGGGTCAGACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCGCGGCGTTCAG	XhoI
569	Forward	AAAAAAGAATTC-CTGATTGCCTTGTGGGAATATGCCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TTATGCATAGACGCTGATAACGGCAAT	Pst I
570	Forward	CGCGGATCCCATATG-GACACCTTCCAAAAAATCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGGCGTTCATTTCTTT	XhoI

571	Forward	AAAAAAGAATTC- ATGGGTATTGCCGGCGCCGTAAATGTTTTGAACCC	Eco RI
	Reverse	AAAAAACTGCAG-TTATGGCCGACGCGCGGCTACCTGACG	Pst I
572	Forward	CGCGGATCCCATATG-GCGCAAAAAGGCAAAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGCAGTGTGCCGATA	XhoI
573	Forward	CGCGGATCCCATATG-CCCTGTTTGTGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GACGGTGTCAATTCGCC	XhoI
574	Forward	CGCGGATCCCATATG-TGGTTTGCCGCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACTTCGATTTTATTCGGG	XhoI
575	Forward	CGCGGATCCCATATG-GTTTCGGGCGAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGAATCTGAACAG	XhoI
576	Forward	CGCGGATCCCATATG-GCCGCCCCCGCATCT	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTACTTTTTTGATGTCGAC	XhoI
577	Forward	CGCGGATCCCATATG-GAAAGGAACGGTGTATTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGCTGTTTGGTAGATTCTG	XhoI
578	Forward	CGCGGATCCCATATG-AGAAGGTTCTGTACAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCAACGCCTCCACG	XhoI
579	Forward	CGCGGATCCCATATG-AGATTGGGCGTTTCCAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGAATTGATGATGTGTATGT	XhoI
580	Forward	CGCGGATCCCATATG-AGGCAGACTTCGCCGA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CACTTCCCCCGAAGTG	XhoI
581	Forward	CGCGGATCCCATATG-CACTTCGCCCAGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGCCGTTTGGCTTTGG	XhoI
582	Forward	AAAAAAGAATTC-TTTGGAGAGACCGCGCTGCAATGCGC	Eco RI
	Reverse	AAAAAATCTAGA-TCAGATGCCGTCCCAGTCGTTGAA	Xba I
583	Forward	AAAAAAGAATTC-ACTGCCGGCAATCGACTGCATAATCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGGAGGTCAATATGATGAAATTG	Pst I
584	Forward	AAAAAAGAATTC- GCGGCTGAAGCATTGAATTACAATATTGTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGAACTGAACCGTCCCATTGACGCT	Pst I
585	Forward	AAAAAAGGTACC-TCTTTCTGGCTGGTGCAGAACACCCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGTTCGCACTTTTTTCTGTTTGGGA	Pst I
586	Forward	CGCGGATCCCATATG-GCAGCCCATCTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTCAGCGAATCAAGTTTC	XhoI
587	Forward	CGCGGATCCCATATG-GACCTGCCCTTGACGA	BamHI-

	Reverse	CCCGCTCGAG-AAATGTATGCTGTACGCC	NdeI
588	Forward	AAAAAAGAATTC-GCCGTCCTGACTTCCTATCAAGAACCAGG	XhoI
	Reverse	AAAAAACTGCAG-TTATTTGTTTTTGGGCAGTTTCACTTC	Eco RI
589	Forward	AAAAAAGAATTC-	Pst I
		ATGCAACAAAAAATCCGTTTCCAAATCGAAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAATCGATTTTACCCGTTTCAGGCG	Pst I
590	Forward	AAAAAAGAATTC-ATGAAAAAACCTTTGATTTCAGTTGCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCTGCGGCTCTGAAACCAT	Pst I
591	Forward	AAAAAAGAATTC-CACTACATCGTTGCCAGATTGTGCGG	Eco RI
	Reverse	AAAAAACTGCAG-CTAACCGAGCAGCCGGGTAAACGTCGTT	Pst I
592a	Forward	AAAAAAGAATTC-CGCGATTACACCGCCAAGCTGAAAATGGG	Eco RI
	Reverse	AAAAAACTGCAG-TTACCAAACGTCGGATTTGATACG	Pst I
593	Forward	CGCGGATCCGCTAGC-CTTGAACCTGAACGGACTC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-GCGGAAGCGGACGATT	XhoI
594a	Forward	AAAAAAGAATTC-GGTAAGTTCGCCGTTTCAGGCCTTTCA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCCGCCGTTTCCTGACACTCGCG	Pst I
595	Forward	AAAAAAGAATTC-TGCCAGCCGCCGGAGGCGGAGAAAGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCAAGCCGAGTATGCCGCG	Pst I
596	Forward	CGCGGATCCCATATG-TCCCAACAATACGTC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-ACGCGTTACCGGTTTGT	XhoI
597	Forward	CGCGGATCCCATATG-CTGCTTCATGTCAGC	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-ACGTATCCAGCTCGAAG	HindIII
601	Forward	CGCGGATCCCATATG-ATATGTTCCCAACCGGCAAT	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-AAAACAATCCTCAGGCAC	XhoI
602	Forward	CGCGGATCCGCTAGC-TTGCTCCATCAATGC	BamHI-
			NheI
	Reverse	CCCGCTCGAG-ATGCAGCTGCTAAAAGCG	XhoI
603	Forward	AAAAAAGAATTC-CTGTCTCGCGTAGGCGGGGACGGGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAGATGCCGGCAAGTTCGGC	Pst I
604	Forward	CGCGGATCCGCTAGC-CCCGAAGCGCACTT	BamHI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCTGCACGG	XhoI
606a	Forward	AAAAAAGAATTC-CGCGAATACCGCGCCGATGCGGGCGC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAAGCGATTTGAGGCGGGCGATACG	Pst I
607	Forward	AAAAAAGAATTC-ATGCTGCTCGACCTCAACCGCTTTTC	Eco RI
	Reverse	AAAAAACTGCAG-TCAGACGGCCTTATGCGATCTGAC	Pst I
608	Forward	AAAAAAGAATTC-ATGTCCGCCCTCCTCCCCATCATCAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGTCTATCCAAATGTCGCGTTC	Pst I
609	Forward	CGCGGATCCCATATG-GTTGTGGATAGACTCG	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-CTGGATTATGATGTCTGTC	XhoI
610	Forward	CGCGGATCCCATATG-ATTGGAGGGCTTATGCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCTTCAACATCTTTGCC	XhoI
611	Forward	CGCGGATCCCATATG-CCGTCTCAAAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGACTTTGAACGCGCAA	XhoI
613	Forward	CGCGGATCCCATATG-TCGCGTTCGAGCCG3	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCCTGTAAAATAAGCGGC	XhoI
614	Forward	CGCGGATCCCATATG-TCCGTCGTGAGCGGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCATACTGCGGCGTTC	XhoI
616	Forward	AAAAAAGAATTC-ATGTCAAACACAATCAAAATGGTTGTCGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAGTCCGGGCGGCAGGCAGCTCG	Xba I
619a	Forward	AAAAAAGAATTC-GGGCTTCTCGCCGCTCGCTTGC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTTTTGTGTTTTAAACGAGATA	Pst I
622	Forward	CGCGGATCCCATATG-GCCGCCCTGCCTAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGTCCAAATGATAAATCTG	XhoI
624	Forward	CGCGGATCCCATATG-TCCCCGCGCTTTTACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGATTCGGGCCTGCGC	XhoI
625	Forward	CGCGGATCCCATATG-TTTGCAACCAGGAAAATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CGGCAAAATTACCGCCTT	XhoI
627a	Forward	AAAAAAGAATTC-AAAGCAGGCGAGGCAGGCGCGCTGGG	Eco RI
	Reverse	AAAAAACTGCAG- TTACGAATGAAACAGGGTACCCGTCATCAAGGC	Pst I
628	Forward	AAAAAAGGTACC-GCCTTACAAACATGGATTTTGC GTTC	Kpn I
	Reverse	AAAAAACTGCAG-CTACGCACCTGAAGCGCTGGCAAA	Pst I
629a	Forward	AAAAAAGAATTC-GCCACCTTTATCGCGTATGAAAACGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACAACACCGCCGTCGGTTCAAACC	Pst I
630a	Forward	AAAAAAGAATTC-GCGGCTTTGGGTATTTCTTTCGG	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGACTTCGCCAATGGAGCCGGG	Pst I
635	Forward	AAAAAAGAATTC- ATGACCCAGCGACGGGTCTGGCAAGCAAAACCG	Eco RI
	Reverse	AAAAAACTGCAG-TTAATCCACTATAATCCTGTGCT	Pst I
638	Forward	AAAAAAGAATTC-ATGATTGGCGAAAAGTTTATCGTAGTTGG	Eco RI
	Reverse	AAAAAACTGCAG-TCACGAACCGATTATGCTGATCGG	Pst I
639	Forward	CGCGGATCCCATATG-ATGCTTTATTTTGTTCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATCGCGGCTGCCGAC	XhoI
642	Forward	CGCGGATCCCATATG-CGGTATCCGCCGCAAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGATTGCGGGGCATTA	XhoI

643	Forward	CGCGGATCCCATATG-GCTTCGCCGTCGGCAG	BamHI- NdeI XhoI
	Reverse	CCCGCTCGAG-AACCGAAAAACAGACCGC	Eco RI
644	Forward	AAAAAAGAATTC- ATGCCGTCTGAAAGGTCGGCGGATTGTTGCCC	Pst I
	Reverse	AAAAAATCTAGA-CTACCCGCAATATCGGCAGTCCAATAT	Eco RI
645	Forward	AAAAAAGAATTC-GTGGAACAGAGCAACACGTTAAATCG	Pst I
	Reverse	AAAAAACTGCAG-CTACGAGGAAACCGAAGACCAGGCCGC	Eco RI
647	Forward	AAAAAAGAATTC-ATGCAAAGGCTCGCCGCAGACGG	Pst I
	Reverse	AAAAAACTGCAG-TTAGATTATCAGGGATATCCGGTAGAA	Eco RI
648	Forward	AAAAAAGAATTC- ATGAACAGGCGCGACGCGCGGATCGAACG	Pst I
	Reverse	AAAAAACTGCAG-TCAAGCTGTGTGCTGATTGAATGCGAC	Eco RI
649	Forward	AAAAAAGAATTC-GGTACGTCAGAACCCGCCACCG	Pst I
	Reverse	AAAAAACTGCAG-TTAACGGCGGAAACTGCCGCCGTC	Eco RI
650	Forward	AAAAAAGAATTC-ATGTCCAAACTCAAACCATCGC	Pst I
	Reverse	AAAAAACTGCAG-TCAGACGGCATGGCGGTCTGTTTT	Kpn I
652	Forward	AAAAAAGGTACC- GCTGCCGAAGACTCAGGCCTGCCGCTTTACCG	Pst I
	Reverse	AAAAAACTGCAG-TTATTTGCCAGTTGGTAGAATGCGGC	Eco RI
653	Forward	AAAAAAGAATTC-GCGGCTTTGCCGGTAATTTTCATCGG	Pst I
	Reverse	AAAAAACTGCAG-CTATGCCGGTCTGGTTGCCGGCGGCGA	Eco RI
656a	Forward	AAAAAAGAATTC-CGGCCGACGTCGTTGCGTCCTAAGTC	Pst I
	Reverse	AAAAAACTGCAG-CTACGATTTGGCGATTTCACATCGT	Eco RI
657	Forward	AAAAAAGAATTC-GCAGAATTTGCCGACCGCCATTTGTGCGC	Pst I
	Reverse	AAAAAACTGCAG-TTATAGGGACTGATGCAGTTTTTTTGC	BamHI- NdeI XhoI
658	Forward	CGCGGATCCCATATG-GTGTCGGAATTGTG	Eco RI
	Reverse	CCCGCTCGAG-GGCAGAATGTTTACCGTT	Pst I
661	Forward	AAAAAAGAATTC- ATGCACATCGGCGGCTATTTTATCGACAACCC	BamHI- NdeI XhoI
	Reverse	AAAAAACTGCAG-TCACGACGTGTCTGTTTCGCCGTCGGGC	Eco RI
663	Forward	CGCGGATCCCATATG-TGTATCGAGATGAAATT	Pst I
	Reverse	CCCGCTCGAG-GTAAAAATCGGGGCTGC	BamHI- NdeI XhoI
664	Forward	CGCGGATCCCATATG-GCGGCTGGCGCGGT	Pst I
	Reverse	CCCGCTCGAG-AAATCGAGTTTTACACCAC	Eco RI
665	Forward	AAAAAAGAATTC-ATGAAATGGGACGAAACGCGCTTCGG	Pst I
	Reverse	AAAAAACTGCAG-TCAATCCAAAATTTGCCGACGATTTC	Eco RI
666	Forward	AAAAAAGAATTC-AACTCAGGCGAAGGAGTGCTTGTTGGC	Xba I
	Reverse	AAAAAATCTAGA-TCAGTTTAGGGATAGCAGGCGTAC	Eco RI
667	Forward	AAAAAAGAATTC- CCGCATCCGTTTGATTTCATTTCGTATTCGTCCG	Pst I
	Reverse	AAAAAACTGCAG-TTAATGACACAATAGGCGCAAGTC	

669	Forward	AAAAAAGAATTC-ATGCGCCGCATCATTAACACACCAGCC	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTATCCGTTTGATGTCGGC	Pst I
670a	Forward	AAAAAAGAATTC-AAAAACGCTTCGGGCGTTTCGTCTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAGGAGCTTTTGGAACGCGTCGGACTGGC	Pst I
671	Forward	CGCGGATCCCATATG-ACCAGCAGGGTAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGCAACTATAAAAAACGCAAG	XhoI
672	Forward	CGCGGATCCCATATG-AGGAAAATCCGCACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGGGATAGGCGGTTG	XhoI
673	Forward	AAAAAAGAATTC-ATGGATATTGAAACCTTCCTTGCAGG	Eco RI
	Reverse	AAAAAACTGCAG-CTACAAACCCAGCTCGCGCAGGAA	Pst I
674	Forward	AAAAAAGAATTC-ATGAAAACAGCCCGCCGCGTTCCCG	Eco RI
	Reverse	AAAAAACTGCAG-TCAACGGCGTTTGGGCTCGTCGGG	Pst I
675	Forward	CGCGGATCCCATATG-AACACCATCGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTCTTCGTCTTCAAACCTGT	XhoI
677a	Forward	AAAAAAGAATTC-AGACGGCATTCCCGATCAGTCGATTTTGA	Eco RI
	Reverse	AAAAAACTGCAG-TTACGTATGCGCGAAATCGACCGCCCG	Pst I
680	Forward	CGCGGATCCGCTAGC-ACGAAGGGCAGTTCGG	BamHI- NheI
	Reverse	CCCGCTCGAG-CATCAAAAACCTGCCGC	XhoI
681	Forward	AAAAAAGAATTC-ATGACGACGCCGATGGCAATCAGTGC	Eco RI
	Reverse	AAAAAACTGCAG-TTACCGTCTTCCGCAAAAAACAGC	Pst I
683	Forward	CGCGGATCCCATATG-TGCAGCACACCGGACAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAGTTTTTTTCCGCATACG	XhoI
684	Forward	CGCGGATCCCATATG-TGCGGTACTGTGCAAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTCGACCATCTGTTGCG	XhoI
685	Forward	CGCGGATCCCATATG-TGTTTGCTTAATAATAAACATT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCA	XhoI
686	Forward	CGCGGATCCCATATG-TGCGGCGGTTTCGGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CATTCCGATTCTGATGAAG	XhoI
687	Forward	CGCGGATCCCATATG-TGCGACAGCAAAGTCCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTGCGCGGCTTTTTGTT	XhoI
690	Forward	CGCGGATCCCATATG-TGTTCTCCGAGCAAAGAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TATTCGCCCCGTGTTTGG	XhoI
691	Forward	CGCGGATCCCATATG-GCCACGGCTTATATCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGGCAGGAAGAAAG	XhoI



694	Forward	CGCGGATCCCATATG-TTGGTTTCCGCATCCGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCTGCGTCGGTGCGGT	XhoI
695	Forward	CGCGGATCCCATATG-TTGCCTCAAACCTCGTCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
696	Forward	CGCGGATCCCATATG-TTGGGTTGCCGGCAGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGATTGCCGCAATGATG	XhoI
700a	Forward	AAAAAAGAATTC-GCATCGACAGACGGTGTGTCGTGGAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACGCTACCGGCACGACTTCCAAACC	Pst I
701	Forward	CGCGGATCCCATATG-AAGACTTGTTTGATACTTC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TGCCGACAACAGCCTC	XhoI
702	Forward	AAAAAAGAATTC-ATGCCGTGTTCCAAAGCCAGTTGGATTTC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACCCCATTCACCCGGAGAACCGA	Pst I
703	Forward	CGCGGATCCGCTAGC-CAAACGCTGGCAACCG	BamHI- NheI
	Reverse	CCCGCTCGAG-TTTTGCAGGTTTGATGTTTG	XhoI
704a	Forward	AAAAAAGAATTC-GCTTCTACCGGTACGCTGGCGCG	Eco RI
	Reverse	AAAAAACTGCAG- TTAGTTTTCGCCGATAATATGGCGGGTGCG	Pst I
707	Forward	CGCGGATCCGCTAGC-GAAATTATTAACGATGCAGA	BamHI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGA	XhoI
708	Forward	CGCGGATCCGCTAGC-CCTTTTAAGCCATCCAAAA	BamHI- NheI
	Reverse	CCCGCTCGAG-TTGACCGGTGAGGACG	XhoI
710	Forward	CGCGGATCCCATATG-GAAACCCACGAAAAAATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AACGGTTTCGGTCAG	XhoI
714	Forward	CGCGGATCCCATATG-AGCTATCAAGACATCTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCGGTAGGTAAATCGGAT	XhoI
716	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTAGAACCGCATTGTC	XhoI
718	Forward	CGCGGATCCCATATG-GAGCCGATAATGGCAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GGCGCGGGCATGGTCTTGTC	XhoI
720	Forward	CGCGGATCCCATATG-AGCGGATGGCATAACC	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTTGCATAGCTGTTGACCA	XhoI
723	Forward	CGCGGATCCCATATG-CGACCCAAGCCCC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AATGCGAATCCGCCGCC	XhoI



725	Forward	CGCGGATCCCATATG-GTGCGCACGGTTAAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTATCCTTAAGGGTTA	XhoI
726	Forward	CGCGGATCCCATATG-ACCATCTATTTCAAAAC	BamHI- NdeI
	Reverse	CCCGCTCGAG-GCCGATGTTTAGCGTCC	XhoI
728	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	XhoI
729	Forward	CGCGGATCCCATATG-TGCACCATGATTCCCCA	BamHI- NdeI
	Reverse	GCCCAAGCTT-TTTGTCGGTTTGGGTATC	HindIII
731	Forward	CGCGGATCCGCTAGC-GCCGTGCCGGAGG	BamHI- NheI
	Reverse	CCCGCTCGAG-ACGGGCGCGGCAG	XhoI
732	Forward	CCGGAATTCTACATATG-TCGAAACCTGTTTTTAAGAA	EcoRI- NdeI
	Reverse	CCCGCTCGAG-CTTCTTATCTTTTTTATCTTTC	XhoI
733	Forward	CGCGGATCCCATATG-GCCTGCGGCGGCAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGCTTGCCTCCTTTAC	XhoI
734	Forward	CGCGGATCCCATATG-GCCGATACTTACGGCTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAGATTTTGAATCAAAGAG	XhoI
735	Forward	CGCGGATCCCATATG-AAGCAGCAGGCGGTCA	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATTTCCGTAGCCGAGGG	XhoI
737	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	BamHI- NdeI
	Reverse	CCCGCTCGAG-GTCGTGCGGCGGGA	XhoI
739	Forward	CGCGGATCCCATATG-GCAAAAAAACCGAACA	BamHI- NdeI
	Reverse	CCCGCTCGAG-GAAGAGTTTGTGCGAGAATT	XhoI
740	Forward	CGCGGATCCCATATG-GCCAATCCGCCGAAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAACGCGCCAAAATAGTG	XhoI
741	Forward	CGCGGATCCCATATG-TGCAGCAGCGGAGGG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTGCTTGGCGGCAAGGC	XhoI
743	Forward	CGCGGATCCCATATG-GACGGTGTGTGCCTGTT	BamHI- NdeI
	Reverse	CCCGCTCGAG-CTTACGGATCAAATTGACG	XhoI
745	Forward	CGCGGATCCCATATG-TTTTGGCAACTGACCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-CAAATCAGATGCCTTTAGG	XhoI
746	Forward	CGCGGATCCCATATG-TCCGAAAACAAACAAAAC	BamHI-

	Reverse	CCCGCTCGAG-TTCATTCGTTACCTGACC	NdeI
747	Forward	CCGGAATTCTAGCTAGC-CTGACCCCTTGGG	XhoI
	Reverse	GCCCAAGCTT-TTTTGATTTTAATTGACTATAGAAC	EcoRI-
749	Forward	CGCGGATCCCATATG-TGCCAGCCGCCG	NheI
	Reverse	CCCGCTCGAG-TTCAAGCCGAGTATGC	HindIII
750	Forward	CGCGGATCCCATATG-TGTTGCCCCGAACCTG	BamHI-
	Reverse	CCCGCTCGAG-CTTTTTCCCCGCCGCAA	NdeI
758	Forward	CGCGGATCCCATATG-AACAATCTGACCGTGTT	XhoI
	Reverse	CCCGCTCGAG-TGGCTCAATCCTTTCTGC	BamHI-
759	Forward	CGCGGATCCGCTAGC-CGTTTACACACACCAC	NdeI
	Reverse	CCCGCTCGAG-CCAGTTGTAGCCTATTTTG	XhoI
763	Forward	CGCGGATCCCATATG-CTGCCTGAAGCATGGCG	BamHI-
	Reverse	CCCGCTCGAG-TTCCGCAAATACCGTTTCC	NdeI
764	Forward	CGCGGATCCCATATG-TTTTCTCCGCCCTGA	XhoI
	Reverse	CCCGCTCGAG-TCGCTCCCTAAAGCTTTC	BamHI-
765	Forward	CGCGGATCCCATATG-TTAAGATGCCGTCCG	NdeI
	Reverse	CCCGCTCGAG-ACGCCGACGTTTTTTATTAA	XhoI
767	Forward	CGCGGATCCCATATG-CTGACGGAAGGGGAAG	BamHI-
	Reverse	CCCGCTCGAG-TTTCTGTACAGCAGGGG	NdeI
768	Forward	CGCGGATCCCATATG-GCCCCGCAAAAACCCG	XhoI
	Reverse	CCCGCTCGAG-TTTCATCCCTTTTTTGAGC	BamHI-
770	Forward	CGCGGATCCCATATG-TGCGGCAGCGGCGAA	NdeI
	Reverse	CCCGCTCGAG-GCGTTTGTCGAGATTTTC	XhoI
771	Forward	CGCGGATCCCATATG-TCCGTATATCGCACCTTC	BamHI-
	Reverse	CCCGCTCGAG-CGGTTCTTTAGGTTTGAG	NdeI
772	Forward	CGCGGATCCCATATG-TTTGCGGCGTTGGTGG	XhoI
	Reverse	CCCGCTCGAG-CAATGCCGACATCAAACG	BamHI-
774	Forward	CGCGGATCCCATATG-TCCGTTTACCCGTTCC	NdeI
	Reverse	CCCGCTCGAG-TCGTTTGCGCACGGCT	XhoI
790	Forward	CGCGGATCCCATATG-GCAAGAAGGTCAAAAAC	BamHI-
			NdeI

	Reverse	CCCGCTCGAG-GGCGTTGTTCCGGATTTCG	XhoI
900	Forward	CGCGGATCCCATATG-CCGTCTGAAATGCCG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ATATGGAAAAGTCTGTTGTC	XhoI
901	Forward	CGCGGATCCCATATG-CCCGATTTTTCGATG	BamHI- NdeI
	Reverse	CCCGCTCGAG-AAAATGGAACAATACCAGG	XhoI
902	Forward.	CCGGAATTCTACATATG-TTGCACTTTCAAAGGATAATC	EcoRI- NdeI
	Reverse	CCCGCTCGAG-AAAAATGTACAATGGCGTAC	XhoI
903	Forward	CCGGAATTCTAGCTAGC-CAGCGTCAGCAGCACAT	EcoRI- NheI
	Reverse	CCCGCTCGAG-GAAACTGTAATTCAAGTTGAA	XhoI
904	Forward	AAAAAAGGTACC-ATGATGCAGCACAAATCGTTTC	Kpn I
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
904a	Forward	AAAAAAGAATTC-CGGCTCGGCATTGTGCAGATGTTGCA	Eco RI
	Reverse	AAACTGCAG-TTAATATCGATAGGTTATATG	Pst I
905	Forward	CGCGGATCCCATATG-AACAAAATATACCGCATC	BamHI- NdeI
	Reverse	CCCGCTCGAG-CCACTGATAACCGACAGAT	XhoI
907	Forward	CGCGGATCCCATATG-GGCGCGCAACGTGAG	BamHI- NdeI
	Reverse	CCCGCTCGAG-ACGCCACTGCCAGCG	XhoI
908	Forward	AAAGAATTC-GCAGAGTTAGTAGGCGTTAATAAAAATAC	Eco RI
	Reverse	AAACTGCAG-TTAATATGGTTTTGTCGTTTCG	Pst I
909	Forward	CGCGGATCCCATATG-TGCGCGTGGGAAACTTAT	BamHI- NdeI
	Reverse	CCCGCTCGAG-TCGGTTTTGAACTTTGGTTTT	XhoI
910	Forward	AAAGAATTC-GCATTGCGCGGCGACTCTGCCGAGCG	Eco RI
	Reverse	AAACTGCAG-TCAGCGATCGAGCTGCTCTTT	Pst I
911	Forward	AAAGAATTC-GCTTCCGCGTGGCCGGCGGTGC	Eco RI
	Reverse	AAAAAACTGCAG-GTCGACTTATTCGGCGGCTTTTCCGC	Pst I
912	Forward	AAAAAAGAATTC- CAAATCCGTCAAACGCCACTCAAGTATTGAG	Eco RI
	Reverse	AAAAAACTGCAG-TTACAGTCCGTCCACGCCTTTCGC	Pst I
913	Forward	CGCGGATCCCATATG-GAAACCCGCCCCGC	BamHI- NdeI
	Reverse	CCCGCTCGAG-AGGTTGTGTTCCAGGTTG	XhoI
915	Forward	CGCGGATCCCATATG-TGCCGGCAGGCGGAA	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGAAAATATAGGTATCAGG	XhoI
914	Forward	AAAGAATTC-GACAGAATCGGCGATTTGGAAGCACG	Eco RI
	Reverse	AAACTGCAG-CTATATGCGCGGCAGGACGCTCAACGG	Pst I
916	Forward	CGCGGATCCCATATG-GCAATGATGGCGGCTG	BamHI- NdeI
	Reverse	CCCGCTCGAG-TTTGGCGGCATCTTTCAT	XhoI

917	Forward	AAAAAAGAATTC-CCTGCCGAAAAACCGGCACCGGC	Eco RI
	Reverse	AAAAAACTGCAG-TTATTTCCCCGCCTTCACATCCTG	Pst I
919	Forward	CGCGGATCCCATATG-TGCCAAAGCAAGAGCATC	BamHI-
	Reverse	CCCGCTCGAG-CGGGCGGTATTCTGGG	NdeI
			XhoI
920	Forward	CGCGGATCCCATATG-CACCGCGTCTGGGTC	BamHI-
	Reverse	CCCGCTCGAG-ATGGTGCGAATGACCGA	NdeI
			XhoI
921	Forward	AAAAAAGAATTC-TTGACGGAAATCCCCGTGAATCC	Eco RI
	Reverse	AAAAAACTGCAG-TCATTTCAAGGGCTGCATCTTCAT	Pst I
922	Forward	CGCGGATCCGCTAGC-TGTACGGCGATGGAGGC	BamHI-
	Reverse	CCCGCTCGAG-CAATCCCGGGCCGCC	NdeI
			XhoI
923	Forward	CGCGGATCCCATATG-TGTTACGCAATATTGTCCC	BamHI-
	Reverse	CCCGCTCGAG-GGACAAGGCGACGAAG	NdeI
			XhoI
925	Forward	CGCGGATCCCATATG-AAACAAATGCTTTTAGCCG	BamHI-
	Reverse	CCCGCTCGAG-GCCGTTGCATTTGATTTT	NdeI
			XhoI
926	Forward	CGCGGATCCCATATG-TGCGCGCAATTACCTC	BamHI-
	Reverse	CCCGCTCGAG-TCTCGTGCGCGCCG	NdeI
			XhoI
927	Forward	CGCGGATCCCATATG-TGCAGCCCCGCAGC	BamHI-
	Reverse	CCCGCTCGAG-GTTTTTTGCTGACGTAGT	NdeI
			XhoI
929a	Forward	AAAAAAGAATTC-CGCGGTTTGCTCAAAACAGGGCTGGG	Eco RI
	Reverse	AAAAAATCTAGA-TTAAGAAAGACGGAACTACTGCC	Xba I
931	Forward	AAAAAAGAATTC-GCAACCCATGTTTTGATGGAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTGCCCCGACAACAACGCGACG	Pst I
935	Forward	AAAAAAGAATTC-GCGGATGCGCCCGCGATTTTGGATGACAAGGC	Eco RI
	Reverse	AAAAAACTGCAG-TCAAAACCGCCAATCCGCCGACAC	Pst I
936	Forward	CGCGGATCCCATATG-GCCGCCGTCGGCGC	BamHI-
	Reverse	CCCGCTCGAG-GCGTTGGACGTAGTTTTG	NdeI
			XhoI
937	Forward	AAAAAAGAATTC-CCGGTTTACATTCAAACCGGCGCAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTAAATGTATGCTGTACGCCAA	Pst I
939a	Forward	AAAAAAGAATTC-GGTTCCGGCAGCTGTGATGAAACC	Eco RI
	Reverse	AAAAAACTGCAG-TTAACGCAAACCTTGGATAAAGTTGGC	Pst I
950	Forward	CGCGGATCCCATATG-GCCAACAAACCGGCAAG	BamHI-
	Reverse	CCCGCTCGAG-TTAGAACCGCATTGTC	NdeI
			XhoI
953	Forward	CGCGGATCCCATATG-GCCACCTACAAAGTGGAC	BamHI-
	Reverse	CCCGCTCGAG-TTGTTTGGCTGCCTCGAT	NdeI
			XhoI
957	Forward	CGCGGATCCCATATG-TTTTGGCTGGGAACGGG	BamHI-

	Reverse	CCCGCTCGAG-GTGAGAAAGGTCGCGC	NdeI
958	Forward	CGCGGATCCCATATG-GCCGATGCCGTTGCG	XhoI
			BamHI-
	Reverse	GCCCAAGCTT-GGGTCGTTTGTTCGTC	NdeI
959	Forward	CGCGGATCCCATATG-CACCACGACGGACACG	HindIII
			BamHI-
	Reverse	CCCGCTCGAG-GTCGTCGCGGCGGGA	NdeI
961	Forward	CGCGGATCCCATATG-GCCACAAGCGACGACG	XhoI
			BamHI-
	Reverse	CCCGCTCGAG-CCACTCGTAATTGACGC	NdeI
972	Forward	AAAAAAGAATTC- TTGACTAACAGGGGGGGAGCGAAATTAAAAAC	XhoI
			Eco RI
	Reverse	AAAAAATCTAGA-TTAAAAATAATCATAATCTACATTTTG	Xba I
973	Forward	AAAAAAGAATTC-ATGGACGGCGCACAAACCGAAAAC	Eco RI
	Reverse	AAAAAACTGCAG-TTACTTCACGCGGGTCGCCATCAGCGT	Pst I
982	Forward	CGCGGATCCCATATG-GCAGCAAAGACGTAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CATCATGCCGCCCATCC	XhoI
983	Forward	CGCGGATCCCATATG-TTAGCTGTTGCAACAACAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACCGGTAGCCTACG	XhoI
987	Forward	CGCGGATCCCATATG-CCCCACTGGAAGAAC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TAATAAACCTTCTATGGGC	XhoI
988	Forward	CGCGGATCCCATATG-TCTTTAAATTACGGGAAAAAG	BamHI-
			NdeI
	Reverse	GCCCAAGCTT-TGATTTGCCTTTCCGTTTT	HindIII
989	Forward	CCGGAATTCTACATATG-GTCCACGCATCCGGCTA	EcoRI-
			NdeI
	Reverse	CCCGCTCGAG-TTTGAATTTGTAGGTGTATTGC	XhoI
990	Forward	CGCGGATCCGCTAGC-TTCAGAGCTCAGCTT	BamHI-
	2		NheI
	Reverse	CCCGCTCGAG-AAACAGCCATTGAGCGA	XhoI
992	Forward	CGCGGATCCCATATG-GACGCGCCCGCCCG	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-CCAAATGCCCAACCATTC	XhoI
993	Forward	CGCGGATCCCATATG-GCAATGCTGATTGAAATCA	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-GAACACATCGCGCCCG	XhoI
996	Forward	CGCGGATCCCATATG-TGCGGCAGAAAATCCGC	BamHI-
			NdeI
	Reverse	CCCGCTCGAG-TCTAAACCCCTGTTTTCTC	XhoI
997	Forward	CCGGAATTCTAGCTAGC-CGGCACGCCGACGTT	EcoRI-
			NheI
	Reverse	CCCGCTCGAG-GACGGCATCGCTCAGG	XhoI

Underlined sequences indicate restriction recognition sites.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1>:

```

g001.seq
1   ATGCTGCCGC AGGGGAAGGC GGC GCGGAGG GTGTCGGCGA ACGAGGTGTG
51  CCGCAGGGCT TGGCCCCGGA TGGTGCTGGT CATCTGCCAG ACGCTGCCGA
101 AACGCGATAC TTAAACGGC TCGGTACGC ATACTTTACC GGTTTGGGCG
151 ATTTTGCCGA GGTGCTTGGC CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GTAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301 CCGTCTGAAG CGATGTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351 CCGGATTGTC CCGGCTTCAT CCGGCAGGTG GGACAATACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2; ORF 001.ng>:

```

g001.pep
1   MLPQKAARR VSANEVSGRA CARMVLVICQ TLPKRDTLNG SGTHTLPVWA
51  ILPRSLRSKS TIITFSARFF GSVNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEAMLRKSS GEKHSVHAD C PASSGRWDNT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3>:

```

m001.seq
1   ATGCTGCCGC AGGGGAAGGC GGC GCGGAGG ATGTCGGCGA ACGAGGTGTG
51  CCGCAssCTT ss.GCTTGGA YGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTTGGGCG
151 ATTTTGCCGA GATCGTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351 CCGGATTGTC CCTCCGCAT CCGGCAGGTG GGACAAGACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 4; ORF 001>:

```

m001.pep
1   MLPQKAARR MSANEVCGXL XAWXVLVICQ TLPKRDTLNG SGTHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PSASGRWDKT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 5>:

```

a001.seq
1   ATGCTGCCGC AGGGGAAGGC GGC GCGGAGG ATGTCGGCGA ACGAGGTGTG
51  CCGCAAGGCT TGGGCTTGGA TGGTGCTGGT CATCTGCCAA ACGCTGCCGA
101 AACGCGATAC TTAAACGGT TCGGTACGC ATACTGTGCC GGTTTGGGCG
151 ATTTTGCCGA GGTGCTTACG CAGCAAATCG ACAATCATCA CGTTTTCGGC
201 GCGGTTTTTC GGTCTGCTT GCAACTCGGC GCGCGGCGT TCGTCTTGTC
251 CGTCGCCCAA AATCGGCGCG GTGCCTTTCA TCGGTTTCGGT GCTGATGGTG
301 CCGTCCGAAC CGATTTTGAG GAAGAGTTCG GCGGAGAAAC ACAGCGTCCA
351 CCGGATTGTC CTTGTGCAT CCGGCAGGTG GGACAAAACG GCATAG

```

This corresponds to the amino acid sequence <SEQ ID 6; ORF 001.a>:

```

a001.pep
1   MLPQKAARR MSANEVCGKA WAWMVLVICQ TLPKRDTLNG SGTHTVPVWA
51  ILPRSLRSKS TIITFSARFF GSACNSAARR SSCPSPKIGA VPFIGSVLMV
101 PSEPILRKSS GEKHSVHAD C PCASGRWDKT A*

```

m001/a001 96.2% identity over a 131 aa overlap

```

          10      20      30      40      50      60
m001.pep  MLPQKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS
          |||||
a001.pep  MLPQKAARRMSANEVCGKAWAWMVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS

```

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	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
a001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
a001.pep	PCASGRWDKTAX					
	130					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 001 shows 89.3% identity over a 131 aa overlap with a predicted ORF (ORF 001.ng) from *N. gonorrhoeae*:

m001/g001

	10	20	30	40	50	60
m001.pep	MLPQGKAARRMSANEVCGXLXAWXVLVICQTLPKRDTLNGSGTHTVPVWAILPRSLRSKS					
g001	MLPQGKAARRVSAANEVSGRACARMVLVICQTLPKRDTLNGSGTHTLPVWAILPRSLRSKS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m001.pep	TIITFSARFFGSACNSAARRSSCPSPKIGAVPFIGSVLMVPSEPILRKSSGEKHSVHADC					
g001	TIITFSARFFGSVCNSAARRSSCPSPKIGAVPFIGSVLMVPSEAMLRKSSGEKHSVHADC					
	70	80	90	100	110	120
	130					
m001.pep	PSASGRWDKTAX					
	:					
g001	PASSGRWDNTAX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 7>:

g003.seq

```

1  ATGGTCGTAT TCGTGGCTGA AGGCGTATTC GGTTCGCGCTG TTTTGGGTCA
51  CTTGGTATTG CTCTTCGGTC AGGGTGCGTT TGAGTTCGGC GTCACCTCGGT
101 TTTTATACG TTGCCCGGTC GAAGCCTTTG CCTTGCGGTG CGGCTTTGGT
151 TTTGCCCGGC AGCGGTTTCGT CGGCTTTGCG GATGTCGATG TGGCAGTAGC
201 CGTTGGGGTT TTTAATCAGG TAGTCCTGAT GGTATTCCTC GGCGTCGTAG
251 AAGTTTTTCA GCGGTTTCGT TTCAACAACG AGGGGCAGTT GGTATTTTGT
301 CTGCTCGCGT TTGAGGGCGG CGGCGATGAC GGCTTTTTCG GCGGGGTCGG
351 TGAGTACAC GCCGCTGCGG TATTGCGTGC CGGTGTCGTT ACCCTGTTTG
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAA TAATATTGCA GGATGTCGTC
451 CAGgCTGagt TTGTCGGCAT CGTaggtcac tTTGACGGTC TCGGCATGAC
501 CCGTATGGCG GTaggacact tctTCgtanc TcGGGtTTTC CGTGttGCCG
551 TTGGCgttac cGGATACCGC gtcaACCACG CCGTcgatgc gttggaAATa
601 ggCTTCCAAG ccccaaaagc agccgccggc gaagtaaata gtgcccgtgt
651 tcatgattGC TGa

```

This corresponds to the amino acid sequence <SEQ ID 8; ORF 003.ng>:

g003.pep

```

1  MVVFVAEGVF GRAVLGHLVL LFGQGAFFFG VTRFFIRCRV EAFALRCGFG
51  FARQRFVGFA DVDVAVAVGV FNQVLMVFL GVVEVFQRFV FNEGQLVFL
101 LLAFEGGGDD GFFGGVGVVH AAVALRAGVV TLFVEAGRIN DAEIILQDVV

```

151 QAEFVGIVGH FDGLGMTRMA VGHEFVRVER VAVGVTGYRV NHAVDALIEIG  
201 FQAPKAAAGE VNGARVHDC.

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 9>:

m003.seq  
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA  
51 CTTGstATTG CTCTTCGGTC AGGGTGC GTT TGAGTTCGGC GTCACCTCGGT  
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGC GGCG CGGTCTTGGT  
151 TTTGCCCCGC AGCGGTTTCGT CAGCKTTGCG GATGTCGATG TGGCAGTAGC  
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG  
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTGG  
301 CTGCTCGCGT TTGAGGGCGk CCGCGATGAC GGCTTTTTTCG kCGGGGTCCG  
351 TGAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG  
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC  
451 TAGGCTGAGT TTGTCCGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGCG  
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGG  
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAATA  
601 GGCTTCCAAG CCCAGAAGC AGCg.CCGGC GAGGTAAATG GTGCGCGTGT  
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 10; ORF 003>:

m003.pep Length: 221  
1 MVVFVAEGIF GRAVLGNLXL LFGQGAFFEG VTRFFIRCRV EAFALRGGLG  
51 FARQRFVSXA DVDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL  
101 LLAFEGXGDD GFFXGVGVVH AAVLRTGVV ALFVEAGRIN DAEIILQDVV  
151 \*AEFVGIVGH FDGFGVARMA VGHVFIARIF RAVGVAGYR VNHAVDALIEI  
201 GFQAPEAAXG EVNGARVHDF \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 11>:

a003.seq  
1 ATGGTCGTAT TCGTGGCTGA AGGCATATTC GGTCGCGCTG TTTTGGGTAA  
51 CTTGGTATTG CTCTTCGGTC AGGGTGC GTT TGAGTTCGGC GTCACCTCGGT  
101 TTTTATACG TTGCCGCGTC GAAGCCTTTG CCTTGC GGCG CGGTCTTGGT  
151 TTTGCCCGGC AGCGGTTTCGT CCGCTTTGCG GATATCGATG TGGCAGTAGC  
201 CGTTGGGGTT TTTAATCAAG TAGTCCTGAT GGTATTCCTC GGCATCGTAG  
251 AAGTTTTtCA GCGGCTCGTT TTCAACAACG AGGGGCAGTT GGTATTTTGG  
301 CTGCTCGCGT TTGAGGGCGG CCGCGATGAC GGCTTTTTTCG GCGGGGTCCG  
351 TGAGTACAC GCCGCTGCGG TATTGCGTAC CGGTGTCGTT GCCCTGTTTG  
401 TTGAGGCTGG TCGGATCAAC GACGCGGAAG AAATATTGCA GGATGTCGTC  
451 TAGGCTGAGT TTGTCCGCAT CGTAGGTCAC TTTGACGGTT TCGGCGTGCG  
501 CCGTATGGCG GTAGGACACG TCTTCATAGC TCGGATTTTT CGTGTGCGG  
551 TTGGCGTAGC CGGATACCGC GTCAACCACG CCGTCGATGC GTTGGAATA  
601 GGCTTCCAAG CCCAGAAGC AGCCGCCGGC GAGGTAGATG GTGCGCGTGT  
651 TCATGATTTT TGA

This corresponds to the amino acid sequence <SEQ ID 12; ORF 003.a>:

a003.pep  
1 MVVFVAEGIF GRAVLGNLVL LFGQGAFFEG VTRFFIRCRV EAFALRCGLG  
51 FARQRFVGFA DIDVAVAVGV FNQVLMVFL GIVEVFQRLV FNNEGQLVFL  
101 LLAFEGGGDD GFFGGGVGVH AAVLRTGVV ALFVEAGRIN DAEIILQDVV  
151 \*AEFVGIVGH FDGFGVARMA VGHVFIARIF RAVGVAGYR VNHAVDALIEI  
201 GFQAPEAAG EVDGARVHDF \*

m003/a003 95.9% identity over a 220 aa overlap

	10	20	30	40	50	60
m003.pep	MVVFVAEGIFGRAVLGNLXLFFGQGAFFEGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
a003	MVVFVAEGIFGRAVLGNLVLFFGQGAFFEGVTRFFIRCRVEAFALRCGLGFARQRFVGFA					
	10	20	30	40	50	60



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	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
a003	DIDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
a003	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
a003	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
	190	200	210	220		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 003 shows 88.6% identity over a 219 aa overlap with a predicted ORF (ORF 003.ng) from *N. gonorrhoeae*:

m003/g003

	10	20	30	40	50	60
m003.pep	MVVFVAEGVIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRGGLGFARQRFVSXA					
g003	MVVFVAEGVIFGRAVLGNLXLLFGQGAFFGVTRFFIRCRVEAFALRCGFGFARQRFVGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m003.pep	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGXGDDGFFXGVGVVH					
g003	DVDVAVAVGVFNQVVLVFLGIVEVFQRLVFNNEGQLVFLLLAFEGGGDDGFFGGGVGVVH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m003.pep	AAAVLRTGVVALFVEAGRINDAEIILQDVVXAEFVGIVGHFDGFGVARMVGHVFIARIF					
g003	AAAVLRAGVTLFVEAGRINDAEIILQDVVQAEFVGIVGHFDGLGMTRMAVGHFFV-RVF					
	130	140	150	160	170	180
	190	200	210	220		
m003.pep	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDFX					
g003	RVAVGVAGYRVNHAVDALFQAEPAAXGEVNGARVHDC					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 13>:

g004.seq

```

1  ATGgtagAAC GGCATATCCA GCATTGCGG AACGGTCATC TTCATTGTAT
51  GCGCCCATGC CAACAagtga gccAAAtgtT CGGCGGCAGG GCCTacgatT
101 TCCGCGCCGA TAAagcggcc gGTGgctTTT tcgGCataca ggcgcaTatg
151 gCCTTTGTTT ACCAgcatca cgcggtgctg accttgatTTT TTGAACGATA
201 CTTCCGCgAT GACAAATTCG TCGGCTTGGT ATTGCGCGGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTTCGgga ctggtaaACA CCACGCCAAT
301 GGTgctgctg cGCAACCGC TGCCGATATt cgGgtagcgg ccccgcggtta
351 ttgcccggca atcttacctt ggtcggcggc ttcATGCAGC AGGGGcagtt
401 ggttgacgc gtcgcccgc ataAAGATAT GCGGAAtgct ggtCTGCATg
451 gtCAGCGGAT CGGCAACGGG tacgccgcgc gcgtctttgt CGATATTGAT
501 GTTTTCCAAA CCGATATtGT CAACGTTCCG ACGGCgACCT ACGGCTGCCA

```

```

551 ACATATATTC GGCAACAAAT ACGCCTTTTT CGCCATCCTG CTCCCAATGG
601 ACTtctACAT TGCCGTCTGC GTCGAGTTG ACCTCGGTTT TAGCATCCAG
651 ATGCAGTTTC AATtctTCTC CGAACACGGC TTTCGCCTCG TCTGAAACAA
701 CGGGGTCGGA AATGCCGCCG ATGATTCCGC CCAAACCGAA AATTTCAACT
751 TTCACACCCA AACGGTGCAA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 14; ORF 004.ng>:

```

g004.pep
  1 MVERHIQHLR NGHLMRPC QQVSQMFGR AYDFRADKAA GGFFGIQAHM
  51 AFVYQHHAHA TLIFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHAN
101 GAAQAATAADI RVAAPRYCPA ILPWSAASCS RGSWLDASPA IKICGMLVCM
151 VSGSATGTPR ASLSILMFSK PILSTFGRRP TAANIYSATN TPFSPSCSQW
201 TSTLPSASSL TSVLASRCSF NSSPNTAFAS SETTGSEMP MIPPKPKIST
251 FTPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 15>:

```

m004.seq
  1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
  51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCAGG GCCTACGATT
101 TCCGCGCCGA TAAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTC ACCAGCATCA CGCGGCTGCG GCCTTGGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATGCGCGGC AACCTGCGCG
251 TATTTAGAC CGACAAAGCC GATTGCGGA CTGGTAAACA CCACGCCGAT
301 GGTGCTGCGC CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCAGCTTC ATGCAGCAGA GGCAGTTGGT
401 TGGACGCATC GCCTGCGATG AAGATATGCG GAATACTGGT CTGCATGGTC
451 AGCGGGTCGG CAACAGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATATT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAGATG
651 CAGTTTCAAT TCTTCGCCGA ACACGGCGTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCGATG ATTCCGCCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 16; ORF 004>:

```

m004.pep
  1 MVERHIQHLR NGHLMCPs QQVRQMFGR AYDFRADKAA GGFFGIQAHM
  51 AFVHQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGKHAD
101 GAAPQTAADI RVAALSPAI LPWSAASCSR GSWLDASPA KICGILVCMV
151 SGSATGTPRA SFSILIFSKE ILSTFGRRP AASIYSATN TPFSPSCSQW
201 STLPSASSLT SVLASRCSFN SSPNTAFAS ETGSEMP MIPPKPKIST
251 TPKRCNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 17>:

```

a004.seq
  1 ATGGTAGAAC GGCATATCCA GCATTTGCGG AACGGTCATC TTCATTTGAT
  51 GTGCCCCAAGC CAACAGGTGC GCCAAATGTT CGGCGGCCGG ACCTACGATT
101 TCTGCGCCGA TGAAGCGGCC GGTGGCTTTT TCGGCATACA GGCGCATATG
151 GCCTTTGTTT ACCAGCATCA CGCGGCTGCG GCCTTGGTTT TTGAACGATA
201 CTTGCGCGAT GACAAATTCG TCGGCTTGGT ATTGCGCGC AACCTGCGCG
251 TATTTCAAAC CGACAAAGCC GATTGCGGA CTGGTGAACA CTACGCCGAT
301 GGTGCTGCGG CGCAAACCGC CGCCGATATT CGGGTAGCGG CCGCGTTATC
351 GCCGGCAATC TTGCCTTGGT CGGCGGCTTC ATGCAGCAGG GGCAGTTGGT
401 TGGACGCGTC GCCCGCAATA AAGATATGCG GAATACTGGT CTGCATAGTC
451 AGCGGATCGG CAACGGGTAC GCCGCGCGCA TCTTTTTCGA TATTGATGT
501 TTCCAAACCG ATATTGTCAA CGTTCGGACG GCGGCCTACG GCTGCCAGCA
551 TATATTCGGC AACAAATACG CCTTTTTCGC CATCCTGCTC CCAATGGACT
601 TCTACATTGC CGTCTGCATC GAGTTTGACC TCGGTTTTAG CATCCAAATG
651 CAGTTTCAAT TCTTACCGA ACACGGCTTT CGCCTCGTCT GAAACGACGG
701 GGTGCGAAAT GCCGCGATG ATGCCACCA AACCGAAAAT TTCAACTTTC
751 ACGCCCAAAC GGTGCAATGC CTGA

```

This corresponds to the amino acid sequence <SEQ ID 18; ORF 004.a>:

a004.pap  
 1 MVERHIQHLR NGHLLMCPS QQVRQMFQGR TYDFCADEAA GGFFGIQAHM  
 51 AFVYQHHAHA ALVFERYFAD DKFVGLVLRG NLRVFQTDKA DLRTGEHYAD  
 101 GAAAQTAADI RVAAALSPAI LPWSAASCSR GSWLDASPAI KICGILVCIV  
 151 SGSATGTPRA SFSILMFSKP ILSTFGRRPT AASIYSATNT PFSPPSCSQWT  
 201 STLPSASSLA SVLASKCSFN SSPNTAFASS ETTGSEMPPM MPPKPKISTF  
 251 TPKRCNA\*

m004/a004 94.9% identity over a 257 aa overlap

m004.pap	10	20	30	40	50	60
	MVERHIQHLRNGHLLMCPSQQVRQMFQGR	YDFRADKAAGGFFGIQAHMAFVHQHHAAA				
a004	MVERHIQHLRNGHLLMCPSQQVRQMFQGR	TYDFRADKAAGGFFGIQAHMAFVYQHHAHA				
	10	20	30	40	50	60
m004.pap	70	80	90	100	110	120
	ALVFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHHADGAAPQTAADIRVAAALSPAI					
a004	ALVFERYFADDKFVGLVLRGNLRVFQTDKADLRTGEHYADGAAAQTAADIRVAAALSPAI					
	70	80	90	100	110	120
m004.pap	130	140	150	160	170	180
	LPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILIFSKPILSTFGRRPT					
a004	LPWSAASCSRGSWLDASPAIKICGILVCIVSGSATGTPRASFSILMFSKPILSTFGRRPT					
	130	140	150	160	170	180
m004.pap	190	200	210	220	230	240
	AASIYSATNTPFSPPSCSQWTSTLPSASSLTVLASRCSFNSSPNTAFASSETTGSEMPPM					
a004	AASIYSATNTPFSPPSCSQWTSTLPSASSLTVLASKCSFNSSPNTAFASSETTGSEMPPM					
	190	200	210	220	230	240
m004.pap	250					
	IPPKPKISTFTPKRCNAX					
a004	MPPKPKISTFTPKRCNAX					
	250					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 004 shows 93.4% identity over a 258 aa overlap with a predicted ORF (ORF 004.ng) from *N. gonorrhoeae*:

m004/g004

m004.pap	10	20	30	40	50	60
	MVERHIQHLRNGHLLMCPSQQVRQMFQGR	YDFRADKAAGGFFGIQAHMAFVHQHHAAA				
g004	MVERHIQHLRNGHLLMRPCQQVQMFQGR	YDFRADKAAGGFFGIQAHMAFVYQHHAHA				
	10	20	30	40	50	60
m004.pap	70	80	90	100	110	119
	ALVFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHHADGAAPQTAADIRVAAA-LSPA					
g004	TLIFERYFADDKFVGLVLRGNLRVFQTDKADLRTGKHANGAAAQTAADIRVAAPRYCPA					
	70	80	90	100	110	120
m004.pap	120	130	140	150	160	170
	ILPWSAASCSRGSWLDASPAIKICGILVCMVSGSATGTPRASFSILIFSKPILSTFGRRP					

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g005.seq
1 ATGGGGATGG ACAATATTGA TATGTTTCATG CCTGAACAAG AGGAAATCCA
51 ATCAATGTGG AAAGAAATTT TACTGAATTA CGGTATTTTC CTGCTCGAAC
101 TGCTTACCGT GTTCGGCGCA ATTGCGCTGA TTGTGTTGGC TATCGTACAG
151 AGTAAGAAAC AGTCGGAAG CCGCAGTGTC GTACTGACAG ATTTTTCGGA
201 AAATTATAAA AAACAGCGGC AATCGTTTGA AACATTCTTT TTAAGCGAGG
251 AAGAGACAAA ACATCAGGAA AAAAAAGAAA AGAAAAAGGA AAAGGCGGAA
301 GCCAAGCAGC AGAAAAAGCT TTTGAAGGAG GCGCGGGAGA AATCTCGCGA
351 AACGCAAAA TCCGCGCTTT TTGTGTTGGA TTTTGACGGC GATTTGTATG
401 CACACGCCGT AGAATCCTTG CGTCATGAGA TTACGCGCGT GCTTTTGTAT
451 GCCAAGCCTG AAGATGAGGT TCTGCTCAGA TTGGAAGATC CGGGCGGCGT
501 GGTTCACGGT TACGGTTTGG CGGCTTCGCA GCTTAGGCGT TTGCGCGAAC
551 GCAATATTCC GCTGAccgtc gccgTCGATA AGGTCGCGGc AAGCGgcggc
601 tatatgatcg cgtgtgtgGC GGATAAAATT GTTTCGCGtc cgtttgcggt
651 catcggttcg gtgvggtgtgg tgCcggaagt gcCGAATATC CAccgCctGT
701 TGAAAAACA TGATATTGAT GTGGATGTGA TGACGGCGGG CGAATTTAAG
751 CGCACGGTTA CTTTTATGGG TGAAAATACG GAAAAGGGCA AACAGAAATT
801 CCGCGAGGAA CTGGAGGAAA CGCATCAGT GTTCAAGCAG TTTGTCAGTG
851 AAAACCGCCC CCGGTTGGAT ATTGAAAAAA TAGCGACGG CGAGCATTTG
901 TTCGCCCGGC AGGCGTTGGC GTTGAACCTG ATTGACGAGA TTTTCACCAG
951 TGATGATTG TTGTTGAAAG CGTTTGAAAA CAAACAGGtt aTCGAAGTGA
1001 AATATCAGGA GAAGCGAAGC CTGATCCAGC GCATTGGTTT GCAGGCGGAA
1051 GCTTCCGTTG AAAAGTTGTT TGCCAAACTT GTCAACCGGC GAGCGGATGT
1101 GATGTAG

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g005.pap
1  MGMNDNIDMF  PEQEEIQSMW  KEILLNYGIF  LLELLTVFGA  IALIVLAIQV
51  SKKQSESGSV  VLTDFSENY  KQRQSFTFF  LSEETKHQE  KKEKKKEKAE
101  AKAEEKRLKE  GGEKSAETQ  SRLFVLDFD  DLYAHAVES  RHEITAVALL
151  AKPEDEVLLR  LSPGGVVHG  YGLAASQLR  LRERNIPLT  AVDKVAASGG
201  YMMACVADKI  VSAPFAVIG  VGVVAEVPNI  HRLKKHDDI  VDMVTAGEFK
251  RTVTFMGENT  EKGKQKFRQ  LEETHQLFK  FVSENRPGL  IEKIATGEHW
301  FGRQALALNL  IDEISTDDL  LLKAFENKV  IEVKYQEK  LIQRIGLQAE
351  ASVEKLFKL  VNRADVM*

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m005.seq
1  ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51  GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGCTATCGT ACAGAGTAAG
151 AAACAGCTCGG AWAGCGGCAG TGTCTACTG ACGGATTTTT CGGAAAATTA
201 TAAAAACAGC CGGCAATCGT TTGAAGCATT CTTTTTAAG CGGGAAGAGG
251 CACAACATCA GGAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA
```

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301 GCAGAGAAAA A.CGTTTGAA GGAGGGTGGG GAGAAATCTG CCGAAACGCA
351 nAAATCACGC CTTTTTGTGT TGGANNNNNN NNNNNNNNNN NNNNNNNNNN
401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNGCGAGCGG CGGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGCTTCC GCTCCGTTTG CGATTGTCGG
651 TTCGTGCGGT GTGGTGGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGAAAAG GGCAAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTTGCAGGC GGAAGCTTCT
1051 GTTGAAGAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGT A
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 22; ORF 005>:

m005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSXSGSVVL TDFSENYKKQ RQSFEAFFLS GEEAQHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSAETXKSR LFLVXXXXXX XXXXXXXXXX XXXXXXXXXX
151 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXXXXXXX XXXXASGGYM
201 MACVADKIAS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG
301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS
351 VEKLFKLVN RRADV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 23>:

a005.seq

```

1 ATGGACAATA TTGACATGTT CATGCCTGAA CAAGAGGAAA TCCAATCAAT
51 GTGGAAAGAA ATTTTACTGA ATTACGGTAT TTTCTGCTC GAACTGCTTA
101 CCGTGTTCGG CGCAATTGCG CTGATTGTGT TGGCTATCGT ACAGAGTAAG
151 AAACAGTCGG AAAGCGGCAG TGTCTACTG ACGGATTTT CGGAAAATTA
201 TAAAAACAG CGGCAATCGT TTGAAGCATT CTTTTTAAGC GGGGAAGAGG
251 CAAAACATCA GGAAAAAGAG GAAAAGAAAA AGGAAAAGGC GGAAGCCAAA
301 GCAGAGAAAA AGCGTTTGAA GGAGGGTGGG GAGAAATCTT CCGAAACGCA
351 AAATCCCGC CTTTTTGTGT TGGATTGGA CGGCGATTG TATGCACACG
401 CCGTAGAATC CTTGCGTCAT GAGATTACGG CGGTGCTTTT GATTGCCAAG
451 CCTGAAGATG AGGTTCTGCT TAGATTGGA AGTCCGGGCG GCGTGGTTCA
501 CGGTTACGGT TTGGCGGCTT CGCAGCTTAG GCGTTTGCGC GAACGCAATA
551 TTCCGCTGAC CGTCGCCGTC GATAAGGTGG CGGCGAGCGG TGTTATATG
601 ATGGCGTGTG TGGCGGATAA AATTGTTTCC GCTCCGTTG CGATTGTCGG
651 TTCGGTGGGT GTTGATGCGG AAGTACCGAA TATCCACCGC CTGTTGAAAA
701 AACATGATAT TGATGTGGAT GTGATGACGG CGGGCGAATT TAAGCGCACG
751 GTTACTTTTA TGGGTGAAAA TACGAAAAG GGCAAACAGA AATCCGACA
801 GGAACGGAG GAAACGCATC AGTTGTTCAA GCAGTTTGTC AGCGAGAACC
851 GCCCTCAATT GGATATTGAG GAAGTGGCAA CGGGCGAGCA TTGGTTCGGT
901 CGGCAGGCGT TGGCGTTGAA CTTGATTGAC GAGATTTCGA CCAGTGATGA
951 TTTGTTGTTG AAAGCGTTTG AAAACAAACA GGTATCGAA GTGAAATATC
1001 AGGAGAAGCA AAGCCTGATC CAGCGCATTG GTTGCAGGC GGAAGCTTCT
1051 GTTGAAGAGT TGTTTGCCAA ACTTGTC AAC CGGCGGGCGG ATGTGATGTA
1101 G

```

This corresponds to the amino acid sequence <SEQ ID 24; ORF 005.a>:

a005.pep

```

1 MDNIDMFMP EEEIQSMWKE ILLNYGIFLL ELLTVFGAIA LIVLAIVQSK
51 KQSESGSVVL TDFSENYKKQ RQSFEAFFLS GEEAKHQEKE EKKKEKAEAK
101 AEKXRLKEGG EKSSSETQKSR LFLVDFDGL YAHAVESLRH EITAVLLIAK
151 PEDEVLLRLE SPGGVVHGYG LAASQLRRLR ERNIPLTVAV DKVAASGGYM
201 MACVADKIVS APFAIVGSVG VVAEVPNIHR LLKKHDIDVD VMTAGEFKRT
251 VTFMGENTEK GKQKFRQELE ETHQLFKQFV SENRPQLDIE EVATGEHWFG

```

301 RQALALNLID EISTSDDLLL KAFENKQVIE VKYQEKQSLI QRIQLQAEAS  
351 VEKLFKLVN RRADVM\*

m005/a005 79.2% identity over a 366 aa overlap

m005.pep	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSGSVVL
a005	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESGSVVL
m005.pep	TDFSENYKKQSQSFEEFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXKSR
a005	TDFSENYKKQSQSFEEFLSGEEAKHQEKEKKKEKAEAKAEKKRLKEGGEKSSSETQKSR
m005.pep	LFVLXX
a005	LFVLDLFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLLESPGGVVHGYGLAASQLRRLR
m005.pep	XXXXXXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDIDVD
a005	ERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAIVGSVGVVAEVPNIHRLKKHDIDVD
m005.pep	VMTAGEFKRTVTFMGENTKKGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG
a005	VMTAGEFKRTVTFMGENTKKGKQKFRQELEETHQLFKQFVSENRPQLDIEEVATGEHWFG
m005.pep	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN
a005	RQALALNLIDEISTSDDLLLKAFENKQVIEVKYQEKQSLIQRIGLQAEASVEKLFKLVN
m005.pep	RRADVMX
a005	RRADVMX

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 005 shows 77.0% identity over a 366 aa overlap with a predicted ORF (ORF 005.ng) from *N. gonorrhoeae*:

m005/g005

m005.pep	MDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQXSGSV
g005	MGMDNIDMFMPQEIEIQSMWKEILLNYGIFLLELLTVFGAIALIVLAIVQSKKQSESGSV
m005.pep	VLTDFSENYKKQSQSFEEFLSGEEAQHQEKEKKKEKAEAKAEKKRLKEGGEKSAETXK
g005	VLTDFSENYKKQSQSFETFFLSEETKHQEKKEKKKEKAEAKAEKKRLKEGGEKSAETQK

	120	130	140	150	160	170
m005. pep	SRLFVLXXX					
		:				
g005	SRLFVLDFDGLYAHAVESLRHEITAVLLIAKPEDEVLLRLESPGGVVHGYGLAASQLRR					
	130	140	150	160	170	180
	180	190	200	210	220	230
m005. pep	XXXXXXXXXXXXXASGGYMMACVADKIASAPFAIVGSVGVVAEVPNIHRLKKHDID					
	:	:     :     :				
g005	LRERNIPLTVAVDKVAASGGYMMACVADKIVSAPFAVIGSVGVVAEVPNIHRLKKHDID					
	190	200	210	220	230	240
	240	250	260	270	280	290
m005. pep	VDVMTAGEFKRTVTFMGENTEGKGQKFRQLEETHQLFKQFVSENRPQLDIEEVATGEHW					
	:     :     :					
g005	VDVMTAGEFKRTVTFMGENTEGKGQKFRQLEETHQLFKQFVSENRPGLDIEKIATGEHW					
	250	260	270	280	290	300
	300	310	320	330	340	350
m005. pep	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKSLIQRIGLQAEASVEKLFACL					
	:     :     :					
g005	FGRQALALNLIDEISTSDDLKAFENKQVIEVKYQEKSLIQRIGLQAEASVEKLFACL					
	310	320	330	340	350	360
	360					
m005. pep	VNRRADV MX					
g005	VNRRADV MX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 25>:

```

g006. seq
1  ATGCTGCTGG TGCTggaatt ttggttCGGc gtGtCGGCGG TGGGCatact
51  tgCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTC CG CCTGAACAAC AGCTTGAAC gcgACAACCA CTTTATCCGA
151 AAAGGCGACG AGCGGCAGCT GTACCGCCAT TACGGACTGG TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCG
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACGGCA GCGCGGGGCA TATTATTTCG GTCGGCACTT ATCTGTGGAT
351 GTTTGCCATG AGTTTGGACG ATGTGCCGCG ATTGGTCGAA CAATATTCCA
401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTCCGAACG GAACATCAAA
451 GCCGGAAC TT GA

```

This corresponds to the amino acid sequence <SEQ ID 26; ORF 006.ng>:

```

g006. pep
1  MLLVLEFWFG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR
51  KGDERQLYRH YGLVSRLRVL ISNREAFGYL CVGAAMGILF GFAFVMMTLK
101 GYGSAGHIYS VGTYLWMFAM SLDDVPRLVE QYSLKDIGQ RIEWSERNIK
151 AGT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 27>:

```

m006. seq
1  ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCCGCGG TGGGCATACT
51  TGCGTTGTTT TTATGGCttt TGCCACGTTT TGCCGCCATC AGCGAAAACC
101 TGTATTTC CG CCTGAACAAC AGCTTGAAC GCGACAACCA CTTTATCCGA
151 AAAGGCGACC GCGGCAGCT GTACCGCCAT TACGGACTGC TTTCGCGCCT
201 GCGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TCGCTCGGCA
251 CGGCGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA
301 GGCTACAGCA GCGCGGGGCA TGTCTATTTC GTCGGCACTT ATCTGTGGAT

```

351 GTTGTCCATG AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA  
 401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA  
 451 GCCGGAACCTGA

This corresponds to the amino acid sequence <SEQ ID 28; ORF 006>:

m006.pep  
 1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLNN SLERDNHFIR  
 51 KGDRRQLYRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK  
 101 GYSSAGHVYS VGTYLWMFAM SLDDVPRLVE QYSLKDIGQ RIEWSERNIK  
 151 AGT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 29>:

a006.seq  
 1 ATGCTGCTGG TGCTGGAATT TTGGGTCGGC GTGTCGGCGG TGGGCATACT  
 51 TGCCTTGTTT TTATGGCTTT TGCCACGTTT TGCCGCCATC AGCGAAAACC  
 101 TGTATTTCCT CCTGAAGAAC AGCTTGAAC GCGACAACCA CTTTATCCGA  
 151 AAAGGCGACG AGCGGCAGCT GGACGCCAT TACGGACTGC TTGCGCGCCT  
 201 CGGTGTGCTG ATTTCCAACC GCGAAGCCTT CGGCTATCTC TGCCTCGGCA  
 251 CGCGGATGGG TATTTTGTTT GGCTTTGCTT TTGTGATGAT GACGCTCAAA  
 301 GGCTACAGCA GCGCGGGGCA TGCTATTTCG GTCGGCACTT ATCTGTGGAT  
 351 GTTTGCCATA AGTTTGGACG ACGTGCCGCG ATTGGTCGAA CAATATTCCA  
 401 ATTTGAAAGA CATCGGACAA CGGATAGAGT GGTGGAACG GAACATCAAA  
 451 GCCGGAACCT GA

This corresponds to the amino acid sequence <SEQ ID 30; ORF 006.a>:

a006.pep  
 1 MLLVLEFWVG VSAVGILALF LWLLPRFAAI SENLYFRLKN SLERDNHFIR  
 51 KGDERQLDRH YGLLARLRVL ISNREAFGYL CVGTAMGILF GFAFVMMTLK  
 101 GYSSAGHVYS VGTYLWMFAI SLDDVPRLVE QYSLKDIGQ RIEWSKRNIK  
 151 AGT\*

m006/a006 96.7% identity over a 153 aa overlap

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIKKGDRRQLYRH					
a006	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLKNSLERDNHFIKKGDERQLDRH					
	10	20	30	40	50	60
m006.pep	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAM					
a006	YGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSAGHVYSVGTYLWMFAI					
	70	80	90	100	110	120
m006.pep	SLDDVPRLVEQYSLKDIGQRIEWSERNIKAGTX					
a006	SLDDVPRLVEQYSLKDIGQRIEWSKRNIKAGTX					
	130	140	150			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 006 shows 95.4% identity over a 153 aa overlap with a predicted ORF (ORF 006.ng) from *N. gonorrhoeae*:

m006/g006

	10	20	30	40	50	60
m006.pep	MLLVLEFWVGVS AVGILALFLWLLPRFAAISENLYFRLNNSLERDNHFIKKGDRRQLYRH					



q006-1.seq

1	ATGTGGA AAA	TGTTGAAACA	CATAGCCAAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCCGGTGC	GA CTGGAAAA	CCTTTTGATG	CTGGGGTATC
101	CGGTGTTTGC	CGGGTCGGCG	ATTAATGCCG	TGATTGCGGG	GAGGGTGTTG
151	CAGCGCTTGC	TGTACGCTTT	GGTTGTATTT	TTGATGTGGC	TGGTCGGTGC
201	GGCACGGCGG	ATTACCGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCCGTGCC	GGTTGTGTTG	GAACAACGGC	AGCGGCAAGT	CCCGCATTCA
301	GCGGTAACTG	CACGGGTTGC	CCTGTCGCGT	GAATTTGTCA	GCTTTTTTGA
351	AGAACACCTG	CCGATTGCCG	CGACATCCGT	CGTATCCATA	TTCCGGCGCT
401	GCATCATGCT	GCTGTGTGCT	GAATTTTGGG	TCGGCGTGTC	GCGCGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCCG	CCATCAGCGA
501	AAACTGTAT	TTCCGCCTGA	ACAAAGCTT	GGAACGCGAC	AACCACTTTA
551	TCCGAAAAGG	CGACGAGCGG	CACCTGTACC	GCCATTACGG	ATCTGGTTTG
601	CGCCTGCGTG	TGCTGATTTT	CGAGCGGCAA	GCCTTCCGCT	ACTCTGCGT
651	CGGCGCGGCG	ATGGGTATTT	TGTTCCGGCT	TGCTTTTGTT	ATGATGACGC
701	TCAAAGGCTA	CGGCAGCGCG	GGGCATATTT	ATTCCGTCGG	CACTTATCTG
751	TGGATGTTTT	CCATGAGTTT	GGACATGTG	CCGCGATTGG	TCGAACAA TA
801	TTCCAATTTG	AAAGACATCG	GACAACGGAT	AGAGTGGTCG	GAACGGAACA
851	TCAAAGCCGG	AACTTGA			

q006-1.pap

1	MWKMLKHIAK	THKRRLIGTF	SPVGLENLLM	LGYPVFGGWA	INAVIAGRVM
51	<u>QALLYALVVF</u>	<u>LMWLGAARR</u>	IADTRTFTRI	YTEIAVPVVL	EQRQRQVPHS
101	AVTARVALSR	EFVSFEEHL	PIAATSVVSI	<u>FGACIMLLVL</u>	<u>EFWVGVSavg</u>
151	<u>ILALFWLLP</u>	RFAAISENLY	FRLNNSLERD	NHFIRKGDGR	QLYRHYGLVS
201	RRLVLISNRE	<u>AFGYLCVGAA</u>	<u>MGILGFAGFV</u>	<u>MMTLKGYSGA</u>	GHIYSVGTYL
251	WRFAMSLDDV	PRLVEQYSNL	KDIGORIEWS	ERNIKAGT*	

m006-1.seq

1	ATGTGGAAAA	TGTTGAAACA	CATAGCCCAA	ACCCACCGCA	AGCGATTGAT
51	TGGCACATTT	TCCCTGGTCG	GACTGGAAAA	CCTTTTGATG	CTGGTGTATC
101	CGGTGTTTGG	CGCGCGGGCG	ATCAATGCCG	TGATTGCGGG	GGAGGTTGCG
151	CAGGCGTTGC	TGTACGCTTT	GGTTGTGCTT	TGTATGTGGC	TGTCGGTGTG
201	GGTGC GCGCG	ATTGCGGATA	CGCGCACGTT	TACGCGGATT	TATACCGAAA
251	TCGCCGTGCC	GGTCGTGTTG	GAACAGCGGC	AGCGACAAGT	CCCGCATTCT
301	GCGGTAAC TG	CGCGGGTTGC	CCTGTGCGCT	GAGTTTGTCA	GCTTTTTTGA
351	AGAACACCTG	CCGATTGCCG	CGAATTCCTT	CGTATCCATA	TTCGGCGCGT
401	GCATCATGCT	GCTGGTGCTG	GAATTTTGGG	TCGGCGTGTC	GGCGGTGGGC
451	ATACTTGCGT	TGTTTTTATG	GCTTTTGCCA	CGTTTTGCCG	CCATCAGCGA
501	AAACCTGTAT	TTCGCGCTGA	ACAACAGCTT	GGAACGCGAC	AACCACTTTA
551	TCCGAAAAGG	CGACCGGCGG	CAGCTGTACC	GCCATTACGC	ACTGCTTTCG
601	CGCCTGCGTG	TGCTGATTTC	CACCGCGGAA	GCGCTTCGGT	ATCTCTGCGT

651 CGGCACGGCG ATGGGTATTT TGTTCCGGCTT TGCTTTTGTG ATGATGACGC  
 701 TCAAAGGCTA CAGCAGCGCG GGGCATGTCT ATTCGGTCGG CACTTATCTG  
 751 TGGATGTTTG CCATGAGTTT GGACGACGTG CCGCGATTGG TCGAACAATA  
 801 TTCCAATTTG AAAGACATCG GACAACGGAT AGAGTGGTCG GAACGGAACA  
 851 TCAAAGCCGG AACTGA

This corresponds to the amino acid sequence <SEQ ID 34; ORF 006-1>:

m006-1.pep

1 MWKMLKHIAQ THRKRLIGTF SLVGLENLLM LVYPVFGGRA INAVIAGEVW  
 51 QALLYALVVL LMWLVGAVRR IADTRTFTRI YTEIAVPVVL EQRQRQVPHS  
 101 AVTARVALSR EFVSFFEEHL PIAATSVVSI FGACIMLLVL EFWVGSAVG  
 151 ILALFLWLLP RFAAISENLY FRLNNSLERD NHFIRKGDORR QLYRHYGLLA  
 201 RLRVLISNRE AFGYLCVGTA MGILFGFAFV MMTLKGYSSA GHVYSVGTYL  
 251 WMFAMSLDDV PRLVEQYSNL KDIGQRIEWS ERNIKAGT\*

m006-1/g006-1 95.5% identity in 288 aa overlap

m006-1.pep	10	20	30	40	50	60
	MWKMLKHIAQTHRKRLIGTFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL					
g006-1	MWKMLKHIAKTHRKRLIGTFSPVGLENLLMLGYPVFGGWAINAVIAGRNVQALLYALVVF					
	10	20	30	40	50	60
m006-1.pep	70	80	90	100	110	120
	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
g006-1	LMWLVGAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL					
	70	80	90	100	110	120
m006-1.pep	130	140	150	160	170	180
	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLNNSLERD					
g006-1	PIAATSVVSIFGACIMLLVLEFWVGSAVGILALFLWLLPRFAAISENLYFRLNNSLERD					
	130	140	150	160	170	180
m006-1.pep	190	200	210	220	230	240
	NHFIRKGDORRQLYRHYGLLARLRVLISNREAFGYLCVGTAAMGILFGFAFVMMTLKGYSSA					
g006-1	NHFIRKGDORRQLYRHYGLVSRVLISNREAFGYLCVGAAMGILFGFAFVMMTLKGYGSA					
	190	200	210	220	230	240
m006-1.pep	250	260	270	280	289	
	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
g006-1	GHIYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 35>:

a006-1.seq (partial)

1 ..AGCCAAAACC ACCGCAAGCG ATTGATTGGC ACATTTTTC TGCTCGGACT  
 51 GGAAAACCTT TTGATGCTGG TGTATCCGGT GTTTGGCGGC TGGGCGATTA  
 101 ATGCCGTGAT TGCGGGGCAG GCGTGGCAGG CGTTGCTGTA CGCTTTGGTT  
 151 GTGCTTTTGA TGTGGCTGGT CCGTGCGGCG CCGCGGATTG CCGATACGCG  
 201 CACGTTTACG CGGATTATA CCGAAATCGC CGTGCCGGTT GTGTTGGAAC  
 251 AGCGGCAGCG GCAAGTCCCG CATTCGGCGG TAAC TGCGCG GGTGCGCCTG  
 301 TCGCGTGAGT TTGTCAGCTT TTTGAAGAA CACCTGCCGA TTGCCGCGAC  
 351 ATCCGTCGTA TCCATATTCG GCGCGTGCAT CATGCTGCTG GTGCTGGAAT  
 401 TTTGGGTCGG CGTGTCGGCG GTGGGCATAC TTGCGTTGTT TTTATGGCTT  
 451 TTGCCACGTT TTGCCGCCAT CAGCGAAAAC CTGTATTTCG GCCTGAAGAA  
 501 CAGCTTGGAA CGCGACAACC ACTTTATCCG AAAAGGCGAC GAGCGGCAGC  
 551 TGGACCGCCA TTACGGACTG CTGCGCGGCC TGCGTGTGCT GATTTCACAC  
 601 CGCGAAGCCT TCGGCTATCT CTGCGTCGGC ACGGCGATGG GTATTTTGT  
 651 CGGCTTTGCT TTTGTGATGA TGACGCTCAA AGGCTACAGC AGCGCGGGGC

701 ATGTCTATTC GGTCGGCACT TATCTGTGGA TGTTTGCCAT AAGTTTGGAC  
 751 GACGTGCCGC GATTGGTCGA ACAATATTCC AATTGAAAG ACATCGGACA  
 801 ACGGATAGAG TGGTCGAAAC GGAACATCAA AGCCGGAAC TGA

This corresponds to the amino acid sequence <SEQ ID 36; ORF 006-1.a>:

a006-1.pep (partial)

1 ..SQNHRKRLIG TFFLVGLENL LMLVYPVFGG WAINAVIAGQ AWQALLYALV  
 51 VLLMWLVGAA RRIADTRTFT RIYTEIAVPV VLEQRQRQVP HSAVTARVAL  
 101 SREFVSFFEE HLPAAATSVV SIFGACIMLL VLEFWGVSA VGILALFLWL  
 151 LPRFAAISEN LYFRLKNSLE RDNHFIRKGD ERQLDRHYGL LARLRVLISN  
 201 REAFGYLCVG TAMGILFGFA FVMMLKGYG SAGHVYSVGT YLWMFAISLD  
 251 DVPRLVEQYS NLKDIGQRIE WSKRNIKAGT \*

a006-1/m006-1 95.7% identity in 280 aa overlap

	10	20	30	40	50
a006-1.pep	SQNHRKRLIGTFFLVGLENLLMLVYPVFGGWAINAVIAGQAWQALLYALVVL				
m006-1	MWKMLKHIAQTHRKRIGTFFSLVGLENLLMLVYPVFGGRAINAVIAGEVWQALLYALVVL				
	10	20	30	40	50
	60	70	80	90	100
a006-1.pep	LMWLVGAAARRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
m006-1	LMWLVGAVRRIADTRTFTRIYTEIAVPVLEQRQRQVPHSAVTARVALSREFVSFFEEHL				
	70	80	90	100	110
	120	130	140	150	160
a006-1.pep	PIAATSVVSIFGACIMLLVLEFWGVSAVGILALFLWLLPRFAAISENLYFRLKNSLERD				
m006-1	PIAATSVVSIFGACIMLLVLEFWGVSAVGILALFLWLLPRFAAISENLYFRLNNSLERD				
	130	140	150	160	170
	180	190	200	210	220
a006-1.pep	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
m006-1	NHFIRKGDERRQLDRHYGLLARLRVLISNREAFGYLCVGTAMGILFGFAFVMMTLKGYSSA				
	190	200	210	220	230
	240	250	260	270	280
a006-1.pep	GHVYSVGTYLWMFAISLDDVPRLVEQYSNLKDIGQRIEWSKRNIKAGTX				
m006-1	GHVYSVGTYLWMFAMSLDDVPRLVEQYSNLKDIGQRIEWSERNIKAGTX				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 37>:

g007.seq

1 atgaACACAA CCCGACTGCC GACCGCCTTC ATCTTGCTGC GCCTCTGcgC  
 51 CGCcGCTTCT GCCGccgaca acAGCatcat gaCaAAAGGG CAAAAAGTGT  
 101 ACGAATCcAa ctGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC  
 151 ACTGCGtTTC CTccgctTTT CCggtcgGac tgtattatga acaAACCGCa  
 201 cgTCctgctg cacagcatgg tcaaaggcAt cgacgggaca ttcaaagtgg  
 251 agcggcaaaa cctacgacgg atttatgCcc gcaaccgcca tcagcgATGC  
 301 GGACATTGCC GCCGTCGCCA CTTATATCAT GAACGCCTTT GA

This corresponds to the amino acid sequence <SEQ ID 38; ORF 007.ng>:

g007.pep

1 MNTTRLPTAF ILCCLCAAAS AADNSIMTKG QKVYESNCIA CHGKKGEGRG  
 51 TAFPPLFRSD CIMNKPVLH HSMVKGIDGT FKVERQNLRR IYARNRHQRC  
 101 GHCRRRHLYH ERL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 39>:



g007                    CIMNKPHVLLHSMVKIDGTFKVERQNLRRYARNRHQRCGHCRRRHLYHERL  
                               70                80                90                100                110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 43>:

g007-1.seq (partial)  
 1 ATGAACACAA CCCGACTGCC GACCGCCTTC ATCTTGTGCT GCCTCTGCGC  
 51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT  
 101 ACGAATCCAA CTGCATCGCC TGCCACGGCA AGAAAGGGGA AGGGCGCGGC  
 151 ACTGCGTTTC CTCCGCTTTT CCGGTCGGAC TATATTATGA ACAAACCGCA  
 201 CGTCCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA  
 251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG  
 301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG  
 351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGGC AAAAAAACA.

This corresponds to the amino acid sequence <SEQ ID 44; ORF 007-1.ng>:

g007-1.pep (partial)  
 1 MNTRLPTAF ILCLCAAAS AADNSIMTKG QKVIYESNCIA CHGKKGEGRG  
 51 TAFPFLFRSD YIMNKPHVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA  
 101 DIAAVATYIM NAFDNGGGSV TEKDVQAKG KKN...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 45>:

m007-1.seq  
 1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCTTCTGCGC  
 51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT  
 101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA  
 151 ACCATGTTTC CGCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACCGCA  
 201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA  
 251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CAACCGCCAT CAGCGATGCG  
 301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG  
 351 CGGAAGCGTT ACCGAAAAAG ACGTAAACA GGCAAAAGC AAAAAAACT  
 401 AA

This corresponds to the amino acid sequence <SEQ ID 46; ORF 007-1>

m007-1.pep  
 1 MNTRLPTAL VLGCFCAAAS AADNSIMTKG QKVIYESNCVA CHGKKGEGRG  
 51 TMFPPLYRSD FIMKKPVLL HSMVKGINGT IKVNGKTYNG FMPATAISDA  
 101 DIAAVATYIM NAFDNGGGSV TEKDVQAKS KKN\*

m007-1 / g007-1 91.7% identity in 133 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTRLPTALVLGCFCAAAS	ADNSIMTKGQKVIYESNCV	ACHGKKGEGRGTMFPPLYRSD			
	:	: :	:			
g007-1	MNTRLPTAFILCLCAAAS	ADNSIMTKGQKVIYESNCI	ACHGKKGEGRGTAFPFLFRSD			
	10	20	30	40	50	60
m007-1.pep	FIMKKPVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDA	DIAAVATYIMNAFDNGGGSV			
	: : :					
g007-1	YIMNKPHVLLHSMVKGINGT	IKVNGKTYNGFMPATAISDA	DIAAVATYIMNAFDNGGGSV			
	70	80	90	100	110	120
m007-1.pep	TEKDVQAKSKKNX					
	:					
g007-1	TEKDVQAKGKKN					
	70	80	90	100	110	120
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 47>:

a007-1.seq (partial)  
 1 ATGAACACAA CCCGACTGCC GACCGCCCTC GTCTTGGGCT GCCTCTGCGC  
 51 CGCCGCTTCT GCCGCCGACA ACAGCATCAT GACAAAAGGG CAAAAAGTGT  
 101 ACGAATCCAA CTGCGTCGCC TGCCACGGCA AAAAGGGCGA AGGCCGCGGA

```

151 ACCATGTTTC CGCCGCTCTA CCGCTCCGAC TTCATCATGA AAAAACC GCA
201 GGTGCTGCTG CACAGCATGG TCAAAGGCAT CAACGGTACA ATCAAAGTCA
251 ACGGCAAAAC CTACAACGGA TTCATGCCCG CCACTGCCAT CAGCGATGCG
301 GACATTGCCG CCGTCGCCAC TTATATCATG AACGCCTTTG ACAACGGCGG
351 CGGAAGCGTT ACCGAAAAAG ACGTAAAAACA GGCAAAAAAC AAAAAA..

```

This corresponds to the amino acid sequence <SEQ ID 48; ORF 007-1.a>:

**a007-1.pep (partial)**

```

1 MNTTRLPTAL VLGCLCAAAS AADNSIMTKG QKVYESNCVA CHGKKGEGRG
51 TMFPPLYRSD FIMKKPQVLL HSMVKINGT IKVNGKTYNG FMPATAISDA
101 DIAAVATYIM NAFDNGGGSV TEKDVQAKN KK..

```

m007-1/a007-1 98.5% identity in 132 aa overlap

	10	20	30	40	50	60
m007-1.pep	MNTTRLPTALVLGCFCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
a007-1	MNTTRLPTALVLGCLCAAAS	AADNSIMTKGQKVYESNCVACHGKKGEGRG	TMFPPLYRSD			
	10	20	30	40	50	60
	70	80	90	100	110	120
m007-1.pep	FIMKKPQVLLHSMVKINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
a007-1	FIMKKPQVLLHSMVKINGTIKVNGKTYNGFMPATAISDADIAAVATYIMNAFDNGGGSV					
	70	80	90	100	110	120
	130					
m007-1.pep	TEKDVQAKSKKNX					
a007-1	TEKDVQAKNKK					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 49>:

**g008.seq**

```

1 ATGAACAACA GACATTTTGC CGTCatcgCC TTGGGCAGCA ACCTTGACAA
51 CCCCGCACAA CAAATacgcy gcgcattaga cgcgctctcg tcccatcctg
101 acatccgggt tgaaCaggtt tcctcactgt aTatgaccgc acctgtcgggt
151 tacgAcaaTC agcccgATT CATCaatgcc gTCTgcaccg TTTCCACCAC
201 CtTGGACGGC ATTGcccTGC TTGCCgaACT CAaccgTATC GAAGCCGATT
251 TCGGACGCGA aCGCAGTTTC CGCAATGCAC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGGCC TTACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATACGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAAATACG GAAAGTTGT CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGACA GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 50; ORF 008.ng>:

**g008.pep**

```

1 MNNRHFAVIA LGSNLDNPAQ QIRGALDALS SHPDIRLEQV SSLYMTAPVG
51 YDNQPDFINA VCTVSTTLDG IALLAELNRI EADFGRRERF RNAPRTLDDLD
101 IIDFDGISSD DPLRTLPHPR AHERSFVIRP LAEILPDFIL GKYGKVVELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 51>:

**m008.seq**

```

1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
51 CCCTGCTCAA CAGGTACGGC CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT TGTCAATGCC GTCTGCACCG TTTCCACCAC
201 TCTGGACGGC ATTGCCyTGC TTGCCGAAT CAACCGTATC GAGGCTGATT
251 TCGGACGCGA ACGCAGCTTC CGCAACGCGC CGCGCACATT GKATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACACsCGAC TcACctTGCC

```

```

351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATCCGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTGTTTTA GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGyTGG GCAATCAAGG TATCCGTCTT TTACCGGACA GGTAAAT

```

This corresponds to the amino acid sequence <SEQ ID 52; ORF 008>:

```

m008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLTG IALLAELNRI EADFGRRERSF RNAPRTLXLD
101 IIDFDGISSD DTRLTLPHPR AHERSFVIRP LAEILPDFVL GKHGKVAELS
151 KRLGNQGIRL LPDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 53>:

```

a008.seq
  1 ATGAACAACA GACATTTTGC CGTCATCGCC CTGGGCAGTA ATCTTGAAAA
 51 CCCTGCCCAA CAGGTACGCG CCGCATTGGA CACGCTGTCG TCCCATCCTG
101 ACATCCGTCT TAAACAGGCT TCCTCACTGT ATATGACCGC GCCCGTCGGT
151 TACGACAATC AGCCCGATT CGTCAATGCC GTCTGCACCG TTTCCACCAC
201 CTTGGACGGC ATTGCCCTGC TTGCCGAACT CAACCGTATC GAAGCCGATT
251 TCGGACGCGA ACGCAGCTT CGCAACGCGC CGCGCACATT GGATTGGAC
301 ATTATCGACT TTGACGGCAT CTCCAGCGAC GACCCCGAC TCACCCTGCC
351 GCATCCGCGC GCGCACGAAC GCAGTTTCGT CATAAGCCCT TTGGCAGAAA
401 TCCTCCCTGA TTTTATTTTG GGAAACACG GAAAGGTTGC CGAATTGTCA
451 AAACGGCTGG GCAATCAAGG CATCCGTCTT TTACCGGATA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 54; ORF 008.a>:

```

a008.pep
  1 MNNRHFAVIA LGSNLENPAQ QVRAALDTLS SHPDIRLKQA SSLYMTAPVG
 51 YDNQPDFVNA VCTVSTTLTG IALLAELNRI EADFGRRERSF RNAPRTLXLD
101 IIDFDGISSD DPRLTLPHPR AHERSFVIRP LAEILPDFIL GKHGKVAELS
151 KRLGNQGIRL LPDK*

```

m008/a008 97.6% identity over a 164 aa overlap

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
a008	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
	10	20	30	40	50	60
m008.pep	VCTVSTTLGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	VCTVSTTLGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
a008	VCTVSTTLGIALLAELNRIEADFGRRERSFRNAPRTLXLDIIDFDGISSDDTRLTLPHPR					
	70	80	90	100	110	120
m008.pep	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
a008	AHERSFVIRPLAEILPDFILGKHGKVAELSKRLGNQGIRLLPDKX					
	130	140	150	160		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 008 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF008.ng) from *N. gonorrhoeae*:

m008/g008

	10	20	30	40	50	60
m008.pep	MNNRHFAVIALGSNLENPAQQVRAALDTLSSHDPDIRLKQASSLYMTAPVGYNQPDFVNA					
g008	MNNRHFAVIALGSNLDNPAQQIRGALDALSSHDPDIRLEQVSSLYMTAPVGYNQPDFINA					

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	10	20	30	40	50	60
m008.pep	70	80	90	100	110	120
	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLXLDDIIDFDGISSDDTRLTLPHR					
g008	VCTVSTTLDGIALLAELNRIEADFGRRERSFRNAPRTLDDIIDFDGISSDDPRLTLPHR					
	70	80	90	100	110	120
m008.pep	130	140	150	160		
	AHERSFVIRPLAEILPDFVLGKHGKVAELSKRLGNQGIRLLPDRX					
g008	AHERSFVIRPLAEILPDFILGKYGKVVELSKRLGNQGIRLLPDRX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 55>:

g009.seq  
 1 ATGCCCCGCG CTGCCGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC  
 51 CGAACAAAAT ACCCATCGCC GCGCCGACGC AGAGATAGCC GAAGGCTTCG  
 101 CGGTTGGAAA TCAGCACACG CAGGCGCGAA ACCAGTCCGT AATGGCGGTA  
 151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTcg CGTTCCAAGC  
 201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC  
 251 AaaGCCATA A

This corresponds to the amino acid sequence <SEQ ID 56; ORF 009.ng>:

g009.pep  
 1 MPRAAFAFER HHHKSKEQN THRRADAEIA EGFAVGNQHT QARNQSVMAV  
 51 QLPLVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 57>:

m009.seq  
 1 ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC  
 51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG  
 101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTA  
 151 CAGCTGCCGC CGGTGCGCTT TTCGGATAAA GTGGTTGTCT CGTTCCAAGC  
 201 TGTGTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC  
 251 AAAAGCCATA A

This corresponds to the amino acid sequence <SEQ ID 58; ORF 009>:

m009.pep  
 1 MPRAAFAFER HHHKSKEQN THRRADAEIA EGFAVGNQHT QARKQSVMAV  
 51 QLPPVAFSDK VVVAFAQVVQ AEIQVFADGG KTWQKP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 009 shows 97.7% identity over a 86 aa overlap with a predicted ORF (ORF 009.ng) from *N. gonorrhoeae*:

m009/g009

	10	20	30	40	50	60
m009.pep	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
g009	MPRAAFAFERHHHKSKEQNTHRRADAEIAEGFAVGNQHTQARNQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
m009.pep	70	80				
	VVVAFAQVVQAEIQVFADGGKTWQKPx					
g009	VVVAFAQVVQAEIQVFADGGKTWQKPx					
	70	80				



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 59>:

```
a009.seq
  1 ATGCCCCGCG CTGCTGTAGC CTTTGAGCGT CATCATCACA AAAGCAAAGC
 51 CGAACAAAAT ACCCATCGCC GTGCCGACGC AGAGATAGCC GAAGGCTTCG
101 CGGTTGGAAA TCAGCACACG CAGGCGCGCA AGCAGTCCGT AATGGCGGTC
151 CAGCTGCCGC TCGTCGCCTT TTCGGATAAA GTGGTTGTCG CGTTCCAAGC
201 TGTTCTTCAG GCGGAAATAC AGGTTTTCGC TGATGGCGGC AAAACGTGGC
251 AAAAGCCATA A
```

This corresponds to the amino acid sequence <SEQ ID 60; ORF 009.a>:

```
a009.pep
  1 MPRAAVAFAER HHHKSKAEQN THRRADAEIA EGFVGNQHT QARKQSVMAV
 51 QLPLVAFSDK VVVAFAQVLQ AEIQVFADGG KTWQKP*
```

m009/a009 97.7% identity over a 86 aa overlap

	10	20	30	40	50	60
m009.pep	MPRAAVAFAERHHHKSKEQNTTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPPVAFSDK					
a009	MPRAAVAFAERHHHKSKEQNTTHRRADAEIAEGFAVGNQHTQARKQSVMAVQLPLVAFSDK					
	10	20	30	40	50	60
	70	80				
m009.pep	VVVAFAQVQAEIQVFADGGKTWQKPX					
	:					
a009	VVVAFAQVLQAEIQVFADGGKTWQKPX					
	70	80				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 61>:

```
g010.seq
  1 ATGGGTTTTTC CTGTTTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGCGG
 51 TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GCGGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTCGC GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTCT TATTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTGCGC CCGTGCGGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGGCGAG GGCGGTATTC TGTGAacgc
801 cgacggcgaa cgcTTTATGG AAcgctatgc GCcgACCGta aAagaCTTGG
851 CTTCTCGCga cgtGGTTTCA CgcgcGatgG CgatggaAat ctatgaaggt
901 cgcggtctgT GtaaaaaaCaA agaCCacgtC TTA CTGAAAA TCGACcAtAt
951 cggTGCAGAA AAAATTATGG AAAAAGTACC GGGCATCCGC GAGATTTCCTA
1001 TTAagtttgc cGGTATCGAT CCGATTAAAG ACCCGATTcc ggttgTGCCG
1051 ACTACCCACT ATATGATGGG CGGCATTCCg aCCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTCCGTAC ACGGTGCGAA CCGTTTGGGT
1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga
```

This corresponds to the amino acid sequence <SEQ ID 62; ORF 010.ng>:

g010.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRDWHMY DTVKGSIDLW DDAIEFMCRAAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNVANTQF FVEWTAQDLI RDENGDVVG TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPT V KDLASRDVVS RAMAMEIYEG
301 RGCCKNDHV LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDFIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 63>:

m010.seq (PARTIAL)

```

1  ..nTCCAATTAT CCAAATCCGG TCTGAATTGT GCCGTTTGT CTAAAGTGTT
51  CCCGACCCGT TCGCATACCG TAGCGGCGCA GGCCTGATT TCCGCTCTn
101 TGGGTAATGT GCAGGAAGAC CGTTGGGACT GGCACATGTA CGATACCCGTG
151 AAAGGTTCCG ACTGGTTGGG CGACCAAGAT GCGATTGAGT TTATGTGCCG
201 CGCCGCGCCT GAAGCCGTAA TTGAGTTGGA ACACATGGGT ATGCCTTTTG
251 ACCGTGTGGA AAGCGGTAAA ATTTATCAGC GTCCTTTCG CCGCCATACT
301 GCCGAACACG GTAAACGCGC GGTAGAACGC GYCTGTGCGG TTGCCGACCG
351 TACAGGTCAT GCGATGCTG ATACTTTGTA CCAACAAAAC GTCCTGTGCCA
401 ATACGCAATT CTTGTGGAA TGGACGCGAC AAGATTTGAT TCGTGATGAA
451 AACGGCGATG TCGTCGGCGT AACC GCCATG GAAATGGAAA CCGGCGAAGT
501 TTATATTTTC CACGCTAAAG CTGTGATGTT TGCTACCGGC GCGGCGGGTC
551 GTATTTATGC GTCTTCTACC AATGCCTATA TGAATACCGG CGATGGTTTG
601 GGTATTTGTG CGCGTGCAGG TATCCCGTTG GAAGACATGG AATTCTGGCA
651 ATTCCAGCCG ACCGCGGTG CCGGTGCGG CGTGTGATT ACCGAA....

```

This corresponds to the amino acid sequence <SEQ ID 64; ORF 010>:

m010.pep (PARTIAL)

```

1  ..XQLSKSGLNC AVLSKVFPT SHTVAAQGGI SASXGNVQED RWDWHMYDTV
51  KGSDWLGDQD AIEFMCRAAP EAVIELEHMG MPFDRVESGK IYQRPFGGHT
101 AEHGKRAVER XCAVADRTGH AMLHTLYQON VRANTQFFVE WTAQDLIRDE
151 NGDVVGVTAM EMETGEVYIF HAKAVMFATG GGGRIYASST NAYMNTGDGL
201 GICARAGIPL EDMFQWQFQ TGVAGAGVLI TE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 65>:

a010.seq

```

1  ATGGGCTTTC CTGTCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGGTATT CCGCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCG GCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCTTTTGA CCGTGTGGAA AGCGGTAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGG GTAGAACGCG
401 CCGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGTTTGG GTATTGTGC GCGTGCAGG ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGCGCGAG GCGGTATTC GTTGAATGC
801 CGACGCGGAA CGCTTATGG AACGCTATG GCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAA TCGACCATAT
951 CCGCGCAGAA AAAATTATGG AAAAAGTCCC GGCATCCGC GAGATTTCCT
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCACT ATATGATGGG CGGTATCCG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTCTC CAAGGCGACG AATACGAAGT GCCTGTAATA GGTCTGTATG
1151 CGGCAGTGA GTGCGCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAATCCC TGCTGGACTT AGTGGTATTC GTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCT TTGCCTGCTA

```

```

1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGGG CAATCAAAC
1351 GATGGTGAAA ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAATCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCACGCGG TCGCGACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGACGCT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 66; ORF 010.a>:

```

a010.pep
1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY
151 QQNV RANTQF FVENTAQDLI RDENG DVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KD LASRDVVS RAMAMEIYEG
301 RCGGK NKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPPIVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEV PVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKP LPANAGELTR QRIERLDNQT
451 DGENVDALRR ELQRSVOLHA GV FRTDEILS KGVREVM AIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLSAE ARKESRG AHA SDDHPERDDE
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKR VY*

```

m010/a010 98.7% identity over a 231 aa overlap

```

                                10      20      30
m010.pep                      XQLSKSGLNCVLSKVF PTRSHTVAAQGGISASXGNV
                                |||
a010      MGFPVRKFDAVIVGGGGAGLRAXLQLSKSGLNCVLSKVF PTRSHTVAAQGGISASLGNV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m010.pep      QEDRWDWHMYDTVKGS DWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                |||
a010      QEDRWDWHMYDTVKGS DWLG DQDAIEFMCR AAPEAVIELEHMGMPFDRVESGKIYQRPFG
                                70      80      90      100     110     120

                                100     110     120     130     140     150
m010.pep      GHTAEHGKRAVERXCAVADR TGHAMLHTLYQQNV RANTQFFV EWT AQDLIR DENG DVVG V
                                |||
a010      GHTAEHGKRAVERACAVADR TGHAMLHTLYQQNV RANTQFFV EWT AQDLIR DENG DVVG V
                                130     140     150     160     170     180

                                160     170     180     190     200     210
m010.pep      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                |||
a010      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
                                190     200     210     220     230     240

                                220     230
m010.pep      FQPTGVAGAGVLITE
                                |:|
a010      FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKD LASRDVVS RAMAMEIYEG
                                250     260     270     280     290     300

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 010 shows 98.7% identity over a 231 aa overlap with a predicted ORF (ORF 010.ng) from *N. gonorrhoeae*:

m010.pap/g010.pap

m010.pap				10	20	30	
				XQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASXGNV			
g010	MGFPVRKFDAVIVGGGAGLRAALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV						
	10	20	30	40	50	60	
m010.pap	40	50	60	70	80	90	
	QEDRWDMHYDITVKGSWDLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG						
g010	QEDRWDMHYDITVKGSWDLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG						
	70	80	90	100	110	120	
m010.pap	100	110	120	130	140	150	
	GHTAEHGKRAVERXCAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDDVVG						
g010	GHTAEHGKRAVERACAVADRTGHAMLHTLYQONVRANTQFFVEWTAQDLIRDENGDDVVG						
	130	140	150	160	170	180	
m010.pap	160	170	180	190	200	210	
	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLDMEFWQ						
g010	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLDMEFWQ						
	190	200	210	220	230	240	
m010.pap	220	230					
	FQPTGVAGAGVLITE						
g010	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVSRAAMEIYEG						
	250	260	270	280	290	300	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 67>:

g010-1.seq..

```

1  ATGGGTTTTCTCTGTTTCGCAA GTTGTATGCC GTGATTGTCG GCGGTGGCGG
51  TGCAGGTTTA CGTGCAGCCC TCCAATTATC CAAATCCGGT TTGAATTGTC
101 CCGTTTGTGTC TAAAGTGTTC CCGACCCGCT CGCATACCGT AGCGGCGCAG
151 GGCAGTATTT CCGCCTCTCT GGGTAATGTG CAGGAGGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGCTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGTGCG GCTGCGCCTG AAGCGGTGAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGCGTTGAA AGCGGCAAAA TTTATCAGCG
351 TCCTTTCGGC GGACATACTG CCGAACATGG TAAACGTGCG GTAGAACGTG
401 CATGTGCGGT TGCCGACCGT ACCGGTCATG CGATGTTGCA TACTTTGTAC
451 CAACAAAACG TCCGTGCCAA TACACAATTC TTTGTGGAAT GGACGGCGCA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC GGGCGAAGTT TATATTTTCC ACGCCAAGGC CGTGATGTTT
601 GCTACCGGTG GCGGCGGTGCT TATTTATGCT TCTTCTACCA ATGCTTATAT
651 GAATACCGGT GACGGTTTGG GCATTTCGCG CCGTGGCGGC ATTCCGTTGG
701 AAGATATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGGCGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGCTATTC TGTGTAACGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTCTTCGCGA CGTGGTTTCA CGCGCGATGG CGATGGAAAT CTATGAAGGT
901 CCGCGCTGTG GTAAAAACAA AGACCACTGC TTAAGTAAAA TCGACCATAT
951 CCGTGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTTGC CCGTATCGAT CCGATTAAAG ACCCGATTCC GGTGTTGCGC
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTATC ACGGTGAAGT
1101 TGTTGTTCCG CAAGGCGACG AGTACGAAGT ACCTGTAAAA GGCCTGTATG
1151 CCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGTTTGGGT

```

1201 ACGAACTCCC TGCTGGACTT GGTGGTGTTC cgcccaaccc cccggtga

This corresponds to the amino acid sequence <SEQ ID 68; ORF 010-1.ng>:

g010-1.pep

```

1  MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCVLSKVF PTRSHTVAAQ
51  GGISASLGNV QEDRWDWHMY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHATAHGKRA VERACAVADR TGHAMLHTLY
151 QQNVRRANTQF FVEWTAQDLI RDENG DVVG TAMEMETGEV YIFHAKAVMF
201 ATGGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG
301 RCGCKNKDHY LLKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF RPTPR*
```

g010-1 / P10444

sp|P10444|DHSA\_ECOLI SUCCINATE DEHYDROGENASE FLAVOPROTEIN SUBUNIT  
 gnl|PID|d1015210 (D90711) Succinate dehydrogenase, flavoprotein [Escherichia coli] gi|1786942  
 (AE000175) succinate dehydrogenase flavoprotein subunit [Escherichia coli] Length = 588  
 Score = 1073 (495.6 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169  
 Identities = 191/303 (63%), Positives = 238/303 (78%)

```

Query: 1  MGFPVRKFDAVIVXXXXXXXXXXXXXSKSGLNCVLSKVF PTRSHTVAAQGGISASLGNV 60
      M  PVR+FDVAV++ S+SG CA+LSKVFPTRSHTV+AQGGI+ +LGN
Sbjct: 1  MKLPVREFDAVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNT 60

Query: 61 QEDRWDWHMYDTVKGSDWLGDQDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG 120
      ED W+WHMYDTVKGSD++GDQDAIE+MC+ PEA++ELEHMG+PF R++ G+IYQRPFG
Sbjct: 61 HEDNWEWHMYDTVKGSDYIGDQDAIEYMCKTGPEAILEHMGLPFSRLDDGRIYQRPFG 120

Query: 121 GHATAHGKRAVERACAVADR TGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENG DVVG 180
      G + G R A ADRTGHA+LHTLYQQN++ +T F EW A DL+++++G VVG
Sbjct: 121 GQSKNFGGEQAARTAAADRTGHALLHTLYQQNLKNHTTIPSEWYALDLVKNDGAVVGC 180

Query: 181 TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ 240
      TA+ +ETGEV F A+A + ATGG GRIY S+TNA++NTGDG+G+ RAG+P++DME WQ
Sbjct: 181 TALCIETGEVVYFKARATVLTATGGAGRIYQSTTNAHINTGDGVGMAIRAGVPVQDMEMWQ 240

Query: 241 FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVS RAMAMEIYEG 300
      FHPTG+AGAGVL+TEG RGEAG LLN GERFMERYAP KDLA RDVV+R++ +EI EG
Sbjct: 241 FHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNAKDLAGRDVVARSIMIEIREG 300

Query: 301 RGC 303
      RGC
Sbjct: 301 RGC 303
```

Score = 249 (115.0 bits), Expect = 6.7e-169, Sum P(2) = 6.7e-169  
 Identities = 53/102 (51%), Positives = 62/102 (60%)

```

Query: 309 HVLLKIDHIGAEKIMEKLPGR EISIQFAGXXXXXXXXXXXXTTHYMMGGIPTNYHGEVV 368
      H LK+DH+G E + +LPGI E+S FA T HYMMGGIPT G+ +
Sbjct: 310 HAKLKLDHLGKEVLESRLPGILELSRTFAHVDPVKEPIPVIPVCHYMMGGIPTKVGTGQAL 369

Query: 369 VPQGEYEVVVKGLYAAGECACASVHGANRLGTNSLLDLVVF 410
      +V V GL+A GE AC SVHGANRLG NSLLDLVVF
Sbjct: 370 TVNEKGEDVVVPGLFVAGGEIACSVHGANRLGGNSLLDLVVF 411
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 69>:

m010-1.seq..

```

1  ATGGGTTTTTC CTGTTTCGCAA GTTGTATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCAGCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTC CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GGCGGTATTT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCGGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTTGTAC
```

```

451 CAACAAACG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGTTCG TATTTATGCG TCTTCTACCA ATGCCTATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC GGGTGGCGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTTCTCGCGA CGTTGTTTCC CGCGCGATGG CGATGGAAAT CTACGAAGGT
901 CGCGGCTGCG GTAAAAACAA AGACCATGTC TTAAGTAAAA TCGACCATAT
951 CGGCGCAGAA AAAATTATGG AAAAAGTGGC GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCC
1051 ACTACCCACT ATATGATGGG CGGCATTCCG ACCAATTACC ACGGCGAAGT
1101 TGTGTTCCG CAAGGTGAAG ATTACGAAGT GCCTGTAAAA GGTCTGTATG
1151 CGGCAGGTGA GTGCGCTTGT GCTTCCGTAC ACGGTGCGAA CCGCTGGGT
1201 ACCAACTCCC TGTGGACTT GGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAACCTT TTGCCTGCTA
1301 ATGCAGGTGA GTTGACCCGC CAACGTATCG AGCGTTTGA CAACCAAACC
1351 GATGGTGAAA ACCTTGATGC ATTGCGTCGC GAACTGCAAC GCTCTGTACA
1401 ACTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGCGTTC
1451 GAGAAGTCAT GGCGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTGATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAAG
1601 AATCAGCGCG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATATCAATA CCTTGTCTTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGATGA

```

This corresponds to the amino acid sequence <SEQ ID 70; ORF 010-1>:

m010-1.pep..

```

1 MGFPVRKFDA VIVGGGGAGL RAALQLSKSG LNCAVLSKVF PTRSHTVAAQ
51 GGISASLGNV QEDRWDMHY DTVKGSWDLG DQDAIEFMCR APEAVIELE
101 HMGMPFDRVE SGKIYQRPFG GHAEHKGRA VERACAVADR TGHAMLHTLY
151 QQNVRAQTQF FVEWTAQDLI RDENGDVVG V TAMEMETGEV YIFHAKAVMF
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG
251 VLITEGVRGE GGILLNADGE RMERYAPT V KDLSRDVVS RAMAMEIYEG
301 RCGGNKNDHV LKIDHIGAE KIMEKLPGR EISIQFAGID PIKDPIPVVP
351 TTHYMMGGIP TNYHGEVVP QGEDYEVVPK GLYAAGECAC ASVHGANRLG
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWK LPANAGELTR QRIERLDNOT
451 DGENVDALRR ELQSVQLHA GVFTDEILS KGVREVMIA ERVKRTEIKD
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPERDDE
551 NWMKHTLYHS DINTLSYKPV HTKPLSVEYI KPAKRVY*

```

m010-1 / g010-1 99.5% identity in 410 aa overlap

```

          10      20      30      40      50      60
m010-1.pep MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
          |||
g010-1      MGFPVRKFDAVIVGGGGAGLRAALQLSKSGLNCAVLSKVFPTRSHTVAAQGGISASLGNV
          10      20      30      40      50      60

          70      80      90     100     110     120
m010-1.pep QEDRWDMHYDTVKGSWDLGDQDAIEFMCRAPAEVIELEHMGMPFDRVESGKIYQRPFG
          |||
g010-1      QEDRWDMHYDTVKGSWDLGDQDAIEFMCRAPAEVIELEHMGMPFDRVESGKIYQRPFG
          70      80      90     100     110     120

          130     140     150     160     170     180
m010-1.pep GHAEHKGRAVERACAVADRTGHAMLHTLYQQNVRAQTQFFVEWTAQDLIRDENGDVVGCV
          |||
g010-1      GHAEHKGRAVERACAVADRTGHAMLHTLYQQNVRAQTQFFVEWTAQDLIRDENGDVVGCV
          130     140     150     160     170     180

          190     200     210     220     230     240
m010-1.pep TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ
          |||
g010-1      TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ

```

190

	190	200	210	220	230	240
	250	260	270	280	290	300
m010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
g010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVDLASRDVVS RAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m010-1.pep	RGCGGNKNDHVLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMGGIP					
g010-1	RGCGGNKNDHVLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m010-1.pep	TNYHGEVVVPQGEDYEVFVKGLYAAGECACASVHGANRLGTNSLLDLVVFGKAAGDSMIK					
g010-1	TNYHGEVVVPQGEDEYEVFVKGLYAAGECACASVHGANRLGTNSLLDLVVFRPTFRK					
	370	380	390	400	410	
	430	440	450	460	470	480
m010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQTDGENVDALRRELQRSVQLHAGVFRTEILS					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 71>:

a010-1.seq..

```

1  ATGGGCTTTC CTGTTGCGCAA GTTTGATGCC GTGATTGTCG GCGGTGGTGG
51  TGCAGGTTTA CGCGCANCCC TCCAATTATC CAAATCCGGT CTGAATTGTG
101 CCGTTTTGTC TAAAGTGTTT CCGACCCGTT CGCATACCGT AGCGGCGCAG
151 GCGGATATT CCGCCTCTCT GGGTAATGTG CAGGAAGACC GTTGGGACTG
201 GCACATGTAC GATACCGTGA AAGGTTCCGA CTGGTTGGGC GACCAAGATG
251 CGATTGAGTT TATGTGCCGC GCCGCGCCTG AAGCCGTAAT TGAGTTGGAA
301 CACATGGGTA TGCCTTTTGA CCGTGTGGAA AGCGGTAAAA TTTATCAGCG
351 TCCTTTCGGC GGCCATACTG CCGAACACGG TAAACGCGCG GTAGAACGCG
401 CCTGTGCNGT TGCCGACCGT ACAGGTCATG CGATGCTGCA TACTTGTATC
451 CAACAAAATG TCCGTGCCAA TACGCAATTC TTTGTGGAAT GGACGGCACA
501 AGATTTGATT CGTGATGAAA ACGGCGATGT CGTCGGCGTA ACCGCCATGG
551 AAATGGAAAC CGGCGAAGTT TATATTTTCC ACGCTAAAGC TGTGATGTTT
601 GCTACCGGCG GCGGCGGCCG TATTTATGCG TCTTCTACCA ATGCCATAT
651 GAATACCGGC GATGGTTTGG GTATTTGTGC GCGTGCAGGT ATCCCGTTGG
701 AAGACATGGA ATTCTGGCAA TTCCACCCGA CCGGCGTGGC AGGTGCGGGC
751 GTGTTGATTA CCGAAGGCGT ACGGCGCGAG GCGGTATTTC TGTTGAATGC
801 CGACGGCGAA CGCTTTATGG AACGCTATGC GCCGACCGTA AAAGACTTGG
851 CTCTCTCGCA CGTTGTTTCC CGCGCGATGG CGATGGAAT CTACGAAGGT
901 CCGGCTGCG GTAAAAACAA AGACCATGTC TTA CTGAAAA TCGACCATAT
951 CCGCGCAGAA AAAATTATGG AAAAAGTCCG GGGCATCCGC GAGATTTCCA
1001 TTCAGTTCGC CGGTATCGAT CCGATTAAAG ACCCGATTCC CGTTGTGCCG
1051 ACTACCCACT ATATGATGGG CGGTATTCGG ACCAACTACC ATGGCGAAGT
1101 TGTCGTTTCT CAAGGCGACG AATACGAAGT GCCTGTAAAA GGTCTGTATG
1151 GCGCAGGTGA GTGCGCCTGT GCTTCCGTAC ACGGTGCGAA CCGCTTGGGT
1201 ACGAACTCCC TGCTGGACTT AGTGGTATTC GGTAAAGCTG CCGGCGACAG
1251 CATGATTAAA TTCATCAAAG AGCAAAGCGA CTGGAAACCT TTGCCTGCTA
1301 ATGCCGGCGA ACTGACCCGC CAACGTATCG AGCGTTTGA CAATCAAAC
1351 GATGGTGAAC ACGTTGATGC ATTGCGCCGC GAACTGCAAC GCTCCGTACA
1401 ATTGCACGCC GCGGTGTTCC GTACTGATGA GATTCTGAGC AAAGGCGTTC
1451 GAGAAGTCAT GCGGATTGCC GAGCGTGTGA AACGTACCGA AATCAAAGAC
1501 AAGAGCAAAG TGTGGAATAC CGCGCGTATC GAGGCTTTGG AATTGGATAA
1551 CCTAATTGAA GTGGCGAAAG CGACTTTGGT GTCTGCCGAA GCACGTAAG
1601 AATCACGCGG TGCGCACGCT TCAGACGACC ATCCTGAGCG CGATGATGAA
1651 AACTGGATGA AACATACGCT GTACCATTCA GATGCCAATA CCTTGCTCTA
1701 CAAACCGGTG CACACCAAGC CTTTGAGCGT GGAATACATC AAACCGGCCA
1751 AGCGCGTTTA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 72; ORF 010-1.a>:

a010-1.pep..

```

1  MGFPVRKFDA VIVGGGGAGL RAXLQLSKSG LNCVLSKV F PTRSHTVAAQ
51  GGISASLGNV QEDRWDRWHY DTVKGS DWLG DQDAIEFMCR AAPEAVIELE
101 HMGMPFDRVE SGKIIYQRPFG GHTAEHGKRA VERACAVADR TGHAMLHTLY

```

151 QQNVRRANTQF FVEWTAQDLI RDENGDDVGV TAMEMETGEV YIFHAKAVMF  
201 ATGGGGRIYA SSTNAYMNTG DGLGICARAG IPLEDMEFWQ FHPTGVAGAG  
251 VLITEGVRGE GGILLNADGE RFMERYAPTV KDLASRDVVS RAMAMEIYEG  
301 RGCGKNKDHV LLKIDHIGAE KIMEKLPGIR EISIQFAGID PIKDPIPVVP  
351 TTHYMMGGIP TNYHGEVVVP QGDEYEVVPK GLYAAGECAC ASVHGANRLG  
401 TNSLLDLVVF GKAAGDSMIK FIKEQSDWKPLPANAGELTR QRIERLDNQT  
451 DGENVDALRR ELQSVQLHA GVFRTEILS KGVREVMIAA ERVKRTEIKD  
501 KSKVWNTARI EALELDNLIE VAKATLVSAE ARKESRGAHA SDDHPPERDE  
551 NWMKHTLYHS DANTLSYKPV HTKPLSVEYI KPAKRVY\*

m010-1 / a010-1 99.3% identity in 587 aa overlap

	10	20	30	40	50	60
a010-1.pep	MGFPVRKFDIAVIVGGGGAGLRLXQLSKSGLNCAVLKVFPTSRHTVAAGGGISASLGNV					
a010-1	MGFPVRKFDIAVIVGGGGAGLRAALQLSKSGLNCAVLKVFPTSRHTVAAGGGISASLGNV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a010-1.pep	QEDRWDMHYDITVKGSDWLGDDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
m010-1	QEDRWDMHYDITVKGSDWLGDDAIEFMCRAAPEAVIELEHMGMPFDRVESGKIYQRPFG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a010-1.pep	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDDVGV					
m010-1	GHTAEHGKRAVERACAVADRTGHAMLHTLYQQNVRRANTQFFVEWTAQDLIRDENGDDVGV					
	130	140	150	160	170	180
	190	200	210	220	230	240
a010-1.pep	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
m010-1	TAMEMETGEVYIFHAKAVMFATGGGGRIYASSTNAYMNTGDGLGICARAGIPLEDMEFWQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
a010-1.pep	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVSRAMAMEIYEG					
m010-1	FHPTGVAGAGVLITEGVRGEGGILLNADGERFMERYAPTVKDLASRDVVSRAMAMEIYEG					
	250	260	270	280	290	300
	310	320	330	340	350	360
a010-1.pep	RGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
m010-1	RGCGKNKDHVLLKIDHIGAEKIMEKLPGIREISIQFAGIDPIKDPIPVVPTTHYMMGGIP					
	310	320	330	340	350	360
	370	380	390	400	410	420
a010-1.pep	TNYHGEVVVPQGDEYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVFKAAGDSMIK					
m010-1	TNYHGEVVVPQGEDYEVVPKGLYAAGECACASVHGANRLGTNSLLDLVVFKAAGDSMIK					
	370	380	390	400	410	420
	430	440	450	460	470	480
a010-1.pep	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRRELQSVQLHAGVFRTEILS					
m010-1	FIKEQSDWKPLPANAGELTRQRIERLDNQT DGENVDALRRRELQSVQLHAGVFRTEILS					
	430	440	450	460	470	480
	490	500	510	520	530	540
a010-1.pep	KGVREVMIAAERVKRTEIKDKSKVWNTARIEALELDNLIEVAKATLVSAEARKESRGAHA					
m010-1	KGVREVMIAAERVKRTEIKDKSKVWNTARIEALELDNLIEVAKATLVSAEARKESRGAHA					
	490	500	510	520	530	540
	550	560	570	580		
a010-1.pep	SDDHPPERDENWMKHTLYHS DANTLSYKPVHTKPLSVEYIKPAKRVYX					



m010-1 SDDHPERDDENWMKHTLYHSDINTLSYKPVHTKPLSVEYIKPAKRVIYX  
550 560 570 580

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 73>:

g011.seq  
1 ATGAAGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTGT CTTTTCAGAC  
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA  
101 GCCTGAAAAC CCGCCTTACC GAAGATATGA AAACCGCGAT GCGCGCCAAA  
151 GATCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAATGCCG CCGTCAAACA  
201 GTTTGAAGTA GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA  
251 TCCTGACCAA AATGGTCAAA CAGCGCAAAG ACGGCGCGAA AATCTACACT  
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGACGT  
351 GCTGCACCGC TACCTGCCGC AAATGCTCTC CGCCGGCGAA ATCCGCACCG  
401 CCGTCGAAGC AGCCGTTGCC GAAACCGGCG CGGCAGGTAT GGCGGATATG  
451 GGCAAAGTGA TGGTCGTATT GAAAACccGC CTCGCCGGCA AAGccgATAT  
501 GGGCGAAGTC AACAAAATCT TGAAAAccGt aCTGACCGCC tga

This corresponds to the amino acid sequence <SEQ ID 74; ORF 011.ng>:

g011.pep  
1 MKTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKTRLT EDMKTAMRAK  
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDGAKIYT  
101 EAGRQDLADK ENAEIDVLHR YLPQMLSAGE IRTAVEAAVA ETGAAGMADM  
151 GKVMVVLKTR LAGKADMGEV NKILKTVLTA \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 75>:

m011.seq (partial)  
1 ATGAGGACAC ACCGCAAGAC CTGCTCTGCG GTGTGTTTGT CTTTTCAGAC  
51 GGCATCGAAA CCCGCCGTTT CCATCCGACA TCCCAGCGAG GACATCATGA  
101 GCCTGAAAAT CCGCCTTACC GAAGACATGA AAACCGCGAT GCGCGCCAAA  
151 GACCAAGTTT CCCTCGGCAC CATCCGCCTC ATCAACGCCG CCGTCAAACA  
201 GTTTGAAGTG GACGAACGCA CCGAAGCCGA CGATGCCAAA ATCACCGCCA  
251 TCCTGACCAA AATGGTCAAA CAGCGAAAAG ACAGCGCGAA AATCTACACT  
301 GAAGCCGGCC GTCAGGATTT GGCAGACAAA GAAAACGCCG AAATCGAGGT  
351 ACTGCACCGC TACCTTCCCC AAATGCTTTC CGCCGGCGAA ATCCGTACCG  
401 AGGTCGAAGC TGCCGTTGCC GAAACCGGCG CGGCAGGTAT GGCGGATATG  
451 GGTAAGTCA TGGGGCTGCT GAAAACCCGC CTCGCAGGTA AAGCCGA...

This corresponds to the amino acid sequence <SEQ ID 76; ORF 011>:

m011.pep (partial)  
1 MRTHRKTCSA VCFAFQTASK PAVSIRHPSE DIMSLKIRLT EDMKTAMRAK  
51 DQVSLGTIRL INAAVKQFEV DERTEADDAK ITAILTKMVK QRKDSAKIYT  
101 EAGRQDLADK ENAEIEVLHR YLPQMLSAGE IRTEVEAAVA ETGAAGMADM  
151 GKVMGLLKTR LAGKA.....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 011 shows 95.8% identity over a 165 aa overlap with a predicted ORF (ORF 011.ng) from *N. gonorrhoeae*:

m011/g011

	10	20	30	40	50	60
m011.pep	MRTHRKTCSAVCF	AFQTASKPAVSIR	HPSEDIMSLKIR	LTEDMKTAMRAK	DQVSLGTIRL	
g011	MRTHRKTCSAVCF	AFQTASKPAVSIR	HPSEDIMSLKTR	LTEDMKTAMRAK	DQVSLGTIRL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m011.pep	INAAVKQFEVDER	TEADDAKITAIL	TKMVKQRKDSAK	IYTEAGRQDLAD	KENAEIEVLHR	
g011	INAAVKQFEVDER	TEADDAKITAIL	TKMVKQRKDGA	KIYTEAGRQDL	ADKENAEIDVL	

193

	70	80	90	100	110	120
	130	140	150	160		
m011.pep	YLPQMLSAGEIRTEVEAAVAETGAAGMADMGKVMGLLKTRLAGKA					
g011	YLPQMLSAGEIRTAEEAAVAETGAAGMADMGKVMVVLKTRLAGKADMGVKNILKTVLTA					
	130	140	150	160	170	180
g011	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 77>:

g012.seq

1	ATGCTCGCCC	GTGCTATTT	TTTCAATATC	CAACCCGGGG	CGGTTTTCAC
51	TGACAAACTG	CTTGAACAAC	TGATGCGTTT	CCTCCAGTTC	CTGCCGGAAT
101	TTCTGTTTGC	CCTTTTCCGT	ATTTTCACCC	ATAAAAGTAA	CCGTGCGCTT
151	AAATTCGCCC	GCCGTCATCA	CATCCACATC	AATATCATGT	TTTTTCAACa
201	gGcggTGGAT	ATTCGgcact	tccgCcacca	caccacccga	accgatgacc
251	gcaaacggaG	CGGAACAAT	TTTATCCGCC	acacacgcca	tcatatagcc
301	gcCGCTTGCC	GCGACCTTAT	CGAcggcgac	ggTCAGCGGA	ATATTGCGTT
351	CGCGCAAACG	CCTAAGCTGC	GAAGCCGCCA	AACCGTAACC	GTGAACCACG
401	CCGCCCGGAC	TTTCCAATCT	GAGCAGAAC	TCATCTTCAG	GCTTGCCAAT
451	CAAAAGCACC	GCCGTAATCT	CATGACGCAA	GGATTCTACG	GCGTGTGCAT
501	ACAAATCGCC	GTCAAAATCC	AACACAAAAA	GGCGGGATT	TTGCGTTTCG
551	GCAGATTCT	CCCCGCCCTC	CTTCAAACGC	TTTTCTCTG	CTTTGGCTTC
601	CGCCTTTTCC	TTTTTCTTTT	CTTTTCTTTC	CTGATGTTTT	GTCTCTTCTC
651	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 78; ORF 012.ng>:

g012.pep

1	MLARRYFFNI	QPGAVETDKL	LEQLMRFLQF	LPEFLFALFR	IFTHKSNRAL
51	KFARRHHIHI	NIMFFQQA	VDIRYFRHHH	THRTDDRKR	SGNFIRHTRH
101	AACRDLIDGD	QORNIAFAQT	PKLRSRQTVT	VNHAARTFQS	EQNLIFRLGN
151	QKHRRNLMTQ	GFYGVCIQIA	VKIQHKKAGF	LRFRFLPAL	LQTLFLCFGF
201	RLFLFLFFFF	LMFCLFLA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 79>:

m012.seq

1	ATGCTCGCCC	GTTGCCACTT	CCTCAATATC	CAATTGAGGG	CGGTTCTCGC
51	TGACAAACTG	CTTGAACAAC	TGATGCGTTT	CCTCCAGTTC	CTGTCCGAAT
101	TTCTGTTTGC	CCTTTTCCGT	ATTTTCACCC	ATAAAAGTAA	CCGTGCGCTT
151	AAATTCGCCC	GCCGTCATCA	CATCCACATC	AATATCATGT	TTTTTCAACA
201	GGCGGTGGAT	ATTCGGTACT	TCCGCCACCA	CACCCACCGA	ACCGACAATC
251	GCAAACGGAG	CGGAAGCAAT	TTTATCCGCC	ACACACGCCA	TCATATAACC
301	GCCGCTCGCn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
351	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
401	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
451	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn	nnnnnnnnnn
501	nnnnnnnnnn	nnnnnnnnnC	AACACAAAAA	GGCGTGATT	TTGCGTTTCG
551	GCAGATTCT	CCCCACCCTC	CTTCAAACGT	TTTTCTCTG	CTTTGGCTTC
601	CGCCTTTTCC	TTTTTCTTTT	CCTCTTTTTC	CTGATGTTGT	GCCTCTTCCC
651	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 80; ORF 012>:

m012.pep

1	MLARCHFLNI	QLRAVLADKL	LEQLMRFLQF	LSEFLFALFR	IFTHKSNRAL
51	KFARRHHIHI	NIMFFQQA	VDIRYFRHHH	THRTDNRK	SGNFIRHTRH
101	AARXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX	XXXXXXXXXX
151	XXXXXXXXXX	XXXXXXXXXX	XXXQHKKAF	XRFRFLPTL	LQTFFLCFGF
201	RLFLFLFLFF	LMLCLFLA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 81>:

```
a012.seq
1   ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CCTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTTGGAT ATTCGGTACT TCCGCTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CGGCAAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TCGCGTTTCG
551 GAAGATTCTT CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 82; ORF 012.a>:

```
a012.pep
1   MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKSGNN FIRHTRHHIT
101 TARRHLIDGD GQRNIAFAQT PKLRSRQTVT VNHAARTFQS KQNLIFRLGN
151 QKHRNLMTO GFYGVCIQIA VKIQHKKAGF LRFRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLFPA*
```

m012/a012 64.2% identity over a 218 aa overlap

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
a012	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXX					
a012	NIMFFQQAVDIRYFRYNTHRTDNRKSGNNFIRHTRHHITTARRHLIDGDGQRNIAFAQT					
	70	80	90	100	110	120
m012.pep	130	140	150	160	170	180
	XXQHKKAXF					
a012	PKLRSRQTVT VNHAARTFQSKQNLIFRLGNQKHRNLMTOGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
m012.pep	190	200	210	219		
	XRFRFLPTLLQTFFLCFGRFLFLFLFFLMLCLFPAX					
a012	LRFRFLPTLLQTLFLCFGRFLFLFLFFLMLCLFPAX					
	190	200	210			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 012 shows 58.7% identity over a 218 aa overlap with a predicted ORF (ORF 012.ng) from *N. gonorrhoeae*:

m012/g012

m012.pep	10	20	30	40	50	60
	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALFRIFTHKSNRALKFARRHHIHI					

195

	10	20	30	40	50	60
m012.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARXXXXXXXXXXXXXXXXXX					
g012	NIMFFQQAVDIRHFRHHTHRTDDRKRSGNNFIRHTRHHIAAACRDLIDGQGNIAFAQT					
	70	80	90	100	110	120
m012.pep	130	140	150	160	170	180
	XXXQHKKAXF					
g012	PKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
m012.pep	190	200	210	219		
	XRFGRFLPTLLQTFFLCFGRFLFLFLFLFFLMLCLFPAX					
g012	LRFGRFLPALQLFLCFGRFLFLFLFFFLMFCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 83>:

m012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTCGGAAT
101 TTCTGTTTGC CTTTTCCTGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTCGCCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GGCGGTGGAT ATTCGGTACT TCCGCCACCA CACCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAGCAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 GCCGCTCGCC GCCACCTTAT CGACGGCGAC GGTGAGCGGA ATATTGCGTT
351 CGCGCAAACG CyTAAGCTGC GAAGCCGCCA AACCCTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT GAGCAGAACC TCATCTTCAG GCTTGGCAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAAATCGCC GTCAAAATCC AACACAAAAA GGCGGGATT TTTGCGTTTCG
551 GCAGATTCTC CCCACCCCTC CTTCAAACGC TTTTCTCTG CTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 84; ORF 012-1>:

m012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALER IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRHHTHR TDNRKRSGSN FIRHTRHHIT
101 AARRHLIDGD GQRNIAFAQT XKLRSRQTVT VNHAARTFQS EQNLIFRLGN
151 QKHRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRFLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFCLEPA*

```

m012-1/g012 91.7% identity in 218 aa overlap

	10	20	30	40	50	60
m012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALERIFTHKSNRALKFARRHHIHI					
g012	MLARRYFFNIQPGAVFTDKLLEQLMRFLQFLPEFLFALERIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
m012-1.pep	70	80	90	100	110	120
	NIMFFQQAVDIRYFRHHTHRTDNRKRSGSNFIRHTRHHITAARRHLIDGQGNIAFAQT					
g012	NIMFFQQAVDIRHFRHHTHRTDDRKRSGNNFIRHTRHHIAAACRDLIDGQGNIAFAQT					
	70	80	90	100	110	120
m012-1.pep	130	140	150	160	170	180
	XKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					
g012	PKLRSRQTVTVNHAARTFQSEQNLI FRLGNQKHRRNLMTQGFYGVCIQIAVKIQHKKAGF					

196

	130	140	150	160	170	180
	190	200	210	219		
m012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	:     :     :     :					
g012	LRFGRLPALQLTLFLCFGRFLFLFLFLFLMFLCLFLAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 85>:

a012-1.seq

```

1  ATGCTCGCCC GTTGCCACTT CCTCAATATC CAATTGAGGG CGGTTCTCGC
51  TGACAAACTG CTTGAACAAC TGATGCGTTT CCTCCAGTTC CTGTGCGAAT
101 TTCTGTTTGC CCTTTTCCGT ATTTTCACCC ATAAAAGTAA CCGTGCGCTT
151 AAATTGCGCC GCCGTCATCA CATCCACATC AATATCATGT TTTTCAACA
201 GCGGTGGAT ATTCGGTACT TCCGTACAA CACCCACCGA ACCGACAATC
251 GCAAACGGAG CGGAAACAAT TTTATCCGCC ACACACGCCA TCATATAACC
301 ACCGCTCGCC GCCACCTTAT CGACGGCGAC GGTCAGCGGA ATATTGCGTT
351 CCGCGAAACG CCTAAGCTGC GAAGCCGCCA AACCGTAACC GTGAACCACG
401 CCGCCCGGAC TTTCCAATCT AAGCAGAACC TCATCTTCAG GCTTGGAAT
451 CAAAAGCACC GCCGTAATCT CATGACGCAA GGATTCTACG GCGTGTGCAT
501 ACAATCGCC GTCAAAATCC AACACAAAAA GCGGGGATT TTGCGTTTCG
551 GAAGATTCTC CCCCACCCTC CTTCAAACGC TTTTCTCTG CTTTGGCTTC
601 CGCCTTTTCC TTTTCTTTT CCTCTTTTC CTGATGTTT GCCTCTTCCC
651 CGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 86; ORF 012-1.a>:

a012-1.pep

```

1  MLARCHFLNI QLRAVLADKL LEQLMRFLQF LSEFLFALFR IFTHKSNRAL
51  KFARRHHIHI NIMFFQQAVD IRYFRYNTHR TDNRKRSNN FIRHTRHHIT
101 TARRHLIDGD QORNIATAQT PKLRSRQVT VNHAARTFQS KQNLIFRLGN
151 QKRRNLMTQ GFYGVCIQIA VKIQHKKAGF LRFGRLPTL LQTLFLCFGF
201 RLFLFLFLFF LMFLCLFPA*

```

a012-1/m012-1 97.2% identity in 218 aa overlap

	10	20	30	40	50	60
a012-1.pep	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	:     :     :     :					
m012-1	MLARCHFLNIQLRAVLADKLEQLMRFLQFLSEFLFALFRIFTHKSNRALKFARRHHIHI					
	10	20	30	40	50	60
	70	80	90	100	110	120
a012-1.pep	NIMFFQQAVDIRYFRYNTHRTDNRKRSNNFIRHTRHHITTARRHLIDGDGQORNIATAQT					
	:     :     :     :					
m012-1	NIMFFQQAVDIRYFRHHTHRTDNRKRSNSNFIRHTRHHITAARRHLIDGDGQORNIATAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a012-1.pep	PKLRSRQVTVNHAARTFQSKQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	:     :     :     :					
m012-1	XKLRSRQVTVNHAARTFQSEQNLIFRLGNQKRRNLMTQGFYGVCIQIAVKIQHKKAGF					
	130	140	150	160	170	180
	190	200	210	219		
a012-1.pep	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	:     :     :     :					
m012-1	LRFGRLPTLLQTLFLCFGRFLFLFLFLFLMFLCLFPAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 87>:

g013.seq

```

1  aTgcctttga ccatgctgtg cagcaGGAcy tGCGGTTtgt tcataatata
51  gtCcgaccgG AAAagcgag GAAaCGCAGT GCCGCGCCCT TCCCTTTCT
101 TGCCGTGGCA GGCGATGCag tTgATTTCGT ACACTTTTG CCCTTTtGtc

```

```

151 atgatGCTgt tgtcggCGGC AGAAGCgGCG GcgCAGAGGC AGCACAAGAT
201 GAAGGCGGTC GGCAGTCGGG TTGTGTtcat tGgcgTTTCC cctaattgtt
251 tgaaaccttg ttttttgatt Ttgcctttac ggggtgaaaa gtttttTtgg
301 cccaaatccg gaatttag

```

This corresponds to the amino acid sequence <SEQ ID 88; ORF 013.ng:

**g013.pep**

```

1 MPLTMLCSRT CGLFIIQSDR KSGGNAVPRP SPFLPWQAMQ LDSYTFCPFV
51 MMLLSAAEAA AQRQHKMKAV GSRVVFIVGS PNVLKPCFLI LPLRGEKFFW
101 PKSGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 89>:

**m013.seq**

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCAGCGCAG TTGGATTCGT ACACTTTTTC CCCTTTTGTC
151 ATGATGCTGT TGTCCGCGGC AGAAGCGGCG GCGCAGAAGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTCAT TGGTGTTC TCCATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT TTTGCCGAAT
301 CAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 90; ORF 013>:

**m013.pep**

```

1 MPLTMLCSST CGFFMMKSER XSGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIVGS FMFETLLLL RSGXKIFLPN
101 Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 91>:

**a013.seq**

```

1 ATGCCTTTGA CCATGCTGTG CAGCAGCACC TCGGGTTTTT TCATGATGAA
51 GTCGGAGCGG TAGAGCGGCG GAAACATGGT TCCGCGGCCT TCGCCCTTTT
101 TGCCGTGGCA GGCAGCGCAG TTGGATTCGT ACACTTTTTC CCCTTTTGTC
151 ATGATGCTGT TGTCCGCGGC AGAAGCGGCG GCGCAGAGGC AGCCCAAGAC
201 GAGGGCGGTC GGCAGTCGGG TTGTGTTTCAT TGGTGTTC TTAATGTTTG
251 AAACCTTGTT GTTGATTTTG CGTAGCGGGT GAAAGATTTT CTTGCCGAAT
301 CGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 92; ORF 013.a>:

**a013.pep**

```

1 MPLTMLCSST CGFFMMKSER *SGGNMVRP SPFLPWQATQ LDSYTFCPFV
51 MMLLSAAEAA AQRQPKTRAV GSRVVFIVGS LMFETLLLL RSG*KIFLPN
101 R*

```

**m013/a013** 97.0% identity over a 101 aa overlap

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
a013	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQRQPKTRAVGSRVVFIVGSFMFETLLLLRSGXKIFLPNQX					
	:     :					
a013	AQRQPKTRAVGSRVVFIVGSLMFETLLLLRSGXKIFLPNRX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 013 shows 73.3% identity over a 101 aa overlap with a predicted ORF (ORF 013.ng) from *N. gonorrhoeae*:

198

## m013/g013

	10	20	30	40	50	60
m013.pep	MPLTMLCSSTCGFFMMKSERXSGGNMVRPSPFLPWQATQLDSYTFCPFVMMLLSAAEAA					
	:  : :: :					
g013	MPLTMLCSRTCGLFIIQSDRKSGGNVPRPSPFLPWQAMQLDSYTFCPFVMMLLSAAEAA					
	10	20	30	40	50	60
	70	80	90	100		
m013.pep	AQKQPKTRAVGSRVVFVIGVSF-MFETLLLILR-SGXKIFLPNQX					
	:    :            :: :        :    :					
g013	AQRQHKMKAVGSRVVFVIGVSPNVLPKPCFLILPLRGEKFFWPKSGIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 93>:

g015.seq

```

1 ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51 CATTTTGGTA TTCAACATCC GTTTTTTCCT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGT CGGCTTTTGG AAAGCACTGC CCCACCTCAA CGACACGATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAG ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGCA CAAAATCCT GCTCCTGTTT GCCTACATCG
251 CACTGGGCAT GGTAATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCTAT GTGTTGCATC GCCTGCATCG TTTACCTTGC
351 CAAAACCAA GTCCTGCCAT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 94; ORF 015.ng>:

g015.pep

```

1 MQYLIVKYSH QIFVTITILV FNIRFFLLWK NPEKPLVGFW KALPHLNDTM
51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLE AYIALGMVMM RARPRSTKFY
101 TVYLLAMCCI ACIVYLAKTK VLPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 95>:

m015.seq (partial)

```

1 ..AAAATCAGAA AAGCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA
51 CGACACCATG CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT
101 TCTCCCCGTT CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC
151 GCCTATATCG CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC
201 CAAGTTCTAC ACCGTTTACC TGCTCGCCAT GTGTTGCGTC GCCTGCATCG
251 TTTACCTTGC CAAAACCAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 96; ORF 015>:

m015.pep (partial)

```

1 ..KIRKALAGFW KALPHLNDTM LLFTGLWLMK ITHFSPFNAP WLGTKILLLE
51 AYIALGMMM RARPRSTKFY TVYLLAMCCV ACIVYLAKTK VLPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 97>:

a015.seq

```

1 ATGCAGTATC TGATTGTCAA ATACAGCCAT CAAATCTTCG TTACCATCAC
51 CATTTTGGTA TTCAACATCC GTGTTTCNT ACTTTGGAAA AATCCAGAAA
101 AGCCCTTGGC GGGCTTTTGG AAGGCACTGC CCCACCTTAA CGACACCATG
151 CTGCTGTTTA CGGGATTGTG GCTGATGAAA ATTACCCATT TCTCCCCGTT
201 CAACGCGCCT TGGCTCGGTA CAAAATCCT GCTTCTGCTC GCCTATATCG
251 CATTGGGTAT GATGATGATG CGCGCCCGTC CGCGTTCGAC CAAGTTCTAC
301 ACCGTTTACC TGCTCGCCAT GTGTTGCCTC ACCTGCATCG TTTACCTTGC
351 CAAAACCAA GTCCTGCCTT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 98; ORF 015.a>:

a015.pep

1 MQYLIVKYSH QIEVTITILV FNIRVFXLWK NPEKPLAGFW KALPHLNDTM  
 51 LLFTGLWLMK ITHFSPFNAP WLGTKILLLL AYIALGMMM RARPRSTKFY  
 101 TVYLLAMCCL TCIVYLAKTK VLPF\*

m015/a015 96.7% identity over a 91 aa overlap

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
a015	LIVKYSHQIFVTITILVFNIRVFXLWKNPEKPLAGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
a015	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCLTCIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
a015	FX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 015 shows 94.5% identity over a 91 aa overlap with a predicted ORF (ORF 015.ng) from *N. gonorrhoeae*:

m015/g015

m015.pep				10	20	30
				KIRKALAGFWKALPHLNDTM	LLFTGLWLMKITH	
g015	LIVKYSHQIFVTITILVFNIRFFLLWKNPEKPLVGFWKALPHLNDTM	LLFTGLWLMKITH				
	10	20	30	40	50	60
m015.pep		40	50	60	70	80
	FSPFNAPWLGTKILLLLAYIALGMMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
g015	FSPFNAPWLGTKILLLLFAYIALGMVMMRRARPRSTK	FYTVYLLAMCCVACIVYLAKTKVLP				
	70	80	90	100	110	120
m015.pep	FX					
g015	FX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 99>:

g018.seq

1 atGCAGCAGG GGCagttggt tggacgcgtc gcccgcaata AAGATATGCG  
 51 GAATgctggt CTGCATggtC AGCGGATCGG CAACGGGtac gccgcgcgcg  
 101 tctttgTCGA TATTGATGTT TTCCAAACCG ATATTgTCAA CGTTCGGACG  
 151 GCgACCTACG GCTGCCAACA TATATTCGGC AACAAATACG CCTTTTCGC  
 201 CATCCTGCTC CCAATGGACT tctACATTGC CGTCTGCGTC GAGTTTGACC  
 251 TCGGTTTtag CATCCAGATG CAGTTTCAAT tctTCTCCGA ACACGGCTTT  
 301 CGCCTCGTCT GA

This corresponds to the amino acid sequence <SEQ ID 100; ORF 018.ng>:

g018.pep

1 MQQGQLVGRV ARNKDMRNAG LHGQRIGNGY AARVFVDIDV FQTDIVNVRT  
 51 ATYGCOHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFSEHGF



101 RLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 101>:

```
m018.seq
1  ATGCAGCAGA GGCAGTTGGT TGGACGCATC GCCTGCGATG AAGATATGCG
51  GAATACTGGT CTGCATGGTC AGCGGGTCGG CAACAGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATATT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCATC GAGTTTGACC
251 TCGGTTTTAG CATCCAGATG CAGTTTCAAT TCTTCGCCGA ACACGGCGTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 102; ORF 018>:

```
m018.pep
1  MQQRQLVGRI ACDEDMRNTG LHGQRVGNRY AARIFFDIDI FQTDIVNVRT
51  AAHGCGHIFG NKYAFAILL PMDFYIAVCI EFDLGFSIQM QFQFFAEHGV
101 RLV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 103>:

```
a018.seq
1  ATGCAGCAGG GGCAGTTGGT TGGACGCGTC GCCGCAATA AAGATATGCG
51  GAATACTGGT CTGCATAGTC AGCGGATCGG CAACGGGTAC GCCGCGCGCA
101 TCTTTTTCGA TATTGATGTT TTCCAAACCG ATATTGTCAA CGTTCGGACG
151 GCGGCCTACG GCTGCCAGCA TATATTCGGC AACAAATACG CCTTTTTCGC
201 CATCCTGCTC CCAATGGACT TCTACATTGC CGTCTGCGTC GAGTTTGGCC
251 TCGGTTTTAG CATCCAAATG CAGTTTCAAT TCTTCACCGA ACACGGCTTT
301 CGCCTCGTCT GA
```

This corresponds to the amino acid sequence <SEQ ID 104; ORF 018.a>:

```
a018.pep
1  MQQGQLVGRV ARNKDMRNTG LHSQRIGNGY AARIFFDIDV FQTDIVNVRT
51  AAYGCGHIFG NKYAFAILL PMDFYIAVCV EFDLGFSIQM QFQFFTEHGF
101 RLV*
```

m018/a018 86.4% identity over a 103 aa overlap

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	:  ::   :     : :       :     :     :					
a018	MQQGQLVGRVARNKDMRNTGLHSQRIGNGYAARIFFDIDVFDIVNVRTAAYGCGHIFG					
	10	20	30	40	50	60
	70	80	90	100		
m018.pep	NKYAFAILLPMDFYIAVCIEFDLGFSIQMQFQFFAEHGVRLVX					
	:     :     :       :     :     :					
a018	NKYAFAILLPMDFYIAVCVEFDLGFSIQMQFQFFTEHGFRLVX					
	70	80	90	100		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 018 shows 84.5% identity over a 103 aa overlap with a predicted ORF (ORF 018.ng) from *N. gonorrhoeae*:

m018/g018

	10	20	30	40	50	60
m018.pep	MQQRQLVGRIACDEDMRNTGLHGQRVGNRYAARIFFDIDIFQTDIVNVRTAAHGCGHIFG					
	:  ::   :     : :       :     :     :					
g018	MQQGQLVGRVARNKDMRNAGLHGQRVGNRYAARVFDIVNVRTATYGCQHIFG					
	10	20	30	40	50	60

	70	80	90	100
m018.pep	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFFAEHGVRLVX			
g018	NKYAFFAILLPMDFYIAVCIEFDLGFSIQMQFFSEHGFRLVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 105>:

g019.seq (partial)

```

1 ..ctgctggcgg ccctggtgct tgccgcgtgt tcttcgACAA ACacacTGCC
51 AGCCGGCAAG ACCCCGGCAG ACAATATAGA AActgcCgAC CTTTCGGCAA
101 GCGTTCCAC cgcCCTGCC GAACCGGAAG GAAAAACGCT GGCAGATTAC
151 GGCGGTACC CGTCCGACT GGATGCAGTG AAACAGAACA ACGATGCGGC
201 AGCCGCCGCC TATTTGAAA Acgcaggaga cagCGcgatg gcGGAAtg
251 tccgaagga gtgGCTGa

```

This corresponds to the amino acid sequence <SEQ ID 106; ORF 019.ng>:

g019.pep (partial)

```

1 ..LLAALVLAAC SSTNTLPAGK TPADNIETAD LSASVPTRPA EPEGKTLADY
51 GGYPSALDAV KQNDAAAAA YLENAGDSAM AENVKLEWL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 107>:

m019.seq (partial)

```

1 ATGTACCTAC CCTCTATGAA GCATTCCCTG CCGTGCTGCG CGGCCCTGGT
51 GCTTGCCGCG TGTTCTTCGA CAAACACACT GCCAGCCGGC AAGACCCCGG
101 CAGACAATAT AGAAACTGCC GACCTTTCGG CAAGCGTTC CACCCGCCCT
151 GCCGAACCCG AAAGAAAAAC GCTGGCAGAT TACGGCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGGCTG
301 AAGTCTTTGG GCGCACGCAG ACAGTGGACG CTGTTGTCAC AGGAATACGC
351 CAAACTCGAA CCGGCAGGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGCTG AACTGGTCAA AAATACGGGC
451 AAAGTGCCTT CCGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCAACGACG CCTGGAGGCG CGTGCGCGGA CTGCTGGCCG
551 GCCGCCAAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CTGCGGCCT TGGACTATTA
801 CGCAAGGTT GCCGACCGCC GCCAATGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGCCTTGCGC GCCCGACGTT GGGACGAGCT GGCCTCGGTT
901 ATCTCGCATA TGCCCGAAAA ACTGCAAAAA AGCCCGACCT GGCTCTACTG
951 GCTGGCACGC AGCCGCGCCG CAACGGGCAA CACGCAAGAG GCGGAAAAAC
1001 TTTACAAACA GCGGCGAGCG ACGGGCAGGA ATTTTATGCG GGTGCTGGCA
1051 GGGGAAGAAT TGGGTCGGAA AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAAAC AGCGTCCGCC GCATGGCGGA AGACGGTGCA GTCAAACCGC
1151 CACTGGTACT GTTCCAAAAC AGCCAATCTG CCGGTGATGC AAAAATGCGC
1201 CGTCAGGCTC AGGCGGAATG GCGTTTTGCC ACACGCGGCT TTGACGAAGA
1251 CAAGCTGCTG ACCGCGCGCG AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCAGCC GCAAACTCAA CTACACCTTG
1351 CGCTATATTT CGCCGTTTAA AGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCTTGGG TTTATGGGCT GATTGCTCAG GAAAGCCGCT
1451 TCGTTATAGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCCTGCCA CCGCGCGCGA AATCGCCGCG AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCGGACG GG...

```

This corresponds to the amino acid sequence <SEQ ID 108; ORF 019>:

m019.pep (partial)

```

1 MYLPSMKHSL PLLAALVLA CSSTNTLPAG KTPADNIETA DLSASVPTRP

```

```

51  AEPERKTLAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LFAQEYAKLE PAGRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSTGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYYGKV ADRRLTDDQ IEWYARAALR ARRWDELASV
301 ISHMPEKLQK SPTWLYWLAR SRAATGNTQE AEKLYKQAAA TGRNFYAVLA
351 GEELGRKIDT RNNVPDAGKN SVRRMAEDGA VKRALVLFQN SQSAGDAKMR
401 RQAQAEWRFA TRGFDEKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL
451 RYISPFKDTV IRHAQNVNVD PAWVYGLIRQ ESRFVIGAQS RVGAQGLMQV
501 MPATAREIAG KIGMDAAQLY TADG...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 109>:

a019.seq

```

1  ATGTACCCAC CCTCTCTGAA GCATTCCCTG CCGCTGCTGG TGGNCCTGGT
51  GCTTGCCCGC TGTCTTNGA CAAACACACT GTCAGCCGAC AAGACCCCGG
101 CAGACAATAT AGAACTGCC GACCTTTCGG CAAGCGTTCC CACCNCCCTT
151 GCCGAACCCG AANGAAAAAC GTNGGCAGAT TACGCCGGCT ACCCGTCCGC
201 ACTGGATGCA GTGAAACAGA AAAACGATGC CGCCGTCGCC GCCTATTGG
251 AAAACGCCGG CGACAGCGCG ATGGCGGAAA ATGTCCGCAA CGAGTGCTG
301 AAGTCTTTGG CGCGCGCAG ACAGTGGACG CTGTNTGCAC ANGAATATGC
351 NAAACTCGAA CCGGCANGGC GCGCCCAAGA AGTCGAATGC TACGCCGATT
401 CGAGCCGCAA CGACTATACG CGTGCCGGCG AACTGGTCAA AAATACGGGC
451 AAACTGCCCT CGGGCTGCAC CAAACTGTTG GAACAGGCAG CCGCATCCGG
501 CTTGTTGGAC GGCACGACG CCTGGAGGCG CGTGCCGCGA CTGCTGGCCG
551 GCCGCCAAC CACAGACGCA CGCAACCTTG CCGCCGCATT GGGCAGCCCG
601 TTTGACGGCG GTACACAAGG TTCGCGCGAA TATGCCCTGT TGAACGTCAT
651 CGGCAAAGAA GCACGCAAAAT CGCCGAATGC CGCCGCCCTG CTGTCCGAAA
701 TGGAAAGCGG TTTAAGCCTC GAACAACGCA GTTTCGCGTG GGGCGTATTG
751 GGGCATTATC AGTCGCAAAA CCTCAATGTG CCTGCCGCCT TGGACTATTA
801 NGGCAAGGTT GCCGACCGCC GCCAACTGAC CGACGACCAA ATCGAGTGGT
851 ACGCCCGCGC CGNNNTNNGC NNNCGNNGTT NGNANGANN TGGCNCNNNN
901 ANCNCGNNNN TGCNNGANAA ACNNNNNNAN AGNCNNANNT NGNTNNANTG
951 NNTGGCACGC AGCCGCGCCG CNACGGGCAA CACGCAANAN GCGGANAAC
1001 TNTACAAACA GCGCGCAGCA NCGGGCANGA ATTTTATGCT NGTGCTGNCN
1051 GGGGAAGAGT TGGGGCGCAN AATCGATACG CGCAACAATG TGCCCGATGC
1101 CGGCAAAANC AGCGTCCTCC GTATGGCGGA AGACGGCGCG ATTAAGCCGC
1151 CGCTGGTGCT GTTCCGAAAC AGCCGAACCG CCGCGATGC GAAAATGCGC
1201 CGTCNGGCTC AGGCGGAATG GCGTTTCGCC ACACGGGCT TCGATGAAGA
1251 CAAGCTGCTG ACCGCCGCGC AAACCGCGTT CGACCACGGT TTTTACGATA
1301 TGGCGGTCAA CAGCGCGGAA CGCACCGACC GCAAACTCAA CTACACCTTG
1351 CGCTACATTT CGNNNNNTNA NGACACGGTA ATCCGCCACG CGCAAAATGT
1401 TAATGTCGAT CCGGCGTGGG TTTACGGGCT GATTGCTCAG GAAAGCCGCT
1451 TCGTTATGGG CGCGCAATCC CGCGTAGGCG CGCAGGGGCT GATGCAGGTT
1501 ATGCTGCGCA CCGCGCGCGA AATCGCCGGC AAAATCGGTA TGGATGCCCG
1551 ACAACTTTAC ACCGCCGACG GCAATATCCG TATGGGGACG TGGTATATGG
1601 CGGACACCAA ACGCCGCTG CAAAACAACG AAGTCCTCGC CACCGCAGGC
1651 TATAACGCCG GTCCCGGCAG GCGCGCCGGA TGGCAGGCG ACACGCCCTT
1701 CGAAGGCGCG GTATATGCCG AAACCATCCC GTTTTCCGAA ACGCGGACT
1751 ATGTCAAAAA AGTGATGGCC AATGCCGCCT ACTACGCTC CCTCTTCGGC
1801 GCGCCGACA TCCCGCTCAA ACAGCGTATG GGCATTGTCC CCGCCCGCTG
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 019.a>:

a019.pep

```

1  MYPPSLKHSL PLLVXLVLAA CSXTNTLSAD KTPADNIETA DLSASVPTXP
51  AEPEKTXAD YGGYPSALDA VKQKNDAAVA AYLENAGDSA MAENVRNEWL
101 KSLGARRQWT LXAXEYAKLE PAXRAQEVEC YADSSRNDYT RAAELVKNTG
151 KLPSTGCTKLL EQAAASGLLD GNDAWRRVRG LLAGRQTDDA RNLAALGSP
201 FDGGTQGSRE YALLNVIGKE ARKSPNAAAL LSEMESGLSL EQRSFAWGLV
251 GHYQSQNLNV PAALDYYGKV ADRRLTDDQ IEWYARAAXX XRXXXXXXXX
301 XXXXXXXXXX XXXXXXXXXAR SRAATGNTQX AXKLYKQAAA XGXNFYAVLX
351 GEELGRXIDT RNNVPDAGKX SVLRMAEDGA IKRALVLFN SRTAGDAKMR
401 RXAQAEWRFA TRGFDEKLL TAAQTAFDHG FYDMAVNSAE RTDRKLNYTL

```

451 RYISXXXTDV IRHAQNVNVD PAWVYGLIRQ ESRFVMAQS RVGAQGLMQV  
 501 MPATAREIAG KIGMDAAQLY TADGNIRMG T WYMADTKRRL QNNEVLATAG  
 551 YNAGPGRARR WQADTFLEGA VYAETIPFSE TRDYVKKVMA NAAYYASLFG  
 601 APHIPLKQRM GIVPAR\*

m019/a019 88.9% identity over a 524 aa overlap

m019.pep	10	20	30	40	50	60
	MYLPSMKHSLPLLAALVLAACSSTNTLPAGKTPADNIETADLSASVPTRPAPERKTLAD					
a019	MYPPSLKHSLPLLVLVLAACSXTNTLSADKTPADNIETADLSASVPTXPAPPEXKTXAD					
	10	20	30	40	50	60
m019.pep	70	80	90	100	110	120
	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLFAQEYAKLE					
a019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKS LGARRQWTLXAXEYAKLE					
	70	80	90	100	110	120
m019.pep	130	140	150	160	170	180
	PAGRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLLEQAAASGLLDGNDAWRRVRG					
a019	PAXRAQEVECYADSSRNDYTRAAELVKNTGKLP SGCTKLLEQAAASGLLDGNDAWRRVRG					
	130	140	150	160	170	180
m019.pep	190	200	210	220	230	240
	LLAGRQTTDARNLAAALGSFFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
a019	LLAGRQTTDARNLAAALGSFFDGGTQGSREYALLNVIGKEARKSPNAAALLSEMESGLSL					
	190	200	210	220	230	240
m019.pep	250	260	270	280	290	300
	EQRSFAWGV LGHYQS QNLNVPAA LDY YGKVADRRQLTDDQIEWYARAALRARRWDELASV					
a019	EQRSFAWGV LGHYQS QNLNVPAA LDY XGKVADRRQLTDDQIEWYARAAXXRXRXRXAXX					
	250	260	270	280	290	300
m019.pep	310	320	330	340	350	360
	ISHMPEKLQKSPTWLYWLARSRAATGNTQAEKLYKQAAATGRNFYAVLAGEELGRKIDT					
a019	XXXXXXXXXXXXXXXXXARSRAATGNTQAXKLYKQAAAXGXNFYAVLXGEELGRXIDT					
	310	320	330	340	350	360
m019.pep	370	380	390	400	410	420
	RNNVPDAGKNSVRRMAEDGAVKRALVLFQNSQSAGDAKMRRQAQAEWRFATRGFDEDKLL					
a019	RNNVPDAGKXSVLRMAEDGAIKRALVLFNRSRTAGDAKMRRXAQAEWRFATRGFDEDKLL					
	370	380	390	400	410	420
m019.pep	430	440	450	460	470	480
	TAAQTAFDHGFYDMAVNSAERTDRKLNYYTLRYISPFKDTVIRHAQNVNVDPAWVYGLIRQ					
a019	TAAQTAFDHGFYDMAVNSAERTDRKLNYYTLRYISXXXTDVIRHAQNVNVDPAWVYGLIRQ					
	430	440	450	460	470	480
m019.pep	490	500	510	520		
	ESRFVIGAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADG					
a019	ESRFVMAQSRVGAQGLMQVMPATAREIAGKIGMDAAQLYTADGNIRMG TWYMADTKRRL					
	490	500	510	520	530	540
a019	QNNEVLATAGYNAGPGRARRWQADTFLEGA VYAETIPFSETRDYVKKVMANAAYYASLFG					
	550	560	570	580	590	600

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 019 shows 95.5% identity over a 89 aa overlap with a predicted ORF (ORF 019.ng) from *N. gonorrhoeae*:

g019/m019

		10	20	30	40	49
g019.pep		LLAALVLAACSSNTNLPAGKTPADNIETADLSASVPTRPAPPEGKTLAD				
m019		MYLPSMKHSLPLLAALVLAACSSNTNLPAGKTPADNIETADLSASVPTRPAPERKTLAD				
		10	20	30	40	50
	50	60	70	80	89	
g019.pep	YGGYPSALDAVKQNNDAAAAYLENAGDSAMAENVRKEWL					
m019	YGGYPSALDAVKQKNDAAVAAYLENAGDSAMAENVRNEWLKSLGARRQWTLFAQEYAKLE					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 111>:

g023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCCAT TACGGTTTGC GCGATTGGGT
51  AATGCAGCGT GCGACTGCCG TTATTATGTT GATTATATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATCCGGCATG GCAGGCATT
151 TTTAGTCAAG CTTGGGTAAA AGTATTTACC CAAGTGAGCT TTATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCTTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT TGtctGGCTG
301 GTCGGCTGCC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 023.ng>:

g023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFL PKEYPAWQAF
51  FSQAWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

m023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCCAT TACGGTTTGC GCGATTGGGT
51  GATGCAACGT GCGACTGCCG TTATTATGTT GATTATATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCCCTG CCTAAAGAAT ATTCGGCATG GCAGGCATT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT
201 ATTCTTGCAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATCA
251 AACCCTTCGG CGTGCCTTTG TTTTTCAGG TTGCCACCAT CGTTTGGCTG
301 GTCGGCTGTC TCGTGTATTC AGTTAAAGTG ATTTGGGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 023>:

m023.pep

```

1  MVERKLTGAH YGLRDWVMQR ATAVIMLIYT VALLVVLFL PKEYSAWQAF
51  FSQTWVKVFT QVSFIQVFLH AWVGIRDLWM DYIKPFGVRL FLQVATIVWL
101 VGCLVYSVKV IWG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

a023.seq

```

1  ATGGTAGAAC GTAAATTGAC CGGTGCCCCAT TACGGTTTGC GGGATTGGGC
51  GATGCAACGT GCGACCGCGG TTATTATGTT GATTATATACC GTTGCACTTT
101 TAGTGGTTCT ATTTGCTCTG CCTAAAGAAT ATTCGGCATG GCAGGCATT
151 TTTAGTCAAA CTTGGGTAAA AGTATTTACC CAAGTGAGCT TCATCGCCGT

```

201 ATTCTTGAC GCTTGGGTGG GTATCCGCGA TTTGTGGATG GACTATATNA  
 251 AACCCCTTCG CGTGCGTTTG TTTTTCAGG TTGCCACCAT CGTCTGGCTG  
 301 GTCGGCTGCT TGGTGTATTC AATTAAAGTA ATTTGGGGGT AA

This corresponds to the amino acid sequence <SEQ ID 116; ORF 023.a>:

a023.pep  
 1 MVERKLTGAH YGLRDWAMQR ATAVIMLIYT VALLVVLFL PKEYSAWQAF  
 51 FSQTWVKVFT QVSFIAVFLH AWVGIRDLWM DYXKPFVRL FLQVATIVWL  
 101 VGCLVYSIKV IWG\*

m023/a023 96.5% identity over a 113 aa overlap

	10	20	30	40	50	60
m023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLSLPKEYSAWQAFFSQTWVKVFT					
	:     :     :     :     :					
a023	MVERKLTGAHYGLRDWAMQRATAVIMLIYTVALLVVLFLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
m023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	:     :     :     :     :					
a023	QVSFIAVFLHAWVGIRDLWMDYXKPFVRLFLQVATIVWLVGCLVYSIKVIWGX					
	70	80	90	100	110	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 023 shows 97.3% identity over a 113 aa overlap with a predicted ORF (ORF 023.ng) from *N. gonorrhoeae*:

g023/m023

	10	20	30	40	50	60
g023.pep	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLPKEYPAWQAFFSQAWVKVFT					
	:     :     :     :     :					
m023	MVERKLTGAHYGLRDWVMQRATAVIMLIYTVALLVVLFLSLPKEYSAWQAFFSQTWVKVFT					
	10	20	30	40	50	60
	70	80	90	100	110	
g023.pep	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	:     :     :     :     :					
m023	QVSFIAVFLHAWVGIRDLWMDYIKPFGVRLFLQVATIVWLVGCLVYSVKVIWGX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 117>:

g025.seq

1 ATGTTGAAAC AAACgACACT TTTGGCAGCT TGTACCGCCG TTGCCGCTCT  
 51 GTTGGGCGGT TGcgCCACCC AACAGCCTGC TccTGTcATT GCAGGCAATT  
 101 CAGGTATGCA GACCGTATCG TCTGCGCCGG TTTACAATCC TTATGGCGCA  
 151 ACGCCGTACA ATGCCGCTCC TGCCGCCAac gatgcGCCgT ATGTGCCGCC  
 201 CGTGCAAact gcgcgggttT ATTCGCTCC TGCTTATGTT CCGCegtCTG  
 251 CACCTGCCGT TTCGggtaca tatgtTCCTT CTTACGCACC CgtcgACATC  
 301 aacgCGGCGa cgCataCTAT TGTGCGTGGC GACACgGtgt acaACATTTc  
 351 caaAcgCtac CATATCTCTC AAGACGATTT CCGTGCCTGG AACGGCATGA  
 401 CCGACAATAC GTTGAGCATC GGTCAGATTG TTAAAGTCAA ACCGGCaggA  
 451 TATGCCGCAC CGAAACCGC AGCCGTAGAA AGCAGGCCCG CCGTACCGGC  
 501 TGCCGCGCAA ACCCTGTGA AACCCGCCGC gcaACCGCCC GTTCAGTCCG  
 551 CGCCGCAACC TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCCGCCCCC  
 601 CGCCCGCCC CGCAATCTCC TGCCGCTTCG CCTCCGCA CGCGTTCGGT  
 651 CGCGGCATT GTTTGGCAGC GTCCGACCCA AGGTAAAGTG GTTGCCGATT

```

701 TCGGCGGCGG CAACAAGG GTGATATTG CCGGCAATGC CGGACAACCC
751 GTTTTGGCGG CGGCTGACGG CAAAGTGGTT TATGCCGGTT CAGGTTTGAG
801 GGGATACGGA AACTTGGTCA TCATCCAGCA CAATTCCTCT TTCCTGACCG
851 CGTACGGGCA CAACCAAAAA TTGCTGGTCG GCGAAGGTCA GCAGGTCAAA
901 CGCGGTGAGC AGGTTGCTTT GATGGGTAAT ACCGATGCTT CCAGAACGCA
951 GCTTCATTTT GAGGTGCGTC AAAACGGCAA ACCGGTTAAC CCGAACAGCT
1001 ATATCGCGTT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 025.ng>:

```

g025.pep
1  MLKQTTLLAA CTAVAALLGG CATQQPAPVI AGNSGMQTVS SAPVYNPYGA
51  TPYNAAPAAN DAPYVPPVQT APVYSPPAYV PPSAPAVSGT YVPSYAPVDI
101 NAATHTIVRG DTVYNISKRY HISQDDFWA NGMTDNTLSI GQIVKVKPAG
151 YAAPKTAAVE SRPAVPAAQ TPVKPAAQPP VQSAPQPAAP AAENKAVPAP
201 APAPQSPAAS PSGTRSVGGI VWQRPTQGV VADFGGNGK VDIAGNAGQP
251 VLAADGKVV YAGSGLRGY NLVIIQHNS FLTAYGHNQK LLVGEGQQVK
301 RGQQVALMGN TDASRTQLHF EVRQNGKPVN PNSYIAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

m025.seq (partial)
1  ..GTGCCGCGG TGCAAAGCGC GCCGGTTTAT ACGCCTCCTG CTTATGTTCC
51  GCCGTCTGCA CCTGCCGTTT CGGGTACATA CGTTCCTTCT TACGCACCCG
101 TCGACATCAA CGCGGCGACG CATACTATTG TCGCGGCGCA CACGGTGTAC
151 AACATTTCCA AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA
201 CGGCATGACC GACAATACGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC
251 CGGCAGGATA TGCCGCACCG AAAGCCGCG CCGTAAAAAG CAGGCCCGCC
301 GTACCGGCTG CCGCGCAACC GCCCGTACAG TCGCACCCG TCGACATTAA
351 CGCGGCGACG CATACTATTG TGCGCGGCGA CACGGTGTAC AACATTTCCA
401 AACGCTACCA TATCTCTCAA GACGATTTC GTGCGTGGAA CGGCATGACC
451 GACAATATGT TGAGCATCGG TCAGATTGTT AAAGTCAAAC CGGCAGGATA
501 TGCCGCACCG AAAACCGCAG CCGTAGAAAG CAGGCCCGCC GTACCGGCTG
551 CCGTGCAAAC CCTGTGAAA CCCGCCGCGC AACCGCCTGT GCAGTCCGCG
601 CCGCAACCTG CCGCGCCCGC TGCGGAAAAT AAAGCGGTT CCGCGCCCGC
651 CCCGCAATCT CCTGCCGCTT CGCCTTCCGG CACGCGTTC GTCGGCGGCA
701 TTGTTTGGA GCGTCCGACG CAAGGTAAAG TGGTTGCCGA TTTCGGCGGC
751 AACAACAAGG GTGTGCATAT TGCCGGTAAT GCGGGACAGC CCGTTTGGC
801 GGCGGCTGAC GGCAAAGTGG TTTATGCCGG TTCAGTTTG AGGGGATACG
851 GAAACTTGGT CATCATCCAG CATAATTCTT CTTTCTGAC CGCATACGGG
901 CACAACCAAA AATTGCTGGT CGGCGAGGGG CAGCAGGTCA AACCGGTCA
951 GCAGGTTGCT TTGATGGGCA ATACCGATGC TTCCAGAACG CAGCTTCATT
1001 TCGAGGTGCG TCAAACGGC AAACCGGTTA ACCCGAACAG CTATATCGCG
1051 TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 110; ORF 025>:

```

m025.pep (partial)
1  ..VPPVQSAPVY TPPAYVPPSA PAVSGTYVPS YAPVDINAAT HTIVRGDTVY
51  NISKRYHISQ DDFRAWNGMT DNTLSIGQIV KVKPAGYAAP KAAAVKSRPA
101 VPAAAQPPVQ SAPVDINAAT HTIVRGDTVY NISKRYHISQ DDFRAWNGMT
151 DNMLSIGQIV KVKPAGYAAP KTAAVESRPA VPAAVQTPVK PAAQPPVQSA
201 PQPAAPAAEN KAVPAPAPQS PAASPSGTRS VGGIVWQRPT QGKVADFGG
251 NNKGVDIAGN AGQPVLAAD GKVVYAGSL RGYNLVIIQ HNSSF LTAYG
301 HNQKLLVGEG QQVKRQQVA LMGNTDASRT QLHFVQRNG KPVNPNSYIA
351 F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

a025.seq
1  ATGTTGACAC CAACAACACT TTAGGTAGCT TGTACCGCCC TGCCGCTCA
51  GTTGGGCGGA TGCCCCACCC AACACCCTTC TCCTGTCAAT GCAGGCAATT
101 CAGGTATGCA GACCGTACCG TCTGCGCCGG TTTACAATCC TTATGGCGCA

```

```

151 ACGCCGTACA ATGCCGCTCC TGCCGCCAAC GATGCGCCGT ATGTGCCCGC
201 GGTGCAAAGC GCGCCGTTTT ATANGCCTCC TGCTTATGTT CCGCCGTCTG
251 CACCTGCCGT TTCGGGTACA TACGTTCCCT CTTACGCANC CGTCGACATC
301 AACGCGGCGA CCCATACTAT TGTGCGCGGC GACACCGTGT ACAAGATTTC
351 CAAATGCTAC CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA
401 CCGACAATAC GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA
451 TATGCCGCAC CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC
501 TGCCGCGCAA CCGCTCGTAC AGTCCGCACC CGTCGACATC AACGCGGCGA
551 CGCATACTAT TGTGCGCGGC GACACGGTGT ACAACATTTC CAAACGCTAC
601 CATATCTCTC AAGACGATTT CCGTGCGTGG AACGGCATGA CCGACAATAC
651 GTTGAGCATC GGTGAGATTG TTAAAGTCAA ACCGGCAGGA TATGCCGCAC
701 CGAAAGCCGC AGCCGTAAAA AGCAGGCCCG CCGTACCGGC TGCCGTGCAA
751 ACCCCTGTGA AACCCGCCGC GCAACCGCCT GTGCAGTCCG CGCCGCAACC
801 TGCCGCGCCC GCTGCGGAAA ATAAAGCGGT TCCGCGCGCC GCCCGCAAT
851 CTCCTGCCGC TTCGCTTCC GGCACGCGTT CGGTGCGCGG CATTGTTTGG
901 CAGCGTCCGA CGCAAGGTAA AGTGGTTGCC GATTTCGGCG GCAACAACAA
951 GGTGTGCGAT ATTGCAGGAA ATGCGGGACA GCCCGTTTTG GCGGCGGCTG
1001 ACGGCAAAGT GGTATTATGCA GGTTCGGTT TGAGGGGATA CGGCAATTTG
1051 GTCATCATCC AGCATAATTC TTCCTTCCTG ACCGCATACG GGCACAACCA
1101 AAAATTGCTG GTCGCGAAG GCCAGCAGGT CAAACGCGGG CAGCAGGTCG
1151 CTTTGATGGG CAATACCGAG GCTTCTAGAA CGCAGCTTCA TTTGAGGTG
1201 CGGCAAAACG GCAAACCGGT TAATCCGAAC AGCTATATCG CGTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 025.a>:

a025.pep

```

1 MLTP TTL*VA CTALAAQLGG CPTQHPSPVI AGNSGMQTVP SAPVYNPYGA
51 TPYNAAPAAN DAPYVPPVQS APVYXPPAYV PPSAPAVSGT YVPSYAXVDI
101 NAATH TIVRG DTVYKISKCY HISQDD FRAW NGMTDNTLSI GQIVKVKPAG
151 YAAPKAAAVK SRPAVPAAAQ PLVQSAPVDI NAATH TIVRG DTVYNI SKRY
201 HISQDD FRAW NGMTDNTLSI GQIVKVKPAG YAAPKAAAVK SRPAVPAAVQ
251 TPVKPAAQPP VQSAPQPAAP AAENKAVPAP APQSPAASPS GTRSVGGIVW
301 QRPTQGVVVA DFGGNNKGVD IAGNAGQPVL AAADGKV VYA GSGLRGYGNL
351 VLIQHNSFL TAYGHNQKLL VEGEQQV KRG QQVALMGNTE ASRTQLHFEV
401 RQNGKPVNPN SYIAF*

```

m025/a025 97.4% identity over a 351 aa overlap

```

                                10      20      30
m025.pep                      VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
                                |||:|||||:|||||:|||||:|||||
a025      GMQTVPSAPVYNPYGATPYNAAPAANDAPYVPPVQSAPVYXPPAYVPPSAPAVSGTYVPS
              40      50      60      70      80      90

              40      50      60      70      80      90
m025.pep    YAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMTDNTLSIGQIVKVKPAGYAAP
              |||:|||||:|||||:|||||:|||||:|||||
a025      YAXVDINAATH TIVRGDTVYKISKCYHISQDD FRAWNGMTDNTLSIGQIVKVKPAGYAAP
              100     110     120     130     140     150

              100     110     120     130     140     150
m025.pep    KAAAVKSRPAVPAAAQPPVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
              |||:|||||:|||||:|||||:|||||:|||||
a025      KAAAVKSRPAVPAAAQPLVQSAPVDINAATH TIVRGDTVYNISKRYHISQDD FRAWNGMT
              160     170     180     190     200     210

              160     170     180     190     200     210
m025.pep    DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              |||:|||||:|||||:|||||:|||||:|||||
a025      DNTLSIGQIVKVKPAGYAAPKAAAVKSRPAVPAAVQTPVKPAAQPPVQSAPQPAAPAAEN
              220     230     240     250     260     270

              220     230     240     250     260     270
m025.pep    KAVPAPAPQSPAASPSGTRSVGGIVWQRPTQGVVADFGGNNKGVDIAGNAGQPVLAAAD
              |||:|||||:|||||:|||||:|||||:|||||

```



m025/g025

```

10          20          30
m025.pep    VPPVQSAPVYTPPAYVPPSAPAVSGTYVPS
              |||||:||||:|||||||
g025         GMQTVSSAPVYNFYGATPYNAAPAANDAPYVPPVQTAPVYSPPAYVPPSAPAVSGTYVPS
              40          50          60          70          80          90

              40          50          60          70          80          90
m025.pep    YAPVDINAATHITVRGDTVYNISKRYHISQDDFWANGMTDNTLSIGQIVKVKPAGYAAP
              |||||:||||:|||||||
g025         YAPVDINAATHITVRGDTVYNISKRYHISQDDFWANGMTDNTLSIGQIVKVKPAGYAAP
              100         110         120         130         140         150

              100         110         120         130         140         150
m025.pep    KAAAVKSRPAVPAAQPPVQSAPVDINAATHITVRGDTVYNISKRYHISQDDFWANGMT
              |
g025         K-----

              160         170         180         190         200         210
m025.pep    DNMLSIGQIVKVKPAGYAAPKTAAVESRPAPVAAQTPVKPAAQPPVQSAPQPAAPAAEN
              |||||:||||:|||||||
g025         -----TAAVESRPAPVAAQTPVKPAAQPPVQSAPQPAAPAAEN
              160         170         180         190

              220         230         240         250         260
m025.pep    KAVPAPAP--QSPAASPSGTRSVGGIIVQWRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
              |||||:||||:|||||||
g025         KAVPAPAPAPQSPAASPSGTRSVGGIIVQWRPTQGKVVADFGGNNKGVDIAGNAGQPVLA
              200         210         220         230         240         250

              270         280         290         300         310         320
m025.pep    ADGKVYVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEQQVKRGQQVALMGNTDAS
              |||||:||||:|||||||
g025         ADGKVYVYAGSGLRGYGNLVIIQHNSSFLTAYGHNQKLLVGEQQVKRGQQVALMGNTDAS
              260         270         280         290         300         310

              330         340         350
m025.pep    RTQLHFEVRQNGKPVNPNPSYIAFX

```

9025

|||||  
 RTQLHFEVRONGKPVNPNSYIAFX  
 320 330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 113>:

g031.seq

```

1 ATGGTGTCCC TCCGCTTCAG ATTCGGCAAC CACTTTAAAC GCCGACATTC
51 TGACAATTTC CTTTTCGCC AGCCAAATAT CATGCGTATC TTTCGGTTCCG
101 GGCTTGTTGG GCATGGCAAC CTCAACAGC CGCGCCATCA CAGGAATCGT
151 CGTTCCCTGA ATCAGCAGCG ACAGCACCAC CACGGCAAAC GCCACATCAA
201 ACAGCAGGTG CGAATTGGGA ACGCCCATCA CCAGCGGCAT CATCGCCAGC
251 GAAATCGGTA CGGCTCCTCG CAAGCCCAAC CAACTGATAT ACGCCTTTTC
301 ACGCAGGCTG TAATTGAATT TCCACAAACC GCCGAACACT GCCAGCGGAC
351 GCGCGACCAG CATCAGGAAC GCCGCAATCG CCAAGGCTTC CGCGCCCTG
401 TCCAACACGC CGGCGGGAGA AACCAGCAGA CCGAGCATGA CGAACAAAGT
451 TGCCTGCGCC AGCCAAGCCA AACCGTCCAT CACACGCAA ACCTGTTCGG
501 TcgcACGGTT GCGCTGGTTA CCGACAATGA TGCCGGCAA GTAACCGGCC
551 AAAAAGCCGC TGCCGCTAT GGTATTGGTA AACGCAACA CAAGCAGCCC
601 GCCCGACACA ATCATCAGCG CGTACAGACC TTCCGTacac acctccaatt
651 cccaatcaac gtcatagtctg tctcccggtg taaaatgttc ttcacttcag
701 aatccccccc ttcttcccag cccgaaacct tcatgtgtta naccctgggg
751 tgccccaacg gatttagtaa cctcccaatg actctgcttg tcgccccctt
801 cgcccgcttt ctccttcgga gaaaacttgt tgtcccgctc ttacattaa

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 031.ng>:

g031.pep

```

1 MVSRLRFRGN HFKRRHSDNF LFRQPNIMRI FRFGLVGHGN LQQRPHHRNR
51 RSLNQQRQHH HGKRHIKQV RIGNAHQQRH HRQRNRYGSS QAQPTDIRLF
101 TOAVIEFPOT AEHCQTRDQ HQERRNRQGF RRPVQHAGGR NQQTEHDEQS
151 CLRQPSQTVH HTQNVFRRTV ALVTDNDAGK VNRQKAAAY GIGKRKHQP
201 ARHNHQRVQT FRTHLQFPIN VIAVSRVKMF FTSESPSSQ PETFMCXTLG
251 CPNGFSNLEP TLLVAPFARF LLPGKLVVFP LH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 115>:

m031.seq (partial)

```

1 ...CGCCTGAAGC ACGGTGTCGG ACTGCATTTT TATTCGGCTA TACGCCTTTT
51 CACGCAGGCT GTAATTGAAT TTCCACAAAC CGCCGAACAC TGCCGACGGA
101 CGCGCGACCA GCATCAGGAA CGCCGCAATC GCCAAgGCTT CCGCCGCCCT
151 GTCCAACACG TTGGCAGGAG AAACCAGCAG CAAAGGCATT CCCAAACGTG
201 CGGACAAAGT GGTGCAAAAC ACGCTCAGAA ACAACAGTGC GCCACCCGGC
251 AG....

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 031>:

m031.pep (partial)

```

1 ...RLKHGVLHF YSAIRLFTQA VIEFPQAEH CRRTRDQHQE RNRQGFRRP
51 VQHVGRNRQQ QRHSQTCGQS GRNHAQKQOC ATRQ....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

a031.seq

```

1 ATACGCCTTT TCACGCAGGC TGTAATTGAA TTCCACAAA CCGCCGAACA
51 CTGCCGGGGG ACGCGCGACC AGCATCAGGA ACGCCGCAAT CGCCAAGGCT
101 TCCGCGCGCC CGTCCAACAC GTTGCCAGGA GAAACCAGCA GCAAAGGCAT
151 TCCCAAACGT GCGGACAAAG TGGTCGAAAC CACGCTCAGA AACAACAGTG
201 CGCCACCCGG CAG

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 031.a>:

a031.pep (partial)

```

1 IRLFTQAVIE FPQTAEHCRH TRDQHQERRN RQGFRRPVQH VGRNRQQQRH
51 SQTGQSGRN HAQKQOCATR Q

```

210

m031/a031 100.0% identity over a 71 aa overlap

	10	20	30	40	50	60
m031.pep	RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH	CRRTDQHQ	ERRNRQGF	RRPVQHVGRNRQ
a031		IRLFTQAVIEFPQTAEH	CRRTDQHQ	ERRNRQGF	RRPVQHVGRNRQ	
		10	20	30	40	

	70	80
m031.pep	QRHSQTCGQSGRNHAQKQ	QCATRQ
a031	QRHSQTCGQSGRNHAQKQ	QCATRQ
	50	60

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 031 shows 60.0% identity over a 85 aa overlap with a predicted ORF (ORF 031.ng) from *N. gonorrhoeae*:

m031/g031

		10	20	30
m031.pep		RLKHGVLH	FYSAIRLFTQ	AVIEFPQTAEH
g031	NQQRQHHHGKRHIKQQVRIGNAHHRQRRNR	RYGSSQAQPTDIRLFTQ	AVIEFPQTAEH	
	60	70	80	90

	40	50	60	70	80
m031.pep	CRRTDQHQERRNRQGFRRPVQHVGRNRQ	QRHS-QTCGQSGRNHAQKQ	QCATRQ		
g031	CQRTDQHQERRNRQGFRRPVQHAGGRNQ	QTEHDEQSCLRQPSQTVHHTQN	VFRRTVALV		
	120	130	140	150	160

g031	TDNDAGKVN	RQAAAA	YGIGKRKH	KQPARH	NHQRVQTFRTHLQFPIN	VIASRVKMF	FTS
	180	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 119>:

g032.seq

```

1  ATGCGGCGAA  ACGTGCCTGC  CGTCGCCGTA  TTGCGCCGCC  CACGATTCGA
51  GGC GTTTT  GATTGGCGT  TGGCTCAGGC  GCGTGCCGTT  CCTGCCGGTA
101 AACAGGGCTT  TGCCGTCCGA  TGC CGTCTGA  CGCAGCGGCA  GATAGTTT
151 CAAGGCTTCC  ACGCTTTTGC  CGGTCAGCGG  AACCTGACGC  TGCTTGCGCC
201 CTTTGCCGGT  AACGTGTACC  CACGCTTCGT  CCAAATATAC  ATCATCTGCA
251 TTC AAGCCGT  GTATCTCGCT  CACGCGCAAA  CCGCTGCCGT  ACATCAGCTC
301 GAACAGCGCG  TGGTCGCGCA  CCGCCAGCGG  GTCGCCGCCG  TCCACGGGCA
351 AATCCAACAT  CCGTTTCAGC  CATTCCTGCG  GCAGGGCTTT  GGGTACGCGC
401 TCGGGCTGCT  TCGGCGGTTT  GATGTCGGCG  GTCGGGTCGG  CGCGCATCAG
451 CCCGCGTTTG  ACCAGCCAGG  CGCAATACTG  CCGCCACGCC  GACAGCTTGC
501 GCGCCAGCGT  CCGACCGTCC  AAACCGCGCT  GCGACAGCCG  CCGCAACGCC
551 GccgTAAAT  CGCGCCGCGA  CAAGTCCTGC  GGCACGCgc  ctgcATCTTC
601 AGACGGCATT  TGTGCCAACA  GTGCAAACAG  TTCTTCCAAA  TCGCGCCGCT
651 ATGCCGCAAC  CGTGTGCTCC  GACTTGCCCT  CGCGCACGAT  GTTTTCCAAA
701 TAAGCGTCAA  AATacgcgc  AAACccgTCC  AAAACCATAA  CCGTCCCACA
751 CAAATATCAA  AAAACCACTG  A

```

This corresponds to the amino acid sequence &lt;SEQ ID 110; ORF 032.ng&gt;:

g032.pep

```

1  MRRNVPVAV  LRRPRFEAF  L  DLALAQARAV  PAGKQGF  AVR  CRLTQRQIVF
51  QGFHAFAGQ  R  NLTLAPFAG  NVYPRFVQIY  IICIQAVYLA  HAQTA  AVHQL

```

```

101 EQRVVAHRQR VAAVHGQIQH PVQPFRLQGF GYALGLLRRF DVGGRVGAHQ
151 PAFDQPGAIL PRRRLARQR PTVQTALRQP PRRRKIAPR QVLRHAACIF
201 RRHLCQQCKQ FFQIAPVCRN RVLRLALAHF VFQISVKIRR KPVQNHNRPT
251 QISKNQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 111>:

```

m032.seq (partial)
  1 ATGCGGCGAA ACGTGCmTGC mGTCGCCGTT KTGCGCCGCC CATTGCGCCA
 51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGACCAGCGG CACCTGCCGC TgTT.GCGCC
201 CTTTGCCGAT AACGTGTACC CACGCTCGT CCAAATAGAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGGGCG TGGTCGCGCA CCGCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTCAGC CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG CGTGTCATCAG
451 GCCGCGCTTT ACCAGCCAAA CGCAATACTG CCGCCAAGAC GAAAGCTTGC
501 GAGCCAGCGT CCGTTCCCCC AAACCGCG...

```

This corresponds to the amino acid sequence <SEQ ID 112; ORF 032>:

```

m032.pep (partial)
  1 MRRNVXAVAV XRRPLRQTFD DLALAQARAV PAGKQGFVR CRLTORQIVF
 51 QGFHAFADQR HLPLXAFAD NVYPRXVOID IICIQAVYLA HAQTAHVHF
101 EQGVVAHRQR VAAVHGQIQH PVQPFRLQGF GYALGLLRRF DVGGRVGVHQ
151 AALYQFNAIL PRRKLASQR PFPQTA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 113>:

```

a032.seq
  1 ATGCGGCGAA ACGTGCCTGC CGTCGCCGTT TTGCGCCGCC CATTGCGCCA
 51 AACGTTTTTG GATTTGGCGT TGGCTCAGGC GCGTGCCGTT CCTGCCGGTA
101 AACAGGGCTT TGCCGTCCGA TGCCGTCTGA CGCAGCGGCA GATAGTTTTT
151 CAGGGCTTCC ACGCTTTTGC CGGTCAGCGG AACCTGCCGC TGCTTGCGTC
201 CTTTGCCGGT AACGTGTACC CACGCTCGT CCAAATATAC ATCATCTGCA
251 TTCAAGCCGT GTATCTCGCT CACGCGCAA CCGTGCCGT ACATCAGTTC
301 GAACAGCGCG TGATCGCGCA CCGCAGCGG GTCGCCGCCG TCCACGGGCA
351 AATCCAGCAT CCGGTTTCAGC CATTCCTGCG GCAGGGCTTT GGGTACGCGC
401 TCGGGCTGCT TCGGCGGTTT GATGTCGGCG GTCGGGTCGG TATGCAGCAG
451 ACCGCGTTTG ACCAGCCAGG CGCAATACTG CCGCCAAGAC GACAGTTTGC
501 GCGCCAGCGT CCGCGCATTC AAACCGCGCT GCGACAGCCG CCGCAACGCC
551 GCCGTAAAT CGCGCTGCGA CAAGCCCTGC GGCACGCCGC CTGCATCTTC
601 AGACGGCATT TGTGCCAACA GCGCAAACAG TTCTTCCAAA TCGCGCCGGT
651 ATGCCGCCAC CGTGTGCTCC GACTTGCCCT CGCGCAGCAT GTTTTCCAAA
701 TAAGCGTCAA AATGCGCGC AAACCGCTCC AAAACCATAA CCGCCCCACA
751 CAAATATCAA AAAACAGTG A

```

This corresponds to the amino acid sequence <SEQ ID 114; ORF 032.a>:

```

a032.pep
  1 MRRNVPAVAV LRRPLRQTFD DLALAQARAV PAGKQGFVR CRLTORQIVF
 51 QGFHAFAGQR NLPLASFAG NVYPRLVQIY IICIQAVYLA HAQTAHVHF
101 EQRVIAHRQR VAAVHGQIQH PVQPFRLQGF GYALGLLRRF DVGGRVGMQQ
151 TAFDQPGAIL PRRRLARQR PRIQTALRQP PRRRKIALR QALRHAACIF
201 RRHLCQQRKQ FFQIAPVCRH RVLRLALAHF VFQISVKMRR KPVQNHNRPT
251 QISKKQ*

```

m032/a032 88.1% identity over a 176 aa overlap

```

m032.pep      10      20      30      40      50      60
MRRNVXAVAVXRRPLRQTFDLDALAQARAVPAGKQGFVRCRLTORQIVFQGFHAFADQR
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a032          10      20      30      40      50      60
MRRNVPAVAVLRRPLRQTFDLDALAQARAVPAGKQGFVRCRLTORQIVFQGFHAFAGQR

```

212

	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHGGIQH					
a032	NLPLLASFAGNVYPRLVQIYIICIQAVYLAHAQTAAVHQFEQQRVIAHRQRVAAVHGGIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPPQTA					
a032	PVQPFLLRQGFYALGLLRRFDVGGVMQQTAFDQPGAILPPRRQLARQRPRIQTALRQP					
	130	140	150	160	170	180
a032	PQRRRKIALRQALRHAACIFRRHLCQQRKQFFQIAPVCRHRVLRLLALAHDFQISVKMRR					
	190	200	210	220	230	240

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 032 shows 86.4% identity over a 176 aa overlap with a predicted ORF (ORF 032.ng) from *N. gonorrhoeae*:

m032/g032

	10	20	30	40	50	60
m032.pep	MRRNVXAVAVXRRPLRQTFDLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFADQR					
g032	MRRNVPAVAVLRRPRFEAFDLALAQARAVPAGKQGFVRCRLTQRQIVFQGFHAFAGQR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m032.pep	HLPLXAPFADNVYPRXVQIDIICIQAVYLAHAQTAAVHQFEQGVVAHRQRVAAVHGGIQH					
g032	NLTLAPFAGNVYPRFVQIYIICIQAVYLAHAQTAAVHQLEQRVVAHRQRVAAVHGGIQH					
	70	80	90	100	110	120
	130	140	150	160	170	
m032.pep	PVQPFLLRQGFYALGLLRRFDVGGRVGVHQAALYQPNAILPPRRKLASQRPFPPQTA					
g032	PVQPFLLRQGFYALGLLRRFDVGGRVGAHQPAFDQPGAILPPRRQLARQRPVQTALRQP					
	130	140	150	160	170	180
g032	PQRRRKIAPRQVLRHAACIFRRHLCQCKQFFQIAPVCRNRVLRLLALAHDFQISVKIRR					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 115>:

g033.seq

```

1  ATGGCGGCGG CGGACAACT CTTGGGCGGC GACCGCCGCA GCGTCGCCAT
51  CATCGGAGAC GCGCGATGA CGCGGGGCA GCGTTTGAA GCCTTGAATT
101 GCGCGGGCGA TATGGATGTG GATTGTCTGG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGCT CGGCGCGTTG CCCAAATATC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAAcgg
251 GCAAGGTATT AGACAAAATA CCCGGCGCGA TGGagtTTGC CCAAAAAGTC
301 GAACaCaAaA TCAAAACCTT TGCCGAAGAA GCCGAACACG CCAAACAGTC
351 GCTGTCGCTG TTTGAAAATT TCGGCTTCCG CTACACCGGC CCCGTGGACG
401 GACACAACGT CGAGAACTCT GTGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGCTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCcg tCaAATACCA CGCCGTGCGc aACCTGCcta
551 AAGAAGGCGG GCGCAAAATg ccGTCTGAAA AAGAACCcAA GCCCGCGcCc
601 aaaccgACCT ATACCCAAGT ATTCGGCAAA TGGCTGTGCG ACCGGCGCGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG

```

```

701 GACTGGTGGG GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTGGGC
751 ATCGCCGAGC AGCACGCCGT tacCTTTGCC GCGGTTTGG CGTGCGAAGG
801 CATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCCG TTTGTTTGCC
901 GTCGACCGTG CGGGCATCGT CGGCGCGGAC GGTCCGACCC ATGCCGGCTT
951 GTACGATTTG AGCTTCTTGC GCTGTGTGCC GAACATGATT GTTGCCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGCTGC TTTCGACCTG CTATCAGGCG
1051 GATGCGCCCG CCGCGTCCG CTATCCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTCAGAC GGCATGAAA CCGTGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCC TtcatTGCCT TCGGCAGTAT GGTGCGCCACC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTCGCGC ATATGCGCTt
1251 cgtcaaacCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAcg
1301 accGCATCGT TACCTTGAA GAAAACGCGC AACAGGGCGG CGCAGGCGGC
1351 GCGGTCTTGG AAGTGTGGC GAAACACGGC ATCTGCAAAAC CCGTTTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGAACA CGGCGATCCG AAAAACTTT
1451 TGGACGATT TGGTTGAGT GCCGAAGCGG TGGAACGCGG GGTGCGCGAG
1501 TGGCTGCCCG ACCGTGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 116; ORF 033.ng>:

```

g033.pep
1 MAAADKLLGG DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51 MSISPNVGAL PKYLASNVVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTAAE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLLKDLRSR
151 KGPQLLHVIT KKGNGYKLA E NDPVKYHAVA NLPKEGGAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLQ RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAT
401 ALAVAEKLNA TVADMRVFKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLLV ADTVTEHGDP KKLLDDLGLS AEAVERVRRE
501 WLPDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 117>:

```

m033.seq
1 ATGGCGGCGG CAGACAACT CTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51 CATCGGCGAC GCGCGGATGA CCGCGGGGCA GCGGTTTGAA GCCTTGAATT
101 GCGCaG.CGA TATGGATGTt GATTTGCTrG TCGTCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAAGT CCGCGCGCTG CCGAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GCCTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAAATA CCGGCGCGCA TGGAGTTTGC CCAAAAAGTC
301 GAACACAAA TCAAAACCCT TGCCGAAGAA GCCGAACACG CCAACAGTC
351 GCTGTCTTTG TTTGAAAAC TCGGCTTCG CTACACGGC CCCGTGGAGC
401 GACACAACGT CGAAAATCTG GTGGACGTAT TGAAAGACTT GCGCAGCCGC
451 AAAGGCCCTC AGTTGTGCA CGTCATCACC AAAAAGGGCA ACGGCTACAA
501 ACTCGCCGAA AACGACCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTGCGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTACCGT TTTGTTTGCC
901 GTCGACCGCG CGGGCATCGT CCGCGCGGAC GGCCCCACCC ATGCCGGTCT
951 GTACGATTTG AGCTTTTTGC GCTGCGTGCC GAACATGATT GTCGCGCGC
1001 CGAGCGATGA AAACGAATGC CGCCTGTTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCGTCCG CTATCGCGC GGCACGGGTA CGGGCGCGCC
1101 GGTTCAGAC GGCATGAAA CCGTGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACGCA TTCATTGCCT TCGGCAGTAT GGTGCGCCCC
1201 GCATTGGCGG TTGCCGAAAA ACTGAACGCC ACCGTCGCGC ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCCTTGCC CGAAGCCAGC

```

```

1301 ACCGCATCGT TACCTTGAA GAAACGCGG AACAGGGCGG CGCAGGCGGG
1351 GCGGTGCTGG AAGTATTGGC GAAACACGGC ATCTGCAAAC CCGTTTGTCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTG GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 118; ORF 033>:

```

m033.pep
1  MAAADKLLGS DRRSVAIIGD GAMTAGQAFE ALNCAXDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDLKDLRSR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLO RAYDQLVHDI ALQNLPLVFA
301 VDRAGIVGAD GPTHAGLYDL SFLRCVPNMI VAAPSDENEC RLLSLSTCYQA
351 DAPAAVRYPR GTGTGAPVSD GMETVEIGKG IIRREGEKTA FIAFGSMVAP
401 ALAVAEKLNA TVADMRFVKP IDEBLIVRLA RSHDRIVTLE ENAEQGGAGG
451 AVLEVLAKHG ICKPVLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA
501 WLSDRDAAN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 119>:

```

a033.seq
1  ATGGCGGCGG CGGACAAACA GTTGGGCAGC GACCGCCGCA GCGTCGCCAT
51  CATCGGCGAC GCGCGCATGA CGGCGGGTCA GCGCTTGAA GCCTTGAAC
101 GCGCGGCGCA TATGGATGTG GATTGCTGG TCGTCCTCAA CGACAACGAA
151 ATGTCGATTT CCCCCAACGT CGGTGCGTTG CCAAATACC TTGCCAGCAA
201 CGTCGTGCGC GATATGCACG GACTGTTGAG TACCGTCAA GCGCAAACGG
251 GCAAGGTATT AGACAAATA CCGGCGCGCA TGGAGTTTGC CCAAAAGTGC
301 GAACATAAAA TCAAACCCCT TGCCGAAGAA GCCGAACACG CCAACAGTGC
351 ACTGCTTTTG TTTGAAACT TCGGCTTCG CTATACCGGC CCCGTGGACG
401 GACACAACGT CGAAAATCTG GTCGATGTAT TGGAAGACCT GCGCGGACGC
451 AAAGGCCCGC AGCTTCTGCA CGTCATCACC AAAAAGGCA ACGGCTACAA
501 ACTCGCCGAA AACGATCCCG TCAAATACCA CGCCGTCGCC AACCTGCCTA
551 AAGAAAGCGC GCGCAAATG CCGTCTGAAA AAGAACCCTA GCCCGCCGCC
601 AAACCGACCT ATACCCAAGT GTTCGGCAAA TGGCTGTGCG ACCGGGCGGC
651 GGCAGATTCC CGACTGGTTG CGATTACCCC CGCCATGCGC GAGGGCAGCG
701 GCTTGGTTGA GTTTGAACAA CGATTCCCCG ACCGCTATTT CGATGTCGGC
751 ATCGCCGAGC AGCACGCCGT TACCTTTGCC GCGGTTTGG CTTGCGAAGG
801 GATGAAGCCC GTCGTGGCGA TTTATTCCAC CTTTTTACAA CGCGCCTACG
851 ACCAACTGGT GCACGACATC GCCCTGCAAA ACCTGCCCGT TTTGTTGCC
901 GTCGACCGCG CGGCATCGT CGGCGCGGAC GGCCCGACCC ATGCCGTTT
951 GTACGATTTA AGCTTTTTCG GCTGCATTCC GAATATGATT GTCGCCGCGC
1001 CGAGCGATGA AAATGAATGC CGCTTGCTGC TTTCGACCTG CTATCAGGCA
1051 GACGCGCCCG CCGCCGTCG CTATCCGCGC GGCACGGGTA CGGGCGTGCC
1101 GGTTCAGAC GGCATGGAAA CCGTGGAAAT CGGCAAGGGC ATTATCCGCC
1151 GCGAAGGTGA GAAAACCGCA TTCATTGCCT TCGGCAGTAT GGTGCCCCCT
1201 GCATTGGCGG TCGCCGAAA ACTGAACGCC ACCGTCGCCG ATATGCGCTT
1251 CGTCAAACCG ATAGACGAAG AGTTGATTGT CCGCTTGCC CGAAGCCAGC
1301 ACCGCATCGT TACCCTTGAA GAAAACGCCG AACAGGGCGG CGCAGGCAGC
1351 GCGGTGCTGG AAGTGTGGC GAAACACGGC ATCTGCAAAC CCGTCTTGCT
1401 TTTGGGCGTT GCCGATACCG TAACCGGACA CGGCGATCCG AAAAACTTT
1451 TAGACGATTG GGGCTTGAGT GCCGAAGCGG TGAACGGCG TGTGCGCGCG
1501 TGGCTGTCGG ATCGGGATGC GGCAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 120; ORF 033.a>:

```

a033.pep
1  MAAADKQLGS DRRSVAIIGD GAMTAGQAFE ALNCAGDMDV DLLVVLNDNE
51  MSISPNVGAL PKYLASNVR DMHGLLSTVK AQTGKVLDKI PGAMEFAQKV
101 EHKIKTLAEE AEHAKQSLSL FENFGFRYTG PVDGHNVENL VDVLEDLRGR
151 KGPQLLHVIT KKGNGYKLAE NDPVKYHAVA NLPKESAAQM PSEKEPKPAA
201 KPTYTQVFGK WLCDRAAADS RLVAITPAMR EGSGLVEFEQ RFPDRYFDVG
251 IAEQHAVTFA GGLACEGMKP VVAIYSTFLO RAYDQLVHDI ALQNLPLVFA

```

301 VDRAGIVGAD GPTHAGLYDL SFLRCIPNMI VAAPSDENEC RLLSTCYQA  
 351 DAPAAVRYPR GTGTGVPVSD GMETVEIGKG IIRREGKTA FIAFGSMVAP  
 401 ALAVAGKLNA TVADMRVVKP IDEELIVRLA RSHDRIVTLE ENAEQGGAGS  
 451 AVLEVLAKHG ICKPVLLLGV ADTVTGHGDP KKLLDDLGLS AEAVERRVRA  
 501 WLSDRDAAN\*

m033/a033 98.4% identity over a 509 aa overlap

m033.pep	10	20	30	40	50	60
	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVLLVVLNDNEMSISPNGAL					
a033	MAAADKQLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVLLVVLNDNEMSISPNGAL					
	10	20	30	40	50	60
m033.pep	70	80	90	100	110	120
	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQVEHKIKTLAEAEHAKQSLSL					
a033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQVEHKIKTLAEAEHAKQSLSL					
	70	80	90	100	110	120
m033.pep	130	140	150	160	170	180
	FENFGFRYTGPDGHNVENLVDVLKDLRSRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
a033	FENFGFRYTGPDGHNVENLVDVLEDLRGRKGPLLHVITKKGNGYKLAENDPVKYHAVA					
	130	140	150	160	170	180
m033.pep	190	200	210	220	230	240
	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
a033	NLPKESAAQMPSEKEPKPAKPTYTQVFGKWLCDRAAADSRLVAITPAMREGSGLVEFEQ					
	190	200	210	220	230	240
m033.pep	250	260	270	280	290	300
	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
a033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA					
	250	260	270	280	290	300
m033.pep	310	320	330	340	350	360
	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
a033	VDRAGIVGADGPTHAGLYDLSFLRCIPNMIVAAPSDENECRLLSTCYQADAPAAVRYPR					
	310	320	330	340	350	360
m033.pep	370	380	390	400	410	420
	GTGTGAPVSDGMETVEIGKGIIRREGKTAFAFGSMVAPALAVAEKLNATVADMRVVKP					
a033	GTGTGVPVSDGMETVEIGKGIIRREGKTAFAFGSMVAPALAVAGKLNATVADMRVVKP					
	370	380	390	400	410	420
m033.pep	430	440	450	460	470	480
	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP					
a033	IDEELIVRLARSHDRIVTLEENAEQGGAGSAGVLEVLAKHGICKPVLLLGVADTVTGHGDP					
	430	440	450	460	470	480
m033.pep	490	500	510			
	KKLLDDLGLSAEAVERRVRAWLSRDAANX					
a033	KKLLDDLGLSAEAVERRVRAWLSRDAANX					
	490	500	510			



Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 033 shows 98.4% identity over a 509 aa overlap with a predicted ORF (ORF 033.ng) from *N. gonorrhoeae*:

m033/g033

m033.pep	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAXDMDVDLLVVLNDNEMSISPVGAL	60
	:	
g033	MAAADKLLGSDRRSVAIIGDGAMTAGQAFEALNCAGDMDVDLLVVLNDNEMSISPVGAL	60
m033.pep	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
g033	PKYLASNVRDMHGLLSTVKAQTGKVLDPGAMEFAQKVEHKIKTLAEAEHAKQSLSL	120
m033.pep	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGQPLLHVITKKGNGYKLAENDPVKYHAVA	180
g033	FENFGFRYTGPVDGHNVENLVDVLKDLRSRKGQPLLHVITKKGNGYKLAENDPVKYHAVA	180
m033.pep	NLPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRVAITPAMREGSGLVEFEQ	240
	:	
g033	NLPKEGGAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRVAITPAMREGSGLVEFEQ	240
m033.pep	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA	300
g033	RFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQLVHDIALQNLPLVFA	300
m033.pep	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
g033	VDRAGIVGADGPTHAGLYDLSFLRCVPMIVAAPSDENECRLLLSTCYQADAPAAVRYPR	360
m033.pep	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVAPALAVAEKLNATVADMRFKVP	420
g033	GTGTGAPVSDGMETVEIGKGIIRREGEKTAFIAGSMVATALAVAEKLNATVADMRFKVP	420
m033.pep	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTGHGDP	480
g033	IDEELIVRLARSHDRIVTLEENAEQGGAGGAVLEVLAKHGICKPVLLLGVADTVTEHGDP	480
m033.pep	KKLLDDLGLSAEAVERRVRWLSDRDAANX	510
g033	KKLLDDLGLSAEAVERRVREWLPRDAANX	510

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 121>:

g034.seq

```

1  ATGAGCCGTT TATGGTTTTT TGCCGTAAAA AACATTATAA TCCGCCTTAT
51  TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGACCA CGCCGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCCG ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TGCGCGCAAA TACGcgGCG
251 CGCCGTTTTT GCGCCACCTG ATTCTGGCGG CAGTCGAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTgtGCCA
351 ACGCTCCATC CAACTGGGCT TCTCTCCGT GATGATGGAC GGCTCTTTGC
401 TCGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACC
451 CGTACCGTCG TCAACTTCTC CCACGCCTGC GCGGTGTCCG TCGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGAAGCAGGC GAAGAAGACG
551 GAGTGGGCGC GGCAGGCAAA CTCTCACAG ACCAAATGCT CACCAGCGTT
601 GAAGATGCCG TGCCTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCAGC GGCATACAA ATTCACCCGT CCGCCACAG

```

```

701 GCGACGTATT GCGTATCGAC CGCATCAAGG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGgtCCAGC TCCGTTCCGC AAGAatgGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG CAAAGTCAAC
901 ATCGATACCG ACCTGCGCCT CGCTTCCACC GCGCGGTAC GCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TTGATCCGCG CAAATACTTG GGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GTTATCTTGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCTGTT TCGTTGGAAA AAATGGCAAG
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 122; ORF 034.ng>:

g034.pep

```

1 MSRLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAIM EAADQVNAIPV IVQASAGARK YAGAPFLRHL ILAAVEEFPFH
101 IPVVMHQDHG ASPDVCORSI QLGFSVMMD GSLEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAAGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIIVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKI NEYGGNIGET YGVFVEEIVE GIKHGVKRVN
301 IDTDLRLAST GAVRRYLAEN PSDFDPRKYL GKTIEAMKQI CLDRYLAFGC
351 EGQAGKIKPV SLEKMASRYA KGELNQIVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 123>:

m034.seq (partial)

```

1 ATGAGCTGTT TATGGTTTTT TGCTGTAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA WACAGCTACG GCyTGCCGGC GTTCAACGTC
151 AACAACTCG WACAGATGCG CGCCATCATG GAGGCTGCAG ACCAAGTCGA
201 CGCCCCCGTC ATCGTACAGG CGAGTGCCGG TCGCGCAAA TATGCGGGTG
251 CGCCGTTTTT ACGCCACCTG ATTTTGGCGG CTGTCGAAGT ATTTCCACAC
301 ATCCCCGTCG TCATGCACCA AGACCACGGC GCATCACCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TCTCCTCTGT AATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTACG AATACAACGT CAACGCCACA
451 CGTACCGTGG TTAACCTTCTC CCACGCTTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAAACCGG CGATGCAGGC GAAGAAGACG
551 GTGTAGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT GACCAGCGTC
601 GAAGATGCCG TATGTTTCGT TAAAGATACC GCGGTTGACG CATTGCTAT
651 TGCCGTCGGC ACCAGCCACG GCGCATACAA ATTCACCCGT CCGCCACAG
701 GCGATGTATT ACGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA C...

```

This corresponds to the amino acid sequence <SEQ ID 124; ORF 034>:

m034.pep (partial)

```

1 MSCLWFFAVK NIIIRLIYLL PKETOMALVS MRQLLDHAAE XSYGLPAFNV
51 NNLXQMRAIM EAADQVDAIPV IVQASAGARK YAGAPFLRHL ILAAVEVFPFH
101 IPVVMHQDHG ASPDVCORSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGDAG EEDGVGAVGK LSHDQMLTSV
201 EDAVCFVKDT GVDALAIIVG TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMH...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 125>:

a034.seq

```

1 ATGAGCCGTT TATGGTTTTT TGCCGCAAAA AACATTATAA TCCGCCTTAT
51 TTACCTATTG CCCAAGGAGA CACAAATGGC ACTCGTATCC ATGCGCCAAC
101 TGCTTGATCA TGCTGCCGAA AACAGCTACG GCCTGCCCGC GTTCAACGTC
151 AACAACTCG AACAAATGCG CGCCATTATG GAAGCCGCGC ACCAAGTCAA
201 CGCGCCCGTC ATCGTACAGG CGAGCGCAGG TCGCGCAAA TACGCGGGCG
251 CGCCGTTTTT GCGCCACCTG ATTTTGGCGG CTGTCGAAGA ATTTCCGCAC
301 ATCCCCGTCG TGATGCACCA AGACCACGGC GCATCGCCCG ACGTGTGCCA
351 ACGCTCCATC CAACTGGGCT TTTCTCTCGT GATGATGGAC GGCTCGCTGA
401 TGGAAGACGG CAAAACCCCT TCTTCTTATG AATACAACGT CAACGCCACC

```

```

451 CGTACCGTGG TTAATTTCTC CCACGCCTGC GCGGTATCCG TTGAAGGCGA
501 AATCGGCGTA TTGGGCAACC TCGAACTGG CGAAGCCGGC GAAGAAGACG
551 GTGTAGGCGC AGTGGGCAAA CTTTCCACG ACCAAATGCT CACCAGCGTC
601 GAAGATGCCG TCGGTTTCGT TAAAGATACC GCGGTTGACG CATTGGCGAT
651 TGCCGTCGGC ACCAGCCACG GCGCGTACAA ATTCACCCGT CCGCCCACAG
701 GCGACGTGTT GCGTATCGAC CGCATCAAAG AAATCCACCA AGCCCTGCCC
751 AATACACACA TCGTGATGCA CGGCTCCAGC TCCGTTCCGC AAGAATGGCT
801 GAAAGTCATC AACGAATACG GCGGCAATAT CGGCGAAACC TACGGCGTGC
851 CGGTTGAAGA AATCGTCGAA GGCATCAAAC ACGGCGTGCG TAAAGTCAAC
901 ATCGATACCG ACTTGCGCCT TGCTTCCACC GCGCGGGTAC GCCGCTACCT
951 TGCCGAAAAC CCGTCCGACT TCGATCCGCG CAAATATTG AGCAAAACCA
1001 TTGAAGCGAT GAAGCAAATC TGCCTCGACC GCTACCTCGC GTTCGGTTGC
1051 GAAGGTCAGG CAGGCAAAAT CAAACCGGTT TCCTTGAAA AAATGGCAAA
1101 CCGTTATGCC AAGGGCGAAT TGAACCAAAT CGTCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 126; ORF 034.a>:

```

a034.pep
1 MSRLWFFAAK NIIIRLIYLL PKETQMALVS MRQLLDHAAE NSYGLPAFNV
51 NNLEQMRAM EAADQVNAPV IVQASAGARK YAGAPFLRHL ILAAVEEFPH
101 IPVVMHQDHG ASPDVCQRSI QLGFSVMMD GSLMEDGKTP SSYEYNVNAT
151 RTVVNFHSHAC GVSVEGEIGV LGNLETGEAG EEDGVGAVGK LSHDQMLTSV
201 EDAVRFVKDT GVDALAIAGV TSHGAYKFTR PPTGDVLRID RIKEIHQALP
251 NTHIVMHGSS SVPQEWLKV NEYGGNIGET YGVPVEEIVE GIKHGVKRVN
301 IDTLRLAST GAVRRYLAEN PSDFDPRKYL SKTIEAMKQI CLDRYLAFCG
351 EGQAGKIKPV SLEKMANRYA KGELNQIVK*

```

m034/a034 96.9% identity over a 257 aa overlap

```

m034.pep      10      20      30      40      50      60
MSCLWFFAVKNIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNNLXQMRAM
|| ||||:|||||||||||||||||||||||||||||||||||||||||||
a034          10      20      30      40      50      60
MSRLWFFAAKNIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNNLEQMRAM

m034.pep      70      80      90      100     110     120
EAADQVDAPVIVQASAGARKYAGAPFLRHLILAAVEVFPHIPVVMHQDHGASPDVCQRSI
|||||:|||||||||||||||||||||||||||||||||||||||||||
a034          70      80      90      100     110     120
EAADQVNAPVIVQASAGARKYAGAPFLRHLILAAVEEFPHIPVVMHQDHGASPDVCQRSI

m034.pep      130     140     150     160     170     180
QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLGNLETGDAG
|||||||||||||||||||||||||||||||||||||||||||||||||
a034          130     140     150     160     170     180
QLGFSVMMDGSLMEDGKTPSSYEYNVNATRTVVNFHSHACGVSVEGEIGVLGNLETGEAG

m034.pep      190     200     210     220     230     240
EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID
|||||||||||||||||||||||||||||||||||||||||||||||||
a034          190     200     210     220     230     240
EEDGVGAVGKLSHDQMLTSVEDAVRFVKDTGVDALAIAGVTSHGAYKFTRPPTGDVLRID

m034.pep      250
RIKEIHQALPNTTHIVMH
||||||||||||||
a034          250     260     270     280     290     300
RIKEIHQALPNTTHIVMHGSSSVPQEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVKRVN

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 034 shows 96.5% identity over a 257 aa overlap with a predicted ORF (ORF 034.ng) from *N. gonorrhoeae*:

## m034/g034

m034 . pep	MSCLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAEXSYGLPAFNVNVLXQMRAIM	60
g034	MSRLWFFAVKNIIIRLIYLLPKETQMALVSMRQLLDHAAENSYGLPAFNVNLEQMRAIM	60
m034 . pep	EAADQVDAPVIVQASAGARKYAGAPFLRHLILA AVEVFPHIPVVMHODHGASPDVCQRSI	120
g034	EAADQVNAPVIVQASAGARKYAGAPFLRHLILA AVEEFPHIPVVMHODHGASPDVCQRSI	120
m034 . pep	QLGFSSVMDGSLMEDGKTPSSYBYNVNATRTVNVNFSHACGVSVEGEIGVLGNLETGDAG	180
g034	QLGFSSVMDGSLLEDGKTPSSYBYNVNATRTVNVNFSHACGVSVEGEIGVLGNLETGEAG	180
m034 . pep	EEDGVGAVGKLSHDQMLTSVEDAVCFVKDTGVDALAI AVGTSHGAYKFTRPPTGDLVRID	240
g034	EEDGVGAAGKLSHDQMLTSVEDAVRFVKDTGVDALAI AVGTSHGAYKFTRPPTGDLVRID	240
m034 . pep	RIKEIHQALPNTHIVMH	257
g034	RIKEIHQALPNTHIVMHGSSSVPEWLKVINEYGGNIGETYGVPVEEIVEGIKHGVRKVN	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 127>:

## g036 . seq

```

1  ATGCTGAAGC  CGTGTGTTGGT  ATACAGTGCC  TGTGCGGCGG  cgttgccCTGC
51  GCGGACTTCG  AGCAGCAGGC  GTTGCCTGCC  TTCGGGCAGA  TGTGCGTACC
101 AATATTCGAG  CAGGGCGGAC  GCAACGCCCC  GTCGGGCGCA  TTCGGGCGCG
151 GTGGCAATCA  GGTGCAGTTC  GGATTCGTCG  GGCAGGTTCT  GCCAAACGAT
201 AAAGGCGGCA  ATCCTGCCGT  CTTTTCGCG  AAGGAAAACC  TGTTCGGACG
251 GCGAAACAAG  CGCGGACTCA  AATTGGCGTT  GCGTCCACGC  GGACGGGTTG
301 CAGACGGTAT  CGAGCGCGGC  CAGTGCAGGC  CAGTCCGACG  GTGAGGCTGG
351 GCGGATGTTT  ATGTTTCGTG  CTTCCGTTCC  GCCTGTTCTT  TGGCAGTCAG
401 GGCGATTTTG  TTGCGGACGT  AGAGCAGTTC  GGCGTGTGCC  GCGCCAGTTG
451 CGGGATAGCC  GCCGCCGAGG  GCGAGCGCGA  GAAAATCGGC  GCGGTCGCGC
501 ATATCGGGTT  TGCCTGAGAA  GGGCGGACGG  TTTTCCAGTG  CGAACGCACT
551 GCCGATGCCG  TCTGAAAGAA  CGTACCCCTC  GGGGAGGGCA  ATGTCTGCCG
601 CCCTACCGAC  TTGATAATCG  CTCAAACGGC  GGCGGTTTCA  CGTGTGCAAC
651 CACGCATAAA  ACACCTCGCC  CATACGCGCG  TCCGACGCGG  CGAGTATGCA
701 GCTTTGCGGC  GCGGCGACGG  AGGCGGCGGC  ATCGAGCGTG  GGGATGCCGA
751 TTAAGGCGT  GTCGAACGGC  GTTGCCAAAC  CTTGCGCCAC  GCCGATGCCG
801 ATACGCAGTC  CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 128; ORF 036.ng>:

## g036 . pep

```

1  MLKPCLVYSA  CAAALPARTS  SSRRCVPSGR  CAYQYSSRAD  ATPRRRHSGA
51  VAIRCSSDSS  GRFCQTIKAA  ILPSFSARKT  CSDGETSADS  NWRCVHADGL
101 QTVSSAASAA  QSDGEAGRMF  MFVPSVPPVL  WQSGRFCCGR  RAVRRVPRQL
151 RDSRRRGRAR  ENRRRSAYRV  CLRRADGFPV  RTHCRCLKR  RTPRGGQCLP
201 PYRLDNRSNG  GGSACRTHK  TLRPYARPQR  RVCSFAAAAA  RRRHRAWGCR
251 LKACRTALPN  LAPRRCRYAV  R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 129>:

## m036 . seq

```

1  ATGCTGAAGC  CGTGCAGCGT  GTACAGTGCC  TGTGCGGCGG  TGTGCTGTC
51  ACGGACTTCG  AGCAGCAGGC  GTTGCCTGTC  TTCGGGCAGA  TGTGTGAACC
101 AATATTCGAG  CAGGGCGGAC  GCAATTCCTT  GCGGCGGCA  TTCGGGCGCG
151 GTGGCAATCA  GGTGCAGTTC  GGATTCGTCG  GGCAGGTTCT  GCCAAACGAT
201 AAAGGCGGCA  ATCCCg.CGT  CTTTTCGCG  AAGGAAAACC  TGTTCGGACG
251 CCGAAACAG  TCGGACTCA  AATTGGCGTT  GCGTCCATGC  GGACGGGTTG
301 CAGACGGCAT  CGAGTGCAGC  CAGCTCCTCA  CAATCGGCAC  AAACGGCAGC

```

```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GCGGATTTTG TTGCGGACGT AGAGCAAACC GCGGTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGCTT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CATACGAGCG TCCGTAGCGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGGGT ATCAAACGGC GTTGCCAAAC CCTGAGCTAC ACCGATGCCG
801 ATACGCAGTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 130; ORF 036>:

```

m036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPXSFSAKRT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRQSAYPV CLRTAELLPA RTRCLCRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*R QGCSFAAAAA RRRHRARVRR
251 LRGYQTALPN PELHRCRYAV R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 131>:

```

a036.seq
1 ATGCTGAAGC CGTGCGCCGT GTACAGTGCC TGTGCGGCGG TGTGCTGCTG
51 ACGGACTTCG AGCAGCAGGC GTTGCCTGTC TTCGGGCAGA TGTGTGAACC
101 AATATTCGAG CAGGGCGGAC GCAATTCCTT GGCGGCGGCA TTCGGGCGCG
151 GTGGCAATCA GGTGCAGTTC GGATTCGTCG GGCAGGTTCT GCCAAACGAT
201 AAAGGCGGCA ATCCGCGCGT CTTTTTCGCG AAGGAAAACC TGTTCGGACG
251 GCGAAACCAG TGCGGACTCA AATTGGCGTT GCGTCCACGC GGACGGGTTG
301 CAGACGGCAT CGAGCGCGGC GAGTGCAGCG CAATCGGCAT AAACGGCGCG
351 GCGGATGTTT ACAGCGCGCG CCTCCGTTCC GCCTGTTCTT TGGCAGTCAA
401 GCGGATTTTG TTGCGGACGT AGAGCAGCTC GCGGTGTGCC GCAGCGACGG
451 CGGGAAAACC GCCTTCAGCC GCCAGATTGA GGAAGTCGGC GGCGGTCCGG
501 ATATCGGGTT TGCCTGAGAA GGGCGGACGG TTTTCCAGCG CGAACGCATT
551 GCCGATGCCG TCTGAAAAGG CGCATCCTTC CGGCAGCCGG ATGTCTGCCG
601 CCCGACCGAC CTGATAATCG CTCAAACGGC GCGGTTTCAG CGTGTGCAAC
651 CATGCATAAA ACACTTCGCC CATACGTGCG TCCGACGGG CAAGGATGCA
701 GCTTTGCGGC GCGGCGAGCG AGGCGGCGGC ATCGAGCGAG GGTACGCCGA
751 TTAAGGGAGT ATCAAACGGC GTTGCCAAAC CTTGCGCCAC GCCGATGCCG
801 ATACGCAGTC CCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 132; ORF 036.a>:

```

a036.pep
1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASAA QSA*TARRMF TGAPSVPPVL WQSRRFCCGR RAARRVPQRR
151 RENRLQPPD* GSRRRSAYRV CLRRADGFPA RTHCRCRLKR RILPAAGCLP
201 PDRPDNRSNG GGSACRTMHK TLRPYVRPQR QGCSFAAAAA RRRHRARVRR
251 LKEYQTALPN LAPRRCRYAV P*

```

m036/a036 85.6% identity over a 270 aa overlap

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACA	AVLPARTSSSR	RCVSSGR	CVNQYSSRAD	AIPWRRHSGA	VAIRCSSDSS
a036	MLKPCAVYSACA	AVLPARTSSSR	RCVSSGR	CVNQYSSRAD	AIPWRRHSGA	VAIRCSSDSS
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAA	IPXSFSAKTC	SADSNWRCV	HADGLQTASSA	ASSSQSAQT	ARRMF
a036	GRFCQTIKAA	IPPSFSARKT	CSDGETSAD	SNWRCVHAD	GLQTASSA	ASAAQSAXT
	70	80	90	100	110	120

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	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMRESRRQSAYPVCRLRTAELLPA					
a036	TGAPSVPPVLWQSGRFCCGRRRAARRVPQRRRENRLQPPDXGSRRRSAYRVCLRRADGFPA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPNDNRNNGGSSAYRTMHKTLRPYERPKRQGCSTFAAAAA					
a036	RTHCRCLKRRILPAAGCLPPDRPDNRNNGGSSACRTMHKTLRPYVRPQRQGCSTFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRRLRGYQTALPNPELHRCRYAVRX					
a036	RRRHRARVRRLKEYQTALPNLAPRRCRYAVPX					
	250	260	270			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 036 shows 74.9% identity over a 271 aa overlap with a predicted ORF (ORF 036.ng) from *N. gonorrhoeae*:

m036/g036

	10	20	30	40	50	60
m036.pep	MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIWRRHSGAVAIRCSSDSS					
g036	MLKPCLVYSACAAALPARTSSSRRCVPSGRCAYQYSSRADATPRRHSGAVAIRCSSDSS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m036.pep	GRFCQTIKAAIPXSFSARKTCSDETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF					
g036	GRFCQTIKAAILPSFSARKTCSDETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m036.pep	TGALSVRPVLWQSGRFCCGRRANRRVRHGRQDNRPWLPMRESRRQSAYPVCRLRTAELLPA					
g036	MFVPSVPPVLWQSGRFCCGRRAVRRVPRQLRDSRRRGRARENRRRSAYRVCLRRADGFVP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m036.pep	RTRCLCRLKRRIPPAAGCLPPARPNDNRNNGGSSAYRTMHKTLRPYERPKRQGCSTFAAAAA					
g036	RTHCRCLKRRTPRGGQCLPPYRLDNRNNGGSSACRTTHKTLRPYARPQRRVCSFAAAAA					
	190	200	210	220	230	240
	250	260	270			
m036.pep	RRRHRARVRRLRGYQTALPNPELHRCRYAVRX					
g036	RRRHRAGCRLKACRTALPNLAPRRCRYAVRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 133>:

m036-1.seq

1	ATGCTGAAGC	CGTGCGCCGT	GTACAGTGCC	TGTGCGGCGG	TGTTGCCTGC
51	ACGGACTTCG	AGCAGCAGGC	GTTGCGTGTC	TTCGGGCAGA	TGTGTGAACC
101	AATATTCGAG	CAGGGCGGAC	GCAATTCCTT	GGCGGCGGCA	TTCGGGCGCG
151	GTGGCAATCA	GGTGCACTTC	GGATTCGTCG	GGCAGGTTCT	GCCAAACGAT
201	AAAGGCGGCA	ATCCCGCCGT	CTTTTCCGCG	AAGGAAAACC	TGTTCCGACG
251	GCGAAACCAG	TGCGGACTCA	AATTGGCGTT	GCGTCCATGC	GGACGGGTTG
301	CAGACGGCAT	CGAGTGCGGC	CAGCTCCTCA	CAATCGGCAC	AAACGGCACG

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```

351 GCGGATGTTT ACGGGCGCGC TCTCCGTTTC GCCTGTTCTT TGGCAGTCAG
401 GGCATTGTTT TTGCGGACGT AGAGCAAACC GGCCTGTGCG GCATGGACGG
451 CAGGATAACC GCCCTTGGCT GCCAATGCGA GAAAGTCGGC GGCAGTCGGC
501 ATATCCGGTC TGCCTGAGAA CGGCGGAGCT TCTTCCAGCG CGAACGCGCT
551 GCCTATGCCG TCTGAAAAGG CGCATCCCTC CGGCAGCCGG ATGTCTGCCG
601 CCCGCCCGAC CTGATAATCG CTCAAACGGT GGCAGTTCAG CGTATCGAAC
651 CATGCATAAA ACACTTCGCC CACACGAGCG TCCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 134; ORF 0036-1>:

```

m036-1.pep
  1 MLKPCAVYSA CAAVLPARTS SSRRCVSSGR CVNQYSSRAD AIPWRRHSGA
 51 VAIRCSSDSS GRFCQTIKAA IPPSFSARKT CSDGETSADS NWRCVHADGL
101 QTASSAASSS QSAQTARRMF TGALSVRPVL WQSGRFCCGR RANRRVRHGR
151 QDNRPWLPMR ESRROSAYPV CLRTAELLPA RTRCLRLKR RIPPAAGCLP
201 PARPDNRSNG GSSAYRTMHK TLRPYERP*

```

m036-1/g036 76.8% identity in 228 aa overlap

```

          10      20      30      40      50      60
m036-1.pep MLKPCAVYSACAAVLPARTSSSRRCVSSGRCVNQYSSRADAIIPWRRHSGAVAIRCSSDSS
          ||||| |||||:||||| ||||: ||||| | ||||| |||||
g036        MLKPCLVYSACAAALPARTSSSRRCVPSGRCAVQYSSRADATPRRRHSGAVAIRCSSDSS
          10      20      30      40      50      60

          70      80      90      100     110     120
m036-1.pep GRFCQTIKAAIPPSFSARKTCS DGETSADSNWRCVHADGLQTASSAASSSQSAQTARRMF
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g036        GRFCQTIKAAIIPPSFSARKTCS DGETSADSNWRCVHADGLQTVSSAASAAQSDGEAGRMF
          70      80      90      100     110     120

          130     140     150     160     170     180
m036-1.pep TGALSVRPVLWQSGRFCCGRANRRVRHGRQDNRPWLPMRESRRQSAYPVCLRTAELLPA
          : || ||||| ||||| ||| : :||| ||||| ||||| ||| : ||:
g036        MFVPSVPPVLWQSGRFCCGRRAVRRVPRQLRDSRRRGRARENRRRSAYRVCLRRADGFPV
          130     140     150     160     170     180

          190     200     210     220     229
m036-1.pep RTRCLRLKRRIPPAAGCLPPARPDNRSNGGSSAYRTMHKTLRPYERPX
          ||: ||||| | : ||||| ||||| || || ||||| ||
g036        RTHCRCLKRRTPRGQCCLPPYRLDNRSNGGSACRTHKTLRPYARPQRRVCSFAAAAA
          190     200     210     220     230     240

g036        RRRHRAWGCRLKACRTALPNLAPRRCRYAVRX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 135>:

```

g038.seq
  1 ATGACTGATT TCCGCCAAGA TTCTCTCAAA TTCTCCCTCG CCCAAAATGT
 51 TTTGAAATTC GGCGAATTTA CCACCAAAGC CGGACGGCGG TCGCCCTATT
101 TCTTCAATGC CGGCTCTTTC AACGACGGCG CGTCCACGCT GCAACTGGCA
151 AAATTCTATG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201 GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGGGCGGCA ACCGCGATGA
251 TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301 GCCAAAGACC GCGGCGAAGG CGGCGTGTG GTGCGGCGCG CGCTTAAAGG
351 GCGCGTGTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401 AATCAATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGCG CGGTGTGCGC
451 ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTAAATTGT CCGCCGTTC
501 GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551 ACGATTGTG TATCCTGTTG CAAAACAACC CCGAATTCG ACAGTTCCTC
601 GAACCCGTCC GCACCTACCG CCGGCAGTAC GCGTAGAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 136; ORF 038.ng>:

```
g038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGASTLQLA
 51  KFYAQSIIES GIRFDMLFGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDRGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GKLSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 137>:

```
m038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCTCTCAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTTA CCACCAAGGC AGGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGTCCC GCCTACAAAG GCATTATTTT GCGGCGCGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451  ATCGCGCTCG ATCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 138; ORF 038>:

```
m038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMLFGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 139>:

```
a038.seq
  1  ATGACCGATT TCCGCCAAGA TTTCTCTCAA TTCTCCCTCG CCCAAAATGT
 51  TTTGAAATTC GCGCAATTTA CCACCAAGC GCGACGGCGG TCGCCCTATT
101  TCTTCAATGC CGGCCTCTTT AACGACGGCT TGTCCACGCT GCAACTGGCA
151  AAATTTTACG CACAATCCAT CATTGAAAGC GGCATCCGAT TCGATATGCT
201  GTTCGGCCCC GCCTACAAAG GCATTATTTT GCGGCGCGCA ACCGCGATGA
251  TGCTGGCGGA AAAAGGCGTG AACGTCCCGT TTGCCTACAA CCGCAAAGAA
301  GCCAAAGACC ACGGCGAAGG CGGCGTGTG GTCGCGCGCG CGCTTAAAGG
351  GCGCGTGCTG ATTATCGACG ACGTGATTTC CGCCGGCACA TCCGTACGCG
401  AATCGATCAA ACTGATTGAA GCGGAGGGTG CAACCCCGC CGGTGTCGCC
451  ATCGCGCTCG ACCGCATGGA AAAAGGCACG GGTGAATTGA GCGCGGTTCA
501  GGAAGTGGAA AAACAATACG GCCTGCCCGT CGCCCCATC GCCAGCCTGA
551  ACGATTGTGT TATTCTGTG CAAAACAACC CCGAATTCGG ACAGTTCCTC
601  GAACCCGTCC GAGCCTACCG TCGGCAGTAC GCGGTAGAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 140; ORF 038.a>:

```
a038.pep
  1  MTDFRQDFLK FSLAQNVLKF GEFTTKAGRR SPYFFNAGLF NDGLSTLQLA
 51  KFYAQSIIES GIRFDMLFGP AYKGIILAAA TAMMLAEKGV NVPFAYNRKE
101  AKDHGEGGVL VGAPLKGRVL IIDDISAGT SVRESIKLIE AEGATPAGVA
151  IALDRMEKGT GELSAVQVEVE KQYGLPVAPI ASLNDLFILL QNNPEFGQFL
201  EPVRAYRRQY GVE*
```

m038/a038 100.0% identity over a 213 aa overlap

```

              10      20      30      40      50      60
m038.pep      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQLAKFYAQSIIES
```



```

|||||
a038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQAKFYAQSIIES
           10      20      30      40      50      60

           70      80      90      100     110     120
m038.pep  GIRFDMLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           |||||||
a038      GIRFDMLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           70      80      90      100     110     120

           130     140     150     160     170     180
m038.pep  IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVEKQYGLPVAPI
           |||||||
a038      IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVEKQYGLPVAPI
           130     140     150     160     170     180

           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           |||||||
a038      ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           190     200     210

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 038 shows 98.1% identity over a 213 aa overlap with a predicted ORF (ORF 038.ng) from *N. gonorrhoeae*:

m038/g038

```

           10      20      30      40      50      60
m038.pep  MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGLSTLQAKFYAQSIIES
           |||||||
g038      MTDFRQDFLKFSLAQNVLKFGEFTTKAGRRSPYFFNAGLFNDGASTLQAKFYAQSIIES
           10      20      30      40      50      60

           70      80      90      100     110     120
m038.pep  GIRFDMLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDHGEGGVLVGAPLKGRVL
           |||||||
g038      GIRFDMLFGPAYKGIILAAATAMMLAEKGVNVPFAYNRKEAKDRGEGGVLVGAPLKGRVL
           70      80      90      100     110     120

           130     140     150     160     170     180
m038.pep  IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGELSAVQVEVEKQYGLPVAPI
           |||||||
g038      IIDDVISAGTSVRESIKLIEAEGATPAGVAIALDRMEKGTGKLSAVQVEVEKQYGLPVAPI
           130     140     150     160     170     180

           190     200     210
m038.pep  ASLNDLFILLQNNPEFGQFLEPVRAYRRQYGVEX
           |||||||
g038      ASLNDLFILLQNNPEFGQFLEPVRTYRRQYGVEX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 141>:

g039.seq

```

1  ATGCCGTC CG AACCACCTGC CGCTTCAGAC GGCATCAAAC CGACACACAC
51  CGAGAAAACA TCATGCCCGC CTGTTTCTGT CCGCACTGCA AAACCCGCCT
101 CTGGGTCAAA GAAAcccagC TCAAcgtCgC ccaagGCTTC GTCGTCTgcc
151 aaAAAtgcga agGGCTgttt aaAgccaaaG accAtctggc aaGcacGAAA
201 gaacctatat tcaacgattg gcccgaagct gtttcgggat gTcaaaCTCG

```

```

251 TCaccgcaT cggcacgcac gccattagca aGAaacagat gtccccgcgac
301 gaaatCgccg atatcctcaa cggcgggtaca acCCTGCACG ATACGCCGCC
351 CGCAACCGCC GCTGCCGCac ctGCCGCCGC ACCGcaggTT TCCGTACCGC
401 CCGCCCGTCA GGAAGGGCTC AACTGGACTA TTGCAACCTT GTTCGCACTT
451 ATCGTCCTCA TTATGCAGCT TTCCTACCTC TTCATCCTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 142; ORF 039.ng>:

**g039.pep**

```

1 MPSEPPAASD GIKPTHTEKT SCPPVSVRTA KPASGSKKPS STSPKASSSA
51 KNAKGCLKPK TIWQARKNLY STIGPKLFRD VKLVHRIGTH AISKQMSRD
101 EIADILNGGT TLHDTTPATA AAAPAAAPQV SVPPARQEGT NWTIATLFAL
151 IVLIMQLSYL FIL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 143>:

**m039.seq**

```

1 ATGCCGTCCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CGnnnnnnnnn nnnnnnnnnn
151 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn
201 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnCCC GAGGCTGTTT
251 CGGATGTCAA ACTCGTTCAC CGTATCGGCA CGCGCGCCAT CGGCAAGAAA
301 CAGATTTCCT GTGACGAAAT CGCCGGCATC CTCAACGGCG GTACAACCCA
351 GCCGATATT CCGCCGCAA CCGCCGCCAC CCCTGCTGCC GCACCGCAGG
401 TTACCGTACC GCCCGCGCG CCGCCCGTC AGGATGGGTT CAACTGGACG
451 ATTGCAACCC TGTTCGCCT TATCGTCCTC ATTATGCAGC TTTCTACCT
501 CGTCATCCTA TGA

```

This corresponds to the amino acid sequence <SEQ ID 144; ORF 039>:

**m039.pep**

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPXXXXXX
51 XXXXXXXXXX XXXXXXXXXX XXXXXXXXXP EAVSDVKLVH RIGTRAIGKK
101 QISRDEIAGI LNGGTTQPD I PPATAATPAA APQVTVPPAA PARQDGFNWT
151 IATLFALIVL IMQLSYLVIL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 145>:

**a039.seq**

```

1 ATGCCGTCCTG AACCGCCTTA CGCCTCAGAC GGCATCAAAC CTGACACACA
51 CGAGGAAATA CCATGCCCGC CTGTTTCTGC CCCCACTGCA AAACCGTCT
101 CTGGGTCAAA GAAACCCAAC TCAATGTCGC CCAAGGCTTC GTCGTCTGCC
151 AAAATGCGA AGGAATGTTT AAAGCCAAAG ACCATCTGGC AAGCACGAAA
201 GAACCATAT TCAACGATT. TGCCCGAAGC TGTTCGGAT GTCAAACCTG
251 TTCACCGCAT CGGCACGAGC GCCATCGGCA AGAAACAGAT TTCCCGTGAC
301 GAAATCGCCG GCATCCTCAA CGGCGGCACA ACCCAGCCCG ATATTCGCC
351 CGCAACCGCC GCCACCCCTG CTGCCGCACC GCAGGTACC GTACCGCCCG
401 CCGCGCCCGC CCGTCAGGAT GGGTCAACT GGACGATTGC AACCTGTTT
451 GCCCTTATCG TCCTCATTAT GCAGCTTTC TACCTCGTCA TCCTATGA

```

This corresponds to the amino acid sequence <SEQ ID 146; ORF 039.a>:

**a039.pep**

```

1 MPSEPPYASD GIKPDTHEEI PCPPVSAPTA KPVSGSKKPN SMSPKASSSA
51 KNAKECLKPK TIWQARKNPY STIXPEAVSD VKLVHRIGTS AIGKKQISR
101 EIAGILNGGT TQPDIPPATA ATPAAAPQVT VPPAAPARQD GFNWTIATLF
151 ALIVLIMQLS YLVL*

```

m039/a039 79.4% identity over a 170 aa overlap

```

              10      20      30      40      50      60
m039.pep      MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPXXXXXXXXXXXXXXXXXX
              |||
a039           MPSEPPYASDGIKPDTHEEIPCPPVSAPTAKPVSGSKKPNMSMPKASSSAKNAKECLKPK

```

226

	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD				
a039	:	:	:	:	:	:
	TIWQARKNPYSTIX----	PEAVSDVKLVHRIGTSAIGKKQISRDEIAGILNGGTTQPD				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAATPAAAPQVTVP	PAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
a039	PPATAATPAAAPQVTVP	PAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
	120	130	140	150	160	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 039 shows 60.8% identity over a 171 aa overlap with a predicted ORF (ORF 039.ng) from *N. gonorrhoeae*:

m039/g039

	10	20	30	40	50	60
m039.pep	MPSEPPYASDGIKPD	THEEIPCPVVSAPTAKPVSGSKPNSMSPXXXXXX				
g039	MPSEPPAASDGIKPTHTEKTSCPPVSVRTAKPASGSKKPSSTSPKASSSAKNAKGCLKPK					
	10	20	30	40	50	60
m039.pep	70	80	90	100	110	120
	XXXXXXXXXXXXXXXXXXXX	PEAVSDVKLVHRIGTRAIGKKQISRDEIAGILNGGTTQPD				
g039	:	:	:	:	:	:
	TIWQARKNLYSTIG----	PKLFRDVKLVHRIGTHAISKKQMSRDEIADIILNGGTTLHDT				
	70	80	90	100	110	
m039.pep	130	140	150	160	170	
	PPATAAT-PAAAPQVTVP	PAAPARQDGFNWTIATLFALIVLIMQLSYLVILX				
g039	PPATAAAAPAAAPQVSVP	PA---RQEGLNWTIATLFALIVLIMQLSYLFILX				
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 147>:

g040.seq

```

1  ATGAACGCGC CCGACAGCTT TGTCGCCCAC TTCCGCGAAG CCGCCCCCTA
51  CATCCGCCAA ATGCGCGGCA CGACACTGGT CGCCGGCATA GAcggCCGCC
101 TGCTCGAAGG CGGCACCTTA AATAAGCTCG CCGCCGACAT CCGGCTGTTG
151 TCGCAACTGG GCATCCGACT CGTCCTCATC CACGGCGCGT ACCACTTCCT
201 CGAcggCCTC GCCGCCGCGC AAGgccGCAC GCCGCATTAT TGCCGgggtt
251 tGCGCGTTAC CGACGaAACc tcGctcgGAC AGGCGCAGCA GtttGCCGGC
301 AccgTCCGCA GCCGTTTTGA agcCGCATTG tgcggcagCG tttcaggatt
351 cgcgCGCGCG CCTTCCGTCC CGCTCGTAtc gggcaacttc ctgacCGCCC
401 GTCcgatggg cgtgattgac ggaACCGata tggaaatacgc gggggttatc
451 cgcaaaaccg ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGATG CCGCCGCTCG GGCATTCTTA CGGCGGCAAA ACCTTCAATC
551 TCGATATGGT GCAGGCCGCC GCTTCCGTCG CCGTCTCGCT TCAGGCCGAA
601 AAACCTGTTT ACCTGACCCT TTCAGACGGC ATTCCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGCCAGCGA AACCCGACGA CTGATTTCGT CCGCCGTTGC CGCGCTCGAA
751 GCGGGCGTGC ATCGCGTCCA AATCCTCAAC GGGGCCGCGC ACGGACGCT
801 GCTGCAAGAA CTCTTCACCC GCAACGGCAT CGGCACGTCC ATTGCCAAG
851 AAGCCTTCGT CTCCATCCGG CAGGCGCACA GCGGCGACAT CCCGCACATC
901 GCCGCCCTCA TCCGCCCGCT GGAAGAACAG GCGGTCCTAT TGCACCGCAG
951 CCGGAATAC CTCGAAAACC ACATTTCCTG ATTTTCATC CTCGAACACG

```

```

1001  ACGGCGACCT GTACGGCTGT GCCGCACTCA AAACCTTTGC CGAAGCCGAT
1051  TCGGGCGAAA TCGCCTGCCT TGCCGTCTCG CCGCAGGCAC AGGACGGCGg
1101  ctACGGCGAA CGCCTGCTTG CCCACATTAT CGATAAGGCG CGCGGCATAG
1151  GCATAAGCAG GCTGTTCGCA CTGTCCACAA ATACCGGCGA ATGGTTTGCC
1201  GAACGCGGCT TTCAGACGGC ATCGGAAGAC GAGCTGCCCG AAACGCGGCG
1251  CAAAGACTAC CGCAGCAACG GACGAAACCC GCATATTCTG GTGCGTCGCC
1301  TGCACCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 148; ORF 040.ng>:

**g040.pep**

```

1  MNAPDSFVAH FREAAPYIRQ MRGTTLVAGI DGRLLGGTLL NKLAADIGLL
51  SQLGIRLVLI HGAYHFLDRL AAAQGRTPHY CRGLRVTDET SLGQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPMGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWM PPLGHSYGGK TFNLDMDVQAA ASVAVSLQAE
201 KLVYLTLSDG ISRPDGTLAE TLSAQEAQSL AEHAASETRR LISSAVAALE
251 GGVHRVQILN GAADGSLLQE LFTRNGIGTS IAKEAFVSIR QAHSGDIPHI
301 AALIRPLEEQ GVLLHRSREY LENHISEFSI LEHDGDLYGC AALKTFAEAD
351 CGEIACLAVS PQAQDGGYGE RLLAHIIDKA RGIGISRLFA LSTNTGEWFA
401 ERGFQTASED ELPETRRKDY RSNGRNPHIL VRRLHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 149>:

**m040.seq**

```

1  ATGAGCGCGC CCGACCTCTT TGTCGCCCAC TTCCGCGAAG CCGTCCCCTA
51  CATCCGCCAA ATGCGCGGCA AAACGCTGGT CGCCGGCATA GACGACCGCC
101 TGCTCGAAGG TGATACCTTA AACAAAGCTCG CCGCCGACAT CGGGCTGTTG
151 TCGCAACTGG GCATCAGGCT CGTCCTCATC CACGGCGCGC GCCACTTCCT
201 CGACCGCCAC GCCGCGCTC AAGGCCGCAC GCCGCATTAT TGCCGGGGCT
251 TGCGCGTTAC CGACGAAACC TCGCTCGAAC AGGCGCagCA GTTTGCCGGC
301 ACCGTCCGCA GCCGTTTGA AGCCGCATTG TGCGGCAGCG TTTCCGGGTT
351 CGCGCGCGCG CCTTCCGTCC CGCTCGTATC GGGCAACTTC CTGACCCGCC
401 GTCCGATAGG TGTGATTGAC GGAACCGATA TGGAAATACG GGGCGTTATC
451 CGCAAAACCG ACACCGCCGC CCTCCGTTTC CAACTCGACG CGGGCAATAT
501 CGTCTGGCTG CCGCCGCTCG GACATTCTTA CAGCGGCAAG ACCTTCTATC
551 TCGATATGCT TCAAACCGCC GCCTCCGCGC CCGTCTCGCT TCAGGCCGAA
601 AAACCTCGTT ACCTGACCCCT TTCAGACGGC ATTCCCGCC CCGACGGCAC
651 GCTCGCCGAA ACCCTCTCGG CACAGGAAGC GCAATCGCTG GCGGAACACG
701 CCGGCGGGCA AACCGGACGG CTGATTTCTG CCGCGAACT CTTCACCCGC
751 AACGGCATCG GCACGTCCAT TGCCAAAGAA GCCTTCGTCT CCATCCGGCA
801 rGCGCAywgG G.CGACATCC CGCACATCGC CGCCCTCATC CGCCCGCTGG
851 AAGAACAGGG CATCCTGCTG CACCGCAs.c GCGAATACCT CGAAAACAC
901 ATTTCCGAAT TTTCCATCCT CGAACACGAC GGCAACCTGT ACGGTTGCGC
951 CGCCCTGAAA ACCTTTGCCG AAGCCGATTG CGGCGAAATC GCCTGCCTTG
1001 CCGTCTCGCC GCag.cACAG GACGGCGGCT ACGGCGAACG CnTGCTTGCC
1051 CACATTATCG ATAAGCGCGC CGGCATAGGC ATAAGCAGGC TGTTCGCACT
1101 GTCCACAAAT ACCGGCGAAT GGTTTGCCGA ACGCGGCTTT CAGACGCAT
1151 CGGAAGACGA GTTGCCCGAA ACGCGGCGCA AAGACTACCG CAGCAACGGA
1201 CGGAACTCGC ATATTCTGGT ACGTCGCTG CACCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 150; ORF 040>:

**m040.pep**

```

1  MSAPDLFVAH FREAVPYIRQ MRGKTLVAGI DDRLLEGDTL NKLAADIGLL
51  SQLGIRLVLI HGARHFLDRH AAAQGRTPHY CRGLRVTDET SLEQAQQFAG
101 TVRSRFEAAL CGSVSGFARA PSVPLVSGNF LTARPIGVID GTDMEYAGVI
151 RKTDTAALRF QLDAGNIVWL PPLGHSYSGK TFYLDMLQTA ASAAVSLQAE
201 KLVYLTLSDG ISRPDGTLAE TLSAQEAQSL AEHAGGQTRR LISSAELFTR
251 NGIGTSIAKE AFVSIRQAHX XDIPHIAALI RPLEEQGILL HRXREYLENH
301 ISEFSILEHD GNLYGCAALK TFAEADCGEI ACLAVSPQXQ DGGYGERXLA
351 HIIDKARGIG ISRLFALSTN TGEWFAERGF QTASEDELPE TRRKDYRSNG
401 RNSHILVRRL HR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 151>:

**a040.seq**

a040.pcp

**m040/a040** 91.5% identity in 436 aa overlap

	10	20	30	40	50	60
m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI					
	:       :       :       :       :       :       :       :					
a040	MIVPDLFVAHFREAAPYIRQMRGKTLVAGIDDRLLEGDTLNKFAADIGLLSQLGIRLVLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m040.pep	HGARHFLLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
a040	HGARHFLLDRHAAAQGRTPHYCRGLRVTDETSLEQAQQFAGTVRSRFEAALCGSVSGFARA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYS GK					
a040	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYS GK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR					
a040	TFHLDMLQTAASAAVSLQAEKLVYLTLSDGISRPDGTLAETLSAQEAQSLAEHAGGQTRR					

	190	200	210	220	230	240
m040.pep	LISSA-----250 260 270					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 040 shows 88.3% identity over a 436 aa overlap with a predicted ORF (ORF 040.ng) from *N. gonorrhoeae*:

m040/g040

m040.pep	MSAPDLFVAHFREAVPYIRQMRGKTLVAGIDDRLLEGDTLNKLAADIGLLSQLGIRLVLI	60
g040	MNAPDSFVAHFREAPYIRQMRGTTLVAGIDGRLLGGTLNKLADIGLLSQLGIRLVLI	60
m040.pep	HGARHFLDRHAAQGRTPHYCRGLRVTDTSLEQAQQFAGTVRSRFEALCGSVSGFARA	120
g040	HGAYHFLDRLAAQGRTPHYCRGLRVTDTSLGQAQQFAGTVRSRFEALCGSVSGFARA	120
m040.pep	PSVPLVSGNFLTARPIGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWLPPLGHSYSGK	180
g040	PSVPLVSGNFLTARPMGVIDGTDMEYAGVIRKTDTAALRFQLDAGNIVWMPPLGHSYGGK	180
m040.pep	TFYLDMLQTAASAAVSLQAEKLVYLTLSDGISRDPDGLAETLSAQEAQSLAEHAGGQTRR	240
g040	TFNLDMVQAAASVAVSLQAEKLVYLTLSDGISRDPDGLAETLSAQEAQSLAEHAASETRR	240
m040.pep	LISSA-----ELFTRNGIGTSIAKEAFVSIRQAHXXDIPHI	276
g040	LISSAVAALGGVHRVQILNGAAGSLLQELFTRNGIGTSIAKEAFVSIRQAHSGDIPHI	300
m040.pep	AALIRPLEEQGILLHRXREYLENHISEFSILEHDGNLYGCAALKTFAEADCGEIACLAVS	336
g040	AALIRPLEEQGVLLHRSREYLENHISEFSILEHDGDLGCAALKTFAEADCGEIACLAVS	360
m040.pep	PQXQDGGYGERXLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	396
g040	PQAQDGGYGERLLAHIIDKARGIGISRLFALSTNTGEWFAERGFQTASEDELPETRRKDY	420
m040.pep	RSGNRNSHILVRRRLHRX	413
g040	RSGNRNPHILVRRRLHRX	437

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 153>:

```
g041.seq
1   ATGAGTTCGC CCAAACACAT CGGCTTGCG AGCGGCAGCA ACGGCGGCCT
51  GATTACCGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GGTGCGCTGG
101 TGTGCGAAGT ACCGCTGACC GATATGATCC GTTATCCGCT GCTGTCCGCC
151 GGTTCAGTTC GGACGGACGA ATACGGCAAT CCGCAGAAAT ACGAAGCCTG
201 CAAACGCCCG CTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCACTC ATTACCACCA GCCTCAGCGA CGACCGCGTC
301 CATCCCGCCC ACGCGCTCAA ATTCTACGCC AAACCTGCGG AAACCTCGCC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCAACGCGCA ATCCGCCGAC AAACCTGCCT GCGTGTGCT GTTTTGTAAA
451 GAATTTTGG GATAA
```

This corresponds to the amino acid sequence <SEQ ID 154; ORF 041.ng>:

```
g041.pep
1   MSSPKHIGLQ GGSNGGLITA AAFVREPSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEACKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPPGGGHT NGTQRESAD KLACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 155>:

```
m041.seq
1   ATCAGTTCGC CCGAACACAT CGGCTTGCG AGCGGCAGCA ACGGCGGACT
51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATC GCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCTC GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCCG TTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CCAACGCGCA ATCCGCCGAC GAACTCGCCT GCGTCTTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 156; ORF 041>:

```
m041.pep
1   ISSPEHIGLQ GGSNGGLITA AAFVREPSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPPGGGHT NGTQRESAD ELACVLLFLK
151 EFLG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 157>:

```
a041.seq
1   ATCAGTTCGC CCGAACACAT CGGCTTGCG AGCGGCAGCA ACGGCGGACT
51  GATTACTGCC GCCGCCTTCG TCGCGGAACC GCAAAGCATA GCGCGCTGG
101 TGTGCGAAGT GCCGCTGACC GACATGATCC GTTATCCGCT GCTCTCCGCC
151 GGTTCAGCTC GGACAGACGA ATACGGCAAT CCGCAAAAAT ACGAAGTCTG
201 CAAACGCCCG TTGGGCGAAT TGTCGCCGTA TCACAATCTT TCAGACGGCA
251 TCGATTATCC GCCCGCGCTC ATTACCACCA GCCTGTCCGA CGATCGCGTC
301 CATCCCGCCC ACGCGCTCAA GTTCTACGCC AAACCTGCGG AAACCTCGGC
351 GCAATCTTGG CTCTACTCGC CTGACGGCGG CGGCCATACC GGCAACGGCA
401 CGCAGCGCGA AGCCGCCGAC GAACTCGCCT GCGTGTGCT GTTTTGTAAA
451 GAGTTTTTGG GCTAA
```

This corresponds to the amino acid sequence <SEQ ID 158; ORF 041.a>:

```
a041.pep
1   ISSPEHIGLQ GGSNGGLITA AAFVREPSI GALVCEVPLT DMIRYPLLSA
51  GSSWTDEYGN PQKYEVCKRR LGELSPYHNL SDGIDYPPAL ITTSLSDDRV
101 HPAHALKFYA KLRETSQSW LYSPPGGGHT NGTQREAAD ELACVLLFLK
```

151 EFLG\*

m041/a041 98.7% identity over a 154 aa overlap

m041.pep	10	20	30	40	50	60
	ISSPEHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
a041	10	20	30	40	50	60
	ISSPEHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
m041.pep	70	80	90	100	110	120
	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSAQSW					
a041	70	80	90	100	110	120
	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSQSW					
m041.pep	130	140	150			
	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
a041	130	140	150			
	LYSPDGGGHTGNGTQREADELACVLLFLKEFLGX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 041 shows 96.8% identity over a 154 aa overlap with a predicted ORF (ORF 041.ng) from *N. gonorrhoeae*:

m041/g041

m041.pep	10	20	30	40	50	60
	ISSPEHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
g041	10	20	30	40	50	60
	MSSPKHIGLQGGSNGLITAAAFVREPOSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGN					
m041.pep	70	80	90	100	110	120
	PQKYEVCKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSAQSW					
g041	70	80	90	100	110	120
	PQKYEACKRRRLGELSPYHNLSGDIDYPPALITTSLSDDRHPAHALKFYAKLRETSQSW					
m041.pep	130	140	150			
	LYSPDGGGHTGNGTQRESADELACVLLFLKEFLGX					
g041	130	140	150			
	LYSPDGGGHTGNGTQRESADKLACVLLFLKEFLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 159>:

g041-1.seq

```

1  ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCG CGCGCACTTT CAGACGGCAT TTTGAATCAA
151 ATGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTT CATCAGAATG CGGAATATCC GAAGGGCGTG TACCGCATGT
251 GTACGGCGGC GACCTACCGT TCCGGCTATC CCGAGTGGAA AATCCTGTTT
301 TCGGTGCGG ATTTGATGA GTTGCTCGGC GACGATGTGT ATTTGGGCGG
351 CGTGTGCGAC TTGGTGGAGC AGCCCAACCG CGCGCTGCTG ACTTTGAACA
401 AATCGGGCGG CGATACGGCG TATACGCTGG AAGTGGATT GGAAGCAGGG
451 GAATTGGTAG AGGGCGGTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGGAAG TGTGGCTGGT GGAACGCGGC

```



```

601 AAGAGTTTCG AGGAAAGCCT GCCGGCGTAC CAAATCGATA AAGGCGCGAT
651 GATGGTAAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AGACGTATTT GCAGGTGTCG
751 TCCGAAGGCG GGGCGAAACC GTTGAACCTG CTAATGATT GCGATGTGGT
801 CGGCTATCTG GCGGGACATC TTTTGCTGAC GCTGCGCAAG GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCGT TGGTGGCGGT GAAACTGAAT
901 CGGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCAAGCCTGC
1001 TGGAGAAATGT ACRAAGCCGT CTGAAAGCGT GCGGTTTTCG CGACAGCAAA
1051 TGGCAGGAAG CCGAGTTGCC GCACCTGCCC TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGCGGCG ACGTGGTTTA TCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAACGACC
1201 GTCATGCGCC TCCAGCCGCA GCAGTTTGT TCAGACGGCA TCGAAGTGCG
1251 GCAGTTTTCG GCGGTGTCTG CCGACGGCGA ACGCATTCCT TATTTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACACGCCGA CCTTAGTCTA TGCTTACGGA
1351 GGTTCGCGCA TTCCTGAATT GCCGCATTAT CTGGGCAGCG TCGGCAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCAACATC CGCGGCGGCG
1451 GAGAATTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAACAC
1501 AAAAGCGTTG ATGATTTGTT GGCAGTCGTG CGTGATTTGT CCGAACGCGG
1551 CATGAGTTCG CCCAAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGCC
1601 TGATTACCGC CGCCGCTTC GTGCGCGAAC CGCAAAGCAT CGGTGCGCTG
1651 GTGTGCGAAG TACCGCTGAC CGATATGATC CGTTATCCGC TGCTGTCCGC
1701 CGGTTCAAGT TGGACGGACG AATACGGCAA TCCGCAGAAA TACGAAGCCT
1751 GCAAACGCCG GCTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCCGCACT CATTACCACC AGCCTCAGCG ACGACCGCGT
1851 CCATCCCGCC CACGCGCTCA AATTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCCGA CAAACTCGCC TCGTGTGTC TGTTTTGA
2001 AGAATTTTGG GATAA

```

This corresponds to the amino acid sequence <SEQ ID 160; ORF 041-1.ng>:

g041-1.pep

```

1 MKSYDPYRH FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILNQ
51 MQDTRQIPFC QEHRARMYHF HQNAEYPKGV YRMCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLNKSGGDTA YTLEVDLEAG
151 ELVEGGFHFAP AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVWLVERG
201 KSFEESLPAY QIDKGAMMVN AWRYLDPOGS PIDLIEASDG FYTKTYLQVS
251 SEGGAAPLNL PNDVDVGYL AGHLLTLRK DWHRANQSYR SGALVAVKLN
301 RGEAGAAQLL FAPDETQALE SVETTKRFV ASLLENVOGR LKAWRFADSK
351 WQEAELPHLP SGALEMTDQP WGGDVVYLA SDFTTPTLTF ALDLNVMELT
401 VMRLQPQFV SDGIEVRQFW AVSSDGERIP YFHVGNKAP DTPTLVYAYG
451 GGIPELPHY LGSVGYWLE EGNFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLAVV RDLSEGMSS PKHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEACKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQRESADKLA CVLLFLKEFL G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 161>:

m041-1.seq

```

1 ATGAAATCCT ACCCGACCC CTACCGCCAT TTTGAAACC TCGATTCCGC
51 CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAGAAAA CGACAAGGCG CGCGCGCTTT CAGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAGAT TCCGTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAGGACG CGGAGTATCC GAAGGGCGTG TACCGCGTGT
251 GTACCGCGGC GACGTATCGT TCCGCTATC CCGAGTGGA AATCCTGTTT
301 TCGGTGGCGG ATTCGACGA ATTGCTTGGC GACGATGTGT ATTGGGCGG
351 CGTGTCGCAC TTGGTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATTGGGCGA CGATACGGCG TACACGCTGG AAGTGGATT GGAAGCAGGG
451 GAGTTGGTCG AAGGCGGTTT TCACTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAACAGCG TGTGGGTGTG TCCGGCTTGG AACGAACGCC
551 AGTTGACCCA ATCGGGCTAT CCGCGCGAAG TATGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCTGTGTAT CAAATCGGCG AAGACGGCAT
651 GATGTGAAC GCGTGGCGTT ATCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCGGACGGT TTTTACACCA AAACCTATTT GCGGCTCTCA

```

```

751 GCCGAAGGCG AGGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTGGT
801 CGGCTATCTG GCGGGGCATC TTTTGCTGAC GCTGCGCAAG GACTGGAACC
851 GCGCGAACCA AAGCTATCCG AGCGGCGCGC TGGTGGCGGT GAAGCTGAAT
901 CCGGGCGAAC TCGGGGCGGC GCAGCTTTTG TTTGCGCCCG ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTGGTG GCGAGCCTGT
1001 TGGAGAACGT ACAAGGCCGT CTGAAAGCAT GGCGGTTTGC CGACGGCAAA
1051 TGGCAGGAAG TCGAATTGCC GCGCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCT TGGGGCGGCG ACCTGCTTGA CTTGCCGCC AGCGATTTC A
1151 CCACGCCGCT GACGCTGTTT GCGCTGGATT TGAACGTGAT GGAAGTGAAC
1201 GTCATGCGCC GCCAGCCGCA GCAGTTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCCT TATTTCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCTACGGC
1351 GGTTTCGGCA TTCCCGAATT GCCGCATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCGAACATC CGCGGCGGCG
1451 GCGAGTTCGG CCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG CGCGATTGT CCGAACGCGG
1551 TATCAGTTCG CCGAACACA TCGGCTTGCA GGGCGGCAGC AACGGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT CGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCG
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTGCGCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCCG
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CGGCAACGGC
1951 ACCCAACGCG AATCCGCGCA CGAACTCGCC TCGCTCTTGC TGTTTTTGAA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 162; ORF 041-1>:

m041-1.pep

```

1 MKSYDPYRHF FENLDSAETQ NFAAEANAET RARFLENDKA RALSDGILAQ
51 LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TSLKLSGSDTA YLEVDLEAG
151 ELVEGGFHFP AGKNHVSWRD ENSVWVCPAW NERQLTQSGY PREVWLVERG
201 KSFEESLPVY QIGEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLRVS
251 AEGEAKPLNL PNDGDVVGYL AGHLLTLRK DWNRRANQSY SGALVAVKLN
301 RGELGAAQLL FAPDETOALE SVETTKRFV ASLLENVQGR LKAWRFADGK
351 WQEVLPRLP SGALEMTDQP WGGDVVYLAA SDFTTPLTLF ALDLNVMELT
401 VMRRQPQQFD SDGINVQQFW TTSADGERIP YFHVGNKAA DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV RDLSEGGISS PEHIGLQGS NGGLITAAAF VREPQSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCRRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHFA HALKFYAKLR ETSAQSWLYS PDGGGHTGNG
651 TQRESADELA CVLLFLKEFL G*

```

m041-1/g041-1 94.6% identity in 671 aa overlap

```

              10      20      30      40      50      60
m041-1.pep  MKSYDPYRHFENLDSAETQNF AAEANAETRARFLENDKARALSDGILAQ LQDTRQIPFC
              |||
g041-1      MKSYDPYRHFENLDSAETQNF AAEANAETRARFLNNDKARALSDGILNQMDTRQIPFC
              10      20      30      40      50      60

              70      80      90      100     110     120
m041-1.pep  QEHRARMYHFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH
              |||
g041-1      QEHRARMYHFHQDAEYPKGVYRMCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH
              70      80      90      100     110     120

              130     140     150     160     170     180
m041-1.pep  LVEQPNRALLTSLKLSGSDTAYTLEVDLEAGELVEGGFHFPAGKNHVSWRDENS VWVCPAW
              |||
g041-1      LVEQPNRALLTLNKGSGDTAYTLEVDLEAGELVEGGFHFPAGKNHVSWRDENS VWVCPAW
              130     140     150     160     170     180

              190     200     210     220     230     240
m041-1.pep  NERQLTQSGYPREVWLVERGKSFEESLPVYQIGEDGMMVN AWRYLDPQGS PIDLIEASDG
              :|||:

```

g041-1	DERQLTESGYPREVWLVERGKSFEESLPAYQIDKGAMMVNAWRYLDPQGSPIDLIEASDG
	190 200 210 220 230 240
m041-1.pep	FYTKTYLRVSAEGEAKPLNLPND CDVVG YLAGHLLLT LRK DWN RAN QSYPS GALVAVKLN
	250 260 270 280 290 300
g041-1	FYTKTYLQVSSEGGAKPLNLPND CDVVG YLAGHLLLT LRK DWH RAN QSYPS GALVAVKLN
	250 260 270 280 290 300
m041-1.pep	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGR LKAWRFADGKWQEVELPRLP
	310 320 330 340 350 360
g041-1	RGELGAAQLLFAPDETQALESVETTKRFVVASLLENVQGR LKAWRFADSKWQEAELPHLP
	310 320 330 340 350 360
m041-1.pep	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRRQPQQFSDSGINVOQFW
	370 380 390 400 410 420
g041-1	SGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRLQPQQFVSDGIEVRQFW
	370 380 390 400 410 420
m041-1.pep	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI
	430 440 450 460 470 480
g041-1	AVSSDGERIPYFHVGNKNAAPDTPTLVYAYGGFGIPELPHYLGSVGVKYWLEEGNAFVLANI
	430 440 450 460 470 480
m041-1.pep	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSE RGISSPEHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
g041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSE RGMSSPKHIGLQGGSNGLITAAAF
	490 500 510 520 530 540
m041-1.pep	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCKRRLGELSPYHNLSDG
	550 560 570 580 590 600
g041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEACKRRLGELSPYHNLSDG
	550 560 570 580 590 600
m041-1.pep	IDYPPALITTSLSDDR VHPAHALKFYAKLRETS AQSWLYSPDGGGHTNGTQRESADELA
	610 620 630 640 650 660
g041-1	IDYPPALITTSLSDDR VHPAHALKFYAKLRETS PQSWLYSPDGGGHTNGTQRESADKLA
	610 620 630 640 650 660
m041-1.pep	CVLLFLKEFLGX
	670
g041-1	CVLLFLKEFLGX
	670

## m041-1/p55577

sp|P55577|Y4NA\_RHISN PROBABLE PEPTIDASE Y4NA >gi|2182536 (AE000086) Y4na [Rhizobium sp. NGR234] Length = 726

Score = 370 bits (940), Expect = e-101

Identities = 217/682 (31%), Positives = 331/682 (47%), Gaps = 22/682 (3%)

Query: 2 KSYDPYRHFENLDSAETQNFAAEANAETRARFLENDKARALSDGILAQLQDTRQIPFCQ 61  
 K DP + +D + + N T + ++ + L LQ T +I  
 Sbjct: 42 KDASDPRAYLNEIDGDKAMTWVEAHNLSTVDKLSKDPYSEYQADALTILQATDRIASPS 101

Query: 62 EHRARMY-HFHQDAEYPKGVYRVCTAATYRSGYPEWKILFSVADFDELLGDDVYLGGVSH 120  
 R M +F QD + +G++R T +YRSG P+W+ + V + G G  
 Sbjct: 102 FARDGMIDNFWQDGHVQGLWRRTTWESYRSGNPQWRITILDVDALSKAEGKTWVFEFGDC 161

Query: 121 LVEQPNRALLTSLKLGSDTAYTLEVDLEAGELVEGGFHFPAKGNHVSWRDENSVMVCPAW 180  
 L N L+ LS G D E D+ GE V+ GF P GK V+W DEN++V W

Sbjct: 162 LPPTSNLCLIRLSGGKDADVREFDIAKGEFVKEGFVLPEGRQSVTVWVDENTIIYVTREW 221

Query: 181 NERQLTQSGYPREVWLVERGKSFEESLPVYQ-----IGEDGMM--VNAWRYLDPQGSPI 232  
 ++T SGY ++V+RG+S ++++ +++ E G++ ++ +D +

Sbjct: 222 TPGEVTSSGYAYVTKVVKRGQSLDQAVEIFRGQKKDVSAERGVLRLDIDGKYVMDTSYRGL 281

Query: 233 DLIEASDGFYTKTYLRVSAEGEAKPLNLPNDCDVVGYLAGHLLTLRKDNWRANQS-YPS 291  
 D FY + + L LP GY G + L+ DW A + + +

Sbjct: 282 DFFNTELAFFPNHG----PDTRKVVLPLPTTAVFSGYYKGQAIYWLKSDWTSAGKTVFHN 337

Query: 292 GALVAVKLNRELGAQAQ----LFAPDETOALESVETTKRFVVASLLENVQGRKAWRFA 347  
 GA++A L A++ LF P+E Q++ TK +V S+L NV ++++ F

Sbjct: 338 GAIIAFDLKAALADPARVEPLVLFMPNEHQSVAGTTQTKNRLVLSILSNVTSEVRSFDFG 397

Query: 348 DGKWQEVLEPRLPSGALEMTDQPWGGDVVYLAASDFTTPTLTFALDLNVMELTVMRRQPQ 407  
 G W +L + L +T D +++ + F P TLF D ++ + P

Sbjct: 398 KGGWSSFKLALPENSTLSLTSSDDESQDLVFSEGFLEPSTLFCADAATGQVEKITSTPA 457

Query: 408 QFDSGGINVQQFWTTSADGERIPYFHVGNKNAAP---DMPTLVYAYGGFGIPELPHYLGS 464  
 +FD+ G+ QQFW TS DG ++PYF V + PT++YAYGGF IP P Y +

Sbjct: 458 RFDAGGLQAQQFWATSKDGTKVYPFLVARKDVKLDGNTPTILYAYGGFQIPMQPSYSAVL 517

Query: 465 GKYWLEEGNAFVLANIRGGGEFGPRWHQAAQGISKHKSVDDLLAVVRDLSEGGISSPEHI 524  
 GK WLE+G A+ LANIRGGGEFGP+WH A ++. DD AV +DL + ++S H+

Sbjct: 518 GKLWLEKGGAYALANIRGGGEFGPKWH DAGLKTNRQRYDDFQAVQDLIAKKVTSTPHL 577

Query: 525 GLOGGSNGGLITAAAFVREPQSIGALVCEVPLTDMIRYPLL SAGSSWTDEYGNPQKYEVC 584  
 G+ GGSNGGL+ ++ P A+V +VPL DM+ + +SAG+SW EYG+P V

Sbjct: 578 GIMGGSNGGLLMGVQMIQRPDLWNAVVIQVPLLDVMVNFTRMSAGASWQAEYGSPPD-PVE 636

Query: 585 KRLGELSPYHNLSGDIDYPPALITTSLSDDRVP HPAHALKFYAKLRETSQSWLYSPDGG 644  
 L +SPYHN+ G+ YP TS DDRV P H A K A + + Y G

Sbjct: 637 GAFLRISISPYHNKAGVAYPEFFETSTKDDRVGPVHARKMAALFEDMGLPFFYYENIEG 696

Query: 645 GHTGNGTQRESADELACVLLFL 666  
 GH +E A A +++

Sbjct: 697 GHAAAANLQEHARRYALEYIYM 718

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 163>:

a041-1.seq

```

1  ATGAAATCCT ACCCCGACCC CTACCGCCAT TTTGAAAACC TCGATTCCGC
51  CGAAACGCAA AACTTCGCTG CTGAAGCGAA TGCCGAAACG CGCGCGCGTT
101 TTTTAAACAA CGACAAGGCA CGCGCATTGT CTGACGGCAT TTTGGCGCAG
151 TTGCAGGACA CGCGGCAAAAT TCCGTTTTGT CAGGAACACC GCGCGCGGAT
201 GTACCATTTC CATCAAGATG CGGAATATCC GAAAGGCGTG TACCGCGTGT
251 GTACCGCGGC GACTTACCGT TCGGGCTATC CTGAGTGGAA AATCCTGTTT
301 TCGGTGGCGG ATTCGACGA ATTGCTCGGT GACGATGTAT ATCTAGGCGG
351 CGTGTGCGAC CTGTTGGAAC AGCCCAACCG CGCGTTGTTA AACTGAGCA
401 AATCGGGCGG CGATACCGCG TACACGCTGG AAGTGGATT TGAAGCAGGG
451 GAGTTGGTAG AAGCGGTTTT TCACTTTCCG GCAGGCAAAA ACCATGTGTC
501 GTGGCGCGAT GAAAAACAGC TGTGGGTGTG TCCGGCTTGG GACGAACGCC
551 AGTTGACCGA ATCGGGCTAT CCGCGCGAGG TGTGGCTGGT GGAACGCGGC
601 AAGAGTTTCG AGGAAAGCCT GCCGGTGATC CAAATTGCTG AAGACGGCAT
651 GATGGTGAAC GCGTGGCGTT ACCTCGATCC GCAGGGTTCG CCGATTGATT
701 TGATTGAAGC GTCTGACGGT TTTTACACCA AAACCTATTT GCAGGTCTCA
751 GCCGAAGGCG AAGCGAAACC GTTAAACCTG CCCAACGATT GCGACGTAGT
801 CGGCTATCTG GCCGGACATC TTTTGTGAC CTGCGTAAA GACTGGCACC
851 GCGCGAACCA AAGCTATCCG AGTGGCGCAT TGGTAGCAGT AAAATTAAAC
901 CGCGGCGAAT TGGGCGCGGC GCAGCTTTTG TTTGCGCCCA ATGAAACGCA
951 GGCATTGGAA AGCGTGGAAA CGACCAAGCG TTTTGTCTGT GCGAGCCTGC
1001 TGGAAAACGT ACAGGGTCGT CTGAAGCGT GCGGTTTTAC TGATGCAAA
1051 TGGCAGGAAA CCGAGTTGCC GCGCCTGCCT TCGGGCGCGT TGGAAATGAC
1101 CGACCAACCG TGGGGGGGCG ACGTAGTTTA CCTTGCCGCC AGCGATTTC
1151 CCACGCCGCT GACGCTGTTT GCATTGGATT TGAACGTGAT GGAAGTACG
1201 GTCATGCGCC GCCAGCCGCA GCAGTTGAT TCAGACGGCA TTAACGTGCA
1251 GCAGTTTGG ACGACTTCGG CTGACGGCGA GCGCATTCTT TATTCCACG
1301 TCGGCAAAAA CGCCGCGCCC GACATGCCGA CGCTGGTCTA TGCCTACGGC
1351 GGTTCGGCA TCCCGAATT GCCGATTAT CTGGGCAGCA TTGGCAAATA
1401 TTGGCTGGAA GAGGGCAATG CCTTTGTATT GGCGAACATC CGCGCGCGCG

```

```

1451 GCGAGTTCGG CCCGCGCTGG CATCAGGCGG CGCAGGGAAT CAGCAAACAT
1501 AAAAGCGTTG ATGATTTATT GGCAGTCGTG AGCGATTTGT CCGAACGCGG
1551 TATCAGTTCG CCCGAACACA TCGGCTTGCA GGGCGGCAGC AACCGCGGAC
1601 TGATTACTGC CGCCGCCTTC GTGCGCGAAC CGCAAAGCAT AGGCGCGCTG
1651 GTGTGCGAAG TGCCGCTGAC CGACATGATC CGTTATCCGC TGCTCTCCGC
1701 CGGTTCAAGC TGGACAGACG AATACGGCAA TCCGCAAAA TACGAAGTCT
1751 GCAAACGCCG GTTGGGCGAA TTGTCGCCGT ATCACAATCT TTCAGACGGC
1801 ATCGATTATC CGCCGCGCT CATTACCACC AGCCTGTCCG ACGATCGCGT
1851 CCATCCCGCC CACGCGCTCA AGTTCTACGC CAAACTGCGC GAAACCTCGC
1901 CGCAATCTTG GCTCTACTCG CCTGACGGCG GCGGCCATAC CCGCAACGGC
1951 ACGCAGCGCG AAGCCGCCGA CGAACTCGCC TGCGTGTTC TGTTTTGA
2001 AGAGTTTTTG GGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 164; ORF 041-1.a>:

a041-1.pep

```

1  MKSYDPYRHF FENLDSAETQ NFAAEANAET RARFLNNDKA RALSDGILAQ
51  LQDTRQIPFC QEHRARMYHF HQDAEYPKGV YRVCTAATYR SGYPEWKILF
101 SVADFDELLG DDVYLGGVSH LVEQPNRALL TLSKSGGDTA YTLEVDLEAG
151 ELVEGGFHFH AGKNHVSWRD ENSVWVCPAW DERQLTESGY PREVLVERG
201 KSFEESLPVY QIAEDGMMVN AWRYLDPQGS PIDLIEASDG FYTKTYLQVS
251 AEGEAKPLNL PNDCDVVGYL AGHLLTLRKL DWHRANQSYR SGALVAVKLN
301 RGELGAAQLL FAPNETQALE SVETTKRFV VASLLENVQGR LKAWRFTDGL
351 WQETELPRLP SGALEMTDQP WGGDVVYLA SDFTTPLTLF ALDLNVMELT
401 VMRRQPQFDF SDGINVQFV TTSADGERIP YFHVGNKNA DMPTLVYAYG
451 GFGIPELPHY LGSIGKYWLE EGNAFVLANI RGGGEFGPRW HQAAQGISKH
501 KSVDDLLAVV SDSLSEGISS PEHIGLOGGS NGGLITAAF VREPOSIGAL
551 VCEVPLTDMI RYPLLSAGSS WTDEYGNPQK YEVCKRRLGE LSPYHNLSDG
601 IDYPPALITT SLSDDRVHPA HALKFYAKLR ETSPQSWLYS PDGGGHTGNG
651 TQREAADELA CVLLFLKEFL G*

```

a041-1/m041-1 97.9% identity in 671 aa overlap

a041-1.pep	10	20	30	40	50	60
m041-1	10	20	30	40	50	60
a041-1.pep	70	80	90	100	110	120
m041-1	70	80	90	100	110	120
a041-1.pep	130	140	150	160	170	180
m041-1	130	140	150	160	170	180
a041-1.pep	190	200	210	220	230	240
m041-1	190	200	210	220	230	240
a041-1.pep	250	260	270	280	290	300
m041-1	250	260	270	280	290	300
a041-1.pep	310	320	330	340	350	360
m041-1	310	320	330	340	350	360

a041-1.pep	370	380	390	400	410	420
	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQFDSGGINVQQFW					
m041-1	SGALEMTDQPWGGDVVYLAASDFTTPLTLFALDLNVMELTVMRRQPQFDSGGINVQQFW					
	370	380	390	400	410	420
a041-1.pep	430	440	450	460	470	480
	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
m041-1	TTSADGERIPYFHVGNKNAAPDMPTLVYAYGGFGIPELPHYLGSIGKYWLEEGNAFVLANI					
	430	440	450	460	470	480
a041-1.pep	490	500	510	520	530	540
	RGGGEFGPRWHQAAQGISKHKSVDLLAVVSDLSEGISSEPHIGLQGGSNGLITAAAF					
m041-1	RGGGEFGPRWHQAAQGISKHKSVDLLAVVRDLSEGISSEPHIGLQGGSNGLITAAAF					
	490	500	510	520	530	540
a041-1.pep	550	560	570	580	590	600
	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCRRRLGELSPYHNLSDG					
m041-1	VREPQSIGALVCEVPLTDMIRYPLLSAGSSWTDEYGNPQKYEVCRRRLGELSPYHNLSDG					
	550	560	570	580	590	600
a041-1.pep	610	620	630	640	650	660
	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQREAADELA					
m041-1	IDYPPALITTSLSDDRVPALHAKFYAKLRETSQSWLYSPDGGGHTGNGTQREADELA					
	610	620	630	640	650	660
a041-1.pep	670					
	CVLLFLKEFLGX					
m041-1	CVLLFLKEFLGX					
	670					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 165>:

## g042.seq

```

1  ATGACGATGA TTTGCTTGCG CTTCCAagcG TTCGTGCCGC ATACCAGCGC
51  GTTATCCAAC ACTTCCACGG CAGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TGCGGTCGAT GATGAAAATC CAGCCGGGGT TTTTCTCTTT GATGTATTCG
151 AAGGAAACGG GCTGCCCGTG CCCTTCGTTG CGTAAAGATT CGTCCACGGG
201 CGGCAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GATTGCGTGC
251 CGAAGGCGGA CACCTTGTTG CCTGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG cggCTTCGCG CTTTGGGCG AACAGCGCGT CAATCTGCGC
351 ATTCAATTCC GCCACGCGCG CTTCTTACC GAAATCCGC GACAGGGTCT
401 CCATCTGCTT CTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAAA
451 TCTATGgtgG TCGCGTTTTT CGCCAACGTG TCATACGCTT CCGCACCCGG
501 CCCGCCGTA ATGACAAACT GCGGATTGTG GCGGTGCAGG GATTGCGCAAT
551 CGGGCTCAA CAGCGTCCCC ACCGTTGCCG CTTGTCAAA TGCAGGCTGC
601 AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 166; ORF 042.ng>:

## g042.pep

```

1  MTMICLRFOA FVPHTSALSN TSTAAGPSCP MAAVRSMKI QPGFFSLMYS
51  KETGCPCLSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRFA NSASICAFNS ATRASLPKIR DRVSICFSPL VRILPLSTVK
151 SMVVAFFANC SYASAPGPV MTNCLWRRC DSQSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 167>:

238

## m042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAmT ACTTCGACAG CCGcCGGCCy TTCyTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCCGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 168; ORF 042>:

## m042.pep

```

1 MTMICLRFOA FVPRTSALSX TSTAAGXSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTSXGLXRRCR ASXSGSNSVP TVAALSNAAG
201 K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 169>:

## a042.seq

```

1 ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51 GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAAC TGCCAACCGC GACTGCGTGC
251 CGAAGGCCGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCCT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCCAACGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA ATGACAAGCT GAGGATTGTA GCGGTGCAGG GCTTCGTAAT
551 CGGGCTCGAA CAGCGTCCCC ACCGTTGCCG CCTTGTCAAA TGCAGGCTGC
601 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 170; ORF 042.a>:

## a042.pep

```

1 MTMICLRFOA FVPRTSALSX TSTAAGPSCP MAAVRSMMKI QSGFFSLMYS
51 KETGCPGPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSPL VRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*GL*RCR AS*SGSNSVP TVAALSNAAG
201 K*

```

m042/a042 99.0% identity over a 201 aa overlap

	10	20	30	40	50	60
m042.pep	MTMICLRFOAFVPRTSALSXTSTAAGXSCPMMAVRSMMKIQSGFFSLMYSKETGCPGPSL					
a042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAVRSMMKIQSGFFSLMYSKETGCPGPSL					
	10	20	30	40	50	60
m042.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
a042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVDSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
m042.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRRCR					
a042	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRRCR					
	130	140	150	160	170	180

```

a042      |||||
          AARASLPKIRAKVSICFSP LVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          130      140      150      160      170      180

          190      200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          |||||
a042      ASXSGSNSVPTVAALSNAGCKX
          190      200

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 042 shows 93.0% identity over a 201 aa overlap with a predicted ORF (ORF 042.ng) from *N. gonorrhoeae*:

m042/g042

```

          10      20      30      40      50      60
m042.pep  MTMICLRFQAFVPTSA LSXTSTAAGXSCPM AAVRSMMKIQSGFFSLMY SKETGCPCPSL
          |||||
g042      MTMICLRFQAFVPTSA LSNTSTAAGPSCPMA AAVRSMMKIQPGFFSLMY SKETGCPCPSL
          10      20      30      40      50      60

          70      80      90      100     110     120
m042.pep  RKDSSTGGRPMSPCIQLANRDCVPKADTLLP VTDSTSPRPLPLAASRVWANSASICAFNS
          |||||
g042      RKDSSTGGRPMSPCIQLANRDCVPKADTLLP VTDSTSPRPLPLAASRFWANSASICAFNS
          70      80      90      100     110     120

          130     140     150     160     170     180
m042.pep  AARASLPKIRAKVSICFSP LVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSXGLXRCR
          |:||||| :|||
g042      ATRASLPKIRD RVSICFSP LVRILPLSTV KSMVVAFFANC SYASAPGPPVMTN CGLWRCR
          130     140     150     160     170     180

          190     200
m042.pep  ASXSGSNSVPTVAALSNAGCKX
          | |||||
g042      DSQSGSNSVPTVAALSNAGCKX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 171>:

m042-1.seq

```

1   ATGACGATGA TTTGCTTGCG CTTCCAAGCG TTCGTGCCGC GTACCAGCGC
51  GTTATCCAAT ACTTCGACAG CCGCCGGCCC TTCCTGCCCG ATGGCGGCGG
101 TACGGTCGAT GATGAAAATC CAATCGGGGT TTTTCTCTTT GATGTATTCTG
151 AAGGAAACAG GCTGCCCGTG CCCCTCGTTG CGTAAAGATT CGTCTACAGG
201 CGGTAGGCCG ATGTCGCCGT GTATCCAACT TGCCAACCGC GACTGCGTGC
251 CGAAGCGGGA CACCTTGTTG CCCGTAACCG ACAGCACCAG CCCGCGTCTT
301 TTGCCTTTGG CGGCTTCGCG CGTTTGGGCG AACAGCGCGT CAATCTGCGC
351 CTTCAATTCC GCCGCGCGCG CTTCCTTGCC GAAAATCCGC GCCAAGGTCT
401 CCATCTGCTT TTCGCCGCTG GTGCGGATAT TGCCGTTGTC CACCGTCAGA
451 TCTATGGTGG TCGCGTTTTT CGCTAACTGT TCATACGCTT CCGCGCCCGG
501 CCCGCCGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 172; ORF 042-1>:

m042-1.pep

```

1   MTMICLRFQA FVPTSA LNSTAAGPSCP MAAVRSMMKI QSGFFSLMY
51  KETGCPPSL RKDSSTGGRP MSPCIQLANR DCVPKADTLL PVDSTSPRP
101 LPLAASRVWA NSASICAFNS AARASLPKIR AKVSICFSP LVRILPLSTVR
151 SMVVAFFANC SYASAPGPPV MTS*

```

m042-1/g042 95.4% identity in 173 aa overlap



240

	10	20	30	40	50	60
m042-1.pep	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	:					
g042	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
g042	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	:     :					
g042	ATRASLPKIRDVSICFSPLVRILPLSTVKSMVVAFFANC SYASAPGPPVMTNCGLWRCR					
	130	140	150	160	170	180
g042	DSQSGSNSVPTVAALSNAGCKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 173>:

a042-1.seq

1	ATGACGATGA	TTTGCTTGCG	CTTCCAAGCG	TTCGTGCCGC	GTACCAGCGC
51	GTTATCCAAT	ACTTCGACAG	CCGCCGGCCC	TTCCTGCCCG	ATGGCGGCGG
101	TACGGTCGAT	GATGAAAATC	CAATCGGGGT	TTTTCTCTTT	GATGTATTCTG
151	AAGGAAACAG	GCTGCCCGTG	CCCCTCGTTG	CGTAAAGATT	CGTCTACAGG
201	CGGTAGGCCG	ATGTCGCCGT	GTATCCAAC	TGCCAACCGC	GACTGCGTGC
251	CGAAGGCGGA	CACCTTGTTG	CCCCTAACCG	ACAGCACCAG	CCCGCGTCTT
301	TTGCCTTTGG	CGGCTTCGCG	CGTTTGGGCG	AACAGCGCGT	CAATCTGCGC
351	CTTCAATTCC	GCCGCGCGCG	CTTCCTTGCC	GAAAATCCGC	GCCAAGGTCT
401	CCATCTGCTT	TTGCGCGCTG	GTGCGGATAT	TGCCGTGTGC	CACCGTCAGA
451	TCATATGGTG	TCGCGTTTTT	CGCCAACGT	TCATACGCTT	CCGCGCCCGG
501	CCCGCCGGTA	A			

This corresponds to the amino acid sequence <SEQ ID 174; ORF 042-1.a>:

a042-1.pep

1	MTMICLRFOA	FVPRTSALSN	TSTAAGPSCP	MAAVRSMMKI	QSGFFSLMYS
51	KETGCPCPSL	RKDSSTGGRP	MSPCIQLANR	DCVPKADTLL	PVTDTSTSPR
101	LPLAASRVWA	NSASICAFNS	AARASLPKIR	AKVSICFSPL	VRILPLSTVR
151	SMVVAFFANC	SYASAPGPPV	MTS*		

m042-1/a042-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
m042-1.pep	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
a042-1	MTMICLRFOAFVPRTSALSNTSTAAGPSCPMAAVRSMMKIQSGFFSLMYSKETGCPCPSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m042-1.pep	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
a042-1	RKDSSTGGRPMSPCIQLANRDCVPKADTLLPVTDTSTSPRPLPLAASRVWANSASICAFNS					
	70	80	90	100	110	120
	130	140	150	160	170	
m042-1.pep	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
a042-1	AARASLPKIRAKVSICFSPLVRILPLSTVRSMVVAFFANC SYASAPGPPVMTSX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 175>:

## g043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GTCGGCCCAT CAGCACTTTT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GCCTGAACGC TTCgttgaAC
101 CGTCCCGCGT ggcggtagcc gcAAAAGTGC ATcGCGGCTT GGATGGTGCT
151 GCCCGATTCTG ATGAGGGGcga gcGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201 GTCCGCGGAC GGTTCGCCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCTGTTCA GCCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGGCG
301 GGC GAATTCTG CTGTTCAAAA TATCGGCGGC TTCGTCTATG CGCCGGCGGC
351 GGTAGCCGTT GTCGTGGCGG CGGAAGGTGA AGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 176; ORF 043.ng>:

## g043.pep

```

1 MVVSNQNIYA VGPSALFHIR RQKSVMPPER FVEPSRVAVA AKVHRGLDGA
51 ARFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQFDA AGDFGDGQRA
101 GEFVQNIIGG FVYAPAAVAV VVAEGEA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 177>:

## m043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT
151 GCCCGATTCTG ATGAGGGCGA GCGCGTGTTC CAGCCGCAGG CGGCGCAGGC
201 ATCCGCGGAC GGTTCGCCG GTTTGCGCTT TGAAATAGCG TTTCAGGTAG
251 CATTCTGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGC GAATTCTG TGTTCAGGA TGTGCGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAAACGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 178; ORF 043>:

## m043.pep

```

1 MVVSNQNIYA AGPSALLHIR RQKSVMPSEF FVEPSRVAVA AKVHGGLDGA
51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAEGEAQ*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 043 shows 89.8% identity over a 128 aa overlap with a predicted ORF (ORF043.a) from *N. gonorrhoeae*:

## m043/g043

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSEFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	:     :     :     :     :     :					
g043	MVVSNQNIYAVGPSALFHIRRQKSVMPPERFVEPSRVAVAAKVHRGLDGAARFDEGERVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	:     :     :     :     :     :					
g043	QPQAAQASGDGFAGLRFEIAFQVAFVQPDAAAGDFGDGQAGEFAVQNIIGGFVYAPAAVAV					
	70	80	90	100	110	120
	130					
m043.pep	VVAEGEAQX					
g043	VVAEGEAXX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 179>:

## a043.seq

```

1 ATGGTTGTTT CAAATCAAAA TATCTATGCC GCCGGCCCT CAGCACTTCT
51 TCACATCCGA AGGCAAAAAT CCGTAATGCC GTCTGAACGC TTCGTTGAAC
101 CGTCCCGCGT GCGGGTAGCC GCAAAAGTGC ATGGCGGCTT GGACGGTGCT

```

242

```

151 GCCGGATTTCG ATGAGGGCGA GCGCGTGTTT CAGCCGCAGG CGGCGCAGGC
201 ATCCGGCGAC GGTTCGCGG GTTTGCCTT TGAAATAGCG TTTCAGGTAG
251 CATTCGTTCA GTCCGACGCG GCGGGCGATT TCGGCGATGG TCAGCGGACG
301 GGCGAATTTCG TGTTCAGGA TGTCGGCGGC TTCGTCTATG CGCCGACGGC
351 GGTAACCGTT GTCGTGGCGG CGGAAGGTGA AGCGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 180; ORF 043.a>:

```

a043.pep
  1 MVVSNQNIYA AGPSALLHIR RQKSVMPSER FVEPSRVAVA AKVHGGLDGA
 51 AGFDEGERVF QPQAAQASGD GFAGLRFEIA FQVAFVQSDA AGDFGDGQRT
101 GEFVLQDVGG FVYAPTAVTV VVAAEGEAQ*

```

m043/a043 100.0% identity in 129 aa overlap

	10	20	30	40	50	60
m043.pep	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
a043	MVVSNQNIYAAGPSALLHIRRQKSVMPSERFVEPSRVAVAAKVHGGLDGAAGFDEGERVF					
	10	20	30	40	50	60
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
m043.pep	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
a043	QPQAAQASGDGFAGLRFEIAFQVAFVQSDAAGDFGDGQRTGEFVLQDVGGFVYAPTAVTV					
	70	80	90	100	110	120
m043.pep	VVAAEGEAQX					
a043	VVAAEGEAQX					
	130					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 181>:

```

g044.seq
  1 ATGCTGCCCG ACCAGAGCGT CGAGTTCTTG CCACAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GCGGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCGTTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGCC TCGATAACG GCGGTCAGCT
201 CCATGCGGTT GTTGGTGGTT TGCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 CGGCTGCCGT AGCGCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 182; ORF 044.ng>:

```

g044.pep
  1 MLPDQSVEFL PQVVVFDGLF GGGFPAVALP TVYPVFHAVF DVLRVGADDD
 51 GAAAFERFQP FDNGGQLHAV VGGLRFAAEK FFFAAVAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 183>:

```

m044.seq
  1 ATGCCGTCCG ACTAGAGCGT CGAGTTCTTT CCAGAAGTCG TCGTTTTTGA
 51 CGGGCTGTTT GGAGGCGGTT TTCCAGCCGT TCGCTTCCA ACCGTGTATC
101 CAGTTTTCCA TGCCATTTTT GACGTATTGC GAGTCGGTGC AGATGATGAC
151 GGTGCAGCGG CGTTTGAGCG ATTTTCAGTCC TCGATGACG GCAGTCAGTT
201 CCATGCGGTT GTTGGTGGTT TGCGCTTCGC CGCCGAAAAG TTCTTTTTCG
251 TGGTACCGT AGCGCAyTaa

```

This corresponds to the amino acid sequence <SEQ ID 184; ORF 044>:

```

m044.pep
  1 MPSPDXSVEFF PEVVVFDGLF GGGFPAVALP TVYPVFHAI F DVLRVGADDD
 51 GAAAFERFQS FDDGSQFHAV VGGLRFAAEK FFFVATVAH*

```



244

501 GG TAGAACCT ACCTGCCCGT TGCCTAAAAT GAGGATTTTC ACGGTATGGG  
551 TCGCCGGGTG A

This corresponds to the amino acid sequence <SEQ ID 188; ORF 046.ng>:

g046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSL RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RYNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLVM AARFCATVEP TCPLPKMRIF TVWVAG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 189>:

m046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAst CCGC.r.sGC gCGcCTGTAT  
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC  
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG  
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTGTGT  
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG  
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG  
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC  
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCGCGTTG CCGAAAACGG  
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG  
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC  
501 GG TAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG  
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 190; ORF 046>:

m046.pep

1 MSAMLRPTSX PXRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSL RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 191>:

a046.seq

1 ATGTCGGCAA TGCTGCGTCC GACAAGCAGT CCGCCGCGCC GCGCCTGTAT  
51 GATGACCATC CGCACGCGGT CGTCTGCAAA ACGTAAAACC TGCAATGCGC  
101 CCGGGCAGTC TATCAGGCCG GCAAGCTGTT CGGTAACGAG CTGTTCCGGG  
151 CTGATGGTTT CGGTTATGCC GAATATGGAA AGGCTGCCGT TTTCGTGTGT  
201 TTCGAGCTTG GGGCTGAGGT ATTCGAGGTA TTCGCTGGAA CGGACGCGCG  
251 CGATGCGGCC GGGGATGTTG AACAGGTCGG CGGCAACTTT GCAGGCGACG  
301 ATGTTGGTTT CGTCGCTGCG GGAGAGCGCG AGCAGCAAGT CGGCATCTTC  
351 CGCGCCGGCG CGTTCTAATG TGAAGGGGGA TCGCGCGTTG CCGAAAACGG  
401 TTTGGACATC GAGGCGGCTG CCTGTTTCCT GCAATGCTTT TTCGTCGATG  
451 TCGATAACGG TTACGTCGTT GTTGGGTATG GCGGCAAGGT TTTGTGCGAC  
501 GG TAGAACCT ACCTGTCCGT TGCCTAAAAT GAGGATTTTC ACGGTGTGGG  
551 TCGCCGAGTG A

This corresponds to the amino acid sequence <SEQ ID 192; ORF 046.a>:

a046.pep

1 MSAMLRPTSS PRRACMMTI RTRSSAKRKT CNAPGQSIRP ASCSVTSCSG  
51 LMVSVMPNME RLPFSLFSSL GLRYSRYSL RTRAMRPGML NRSAATLQAT  
101 MLVSSLRESA SSKSASSAPA RSNVKGDAPL PKTVWTSRRL PVSCNAFSSM  
151 SITVTSLLGM AARFCATVEP TCPLPKMRIF TVWVAE\*

m046/a046 98.4% identity over a 186 aa overlap

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					
a046	MSAMLRPTSSPPRRACMMTIRTRSSAKRKT CNAPGQSIRP ASCSVTSCSG LMVSVMPNME					

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	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
a046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
a046	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
a046	TVWVAEX					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 046 shows 97.3% identity over a 185 aa overlap with a predicted ORF (ORF 046.ng) from *N. gonorrhoeae*:

m046/g046

	10	20	30	40	50	60
m046.pep	MSAMLRPTSPXXRACMMTIRTRSSAKRKTGNAPGQSIRPASCSTSCSGLMVSVMPNME					
g046	MSAMLRPTSPPPRACMMTIRTRSSAKRKTGNAPGQSIRPASCSTSCSGLMVSVMPNME					
	10	20	30	40	50	60
m046.pep	70	80	90	100	110	120
	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
g046	RLPFSLFSSLGLRYSRYSLETRAMRPGMLNRSAAATLQATMLVSSLRESASSKSASSAPA					
	70	80	90	100	110	120
m046.pep	130	140	150	160	170	180
	RSNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLGMAARFCATVEPTCPLPKMRIF					
g046	RYNVKGDAPLPKTVWTSRRLPVSCNAFSSMSITVTSLLVMAARFCATVEPTCPLPKMRIF					
	130	140	150	160	170	180
m046.pep	TVWVAEX					
g046	TVWVAGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 193>:

g047.seq

1	ATGGTCATCA	TACAGGCGcg	gcGCGGCGGG	CTGCTTGTCG	GACGCAGCAT
51	TGCCGACATC	GCCCAAGATT	TGCCCGACGG	GGCCGACTGC	CAAATCTGCG
101	CCGTTTACCG	CAACAACCGC	CTCATCGTCC	CCGCGCCGCA	AACCGTCATC
151	ATCGAAGGCG	ACGAAATCCT	GTTTGCCGCC	GCCGCGGAAA	ACATCGGGGC
201	GGTCATACCc	gaATTGCGCC	CCAAAGAAAC	CAGCACCCGC	CGCATCATGA
251	TTGCCGCGCG	CGGCAACATc	tgctACCGCC	TCGCCAAGCA	GCTCGAACAC

```

301 GCATAcacG TCAAAATCAT CGAATGCCGG CCGCGCcggtg ccgaATGGAT
351 AGCCGAAAC ctcgAcaaCA CCCTCGTCCT GCAAGGTTTCG Gcaaccgacg
401 aAaccctgct cgAcaacgaa tacatcgacg aaatcgaCGT ATTCTGCGCC
451 CTGACCAACG ACGACGAAAG CAACATTAtg tCCGCCCTTT TGGCGAAAAA
501 CCTcggcgCG AAGCgcgtca tcggCATCGT CAACCGCTCA AGCTACGTCG
551 ATTTGCTCGA AGGCAACAAA ATCGACATCG TCGTCTCCCC CCACCTCATC
601 ACCATCGGCT CGATACTCGC CCACATCCGG CGCGGCGACA TCGTTGCCGT
651 CCACCCCATC CGGCGCGGCA CGGCGGAAGC CATCGAAGTC GTCGCGCAGC
701 GCGACAAAAA AACTTCCGCC ATCATCGGCA GGCGCATCAG CGGCATCAAA
751 TGGCCCGAAG GCTGCCACAT TGCCGCCGTC GTCCGCGCCG GAACCGGCGA
801 AACCATTATG GGACACCATA CCGAAACCGT CATCCAAGAC GGTGACCACA
851 TCATCTTTTT CGTCTCGCGC CGGCGCATCC TGAACGAACT GGAGAAATC
901 ATCCAAGTCA AAATGGGCTT TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 194; ORF 047.ng>:

g047.pep

```

1 MVIIQARRGG LLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETSTR RIMIAGGGNI CYRLAKQLEH
101 AYNVKIIECR PRRAEWIAEN LDNTLVLQGS ATDETLLDNE YIDEIDVFCA
151 LTNDDESNI M SALLAKNLGA KRVIGIVNRS SYVDLLEGNK IDIVVSPHLI
201 TIGSILAHIR RGDIVAVHPI RRGTAEAIEV VAHGDKKTS A IIGRRISGIK
251 WPEGCHIAAV VRAGTGETIM GHHTETVIQD GDHIIFFVSR RRILNELEKL
301 IQVKMGFFG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 195>:

m047.seq

```

1 ATGGTCATCA TACAGgCGcG C..syGCGGA sTGCTTGTCTG GACGCAGCAT
51 TGCCGACATC GCCCAAGATT TGCCCGACGG GGCCGACTGC CAAATCTGCG
101 CCGTTTACCG CAACAACCGC CTCATCGTCC CCGCGCCGCA AACCCTCATC
151 ATCGAAGGCG ACGAAATCCT ATTTGCCGCC GCCGCCGAAA ACATCGGCGC
201 GGTCAATCCC GAATTGCGCC CCAAAGAAAC CCAAAGAAAC CAGCcCmgmm
251 GcATCATGAT TkCCGGCGGC GGCAACATCG GCTACCGTCT CGCCAAGCAG
301 CTCGAACACG CATACAACGT yAAATCATC GAATGCCGGC CGCGCCGTGC
351 CGAATGGATA GCCGAAAACC TCGACAACAC CCTCGTcyTG CAAGGTTTCG
401 CAACCGACGA AACCTTGCTC GACAACGAAT ACATCGACGA AATCGACGTA
451 TTCTGCGCCC TGACCAACGA CGACGAAAGC AACATTATGT CCGCCCTTTT
501 GCGGAaAAAC CTCGGCGCGA AGCGCGTCAT CGGCATCGTC AACCCTCAA
551 GCTACGTCGA TTTGCTCGAA GGCAACAAA TCGACATCGT CGTCTCCCCC
601 CACCTCATCA CCATCGGCTC GATACTCGCC CACATCCGGC GCGGCGACAT
651 CGTGCGCGTC CACCCATCC GCGCGGCAC GGCGGAAGCC ATCGAAGTCG
701 TCGCACACGG CGACAAAAA ACTTCCGCCA TCATCGGCAG GCGCATCAGC
751 GGCATCAAAT GGCCCGAAGG CTGCCACATT GCCGCCGTCT TCCGCGCCGG
801 AACC GGCGAA ACCATTATGG GACACCATAC CGAAACCGTC ATCCAAGACG
851 GCGACCACAT CATCTTTTTC GTCTCGCGCC GGCGCATCCT GAACGAACTG
901 GAAAACTCA TCCAGGTCAA AATGGGCTTT TTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 196; ORF 047>:

m047.pep

```

1 MVIIQARXXG XLVGRSIADI AQDLPGADC QICAVYRNNR LIVPAPQTVI
51 IEGDEILFAA AAENIGAVIP ELRPKETQRN QPXXIMIXGG GNIGYRLAKQ
101 LEHAYNVKII ECRPRRAEWI AENLDNTLV L QGSATDETL DNEYIDEIDV
151 FCALTNDDES NIMSALLAKN LGAKRVIGIV NRSSYVDLLE GNKIDIVVSP
201 HLITIGSILA HIRRGDIVAV HPIRRGTAE A IEVVAHGDKK TSAIIGRRIS
251 GIKWPEGCHI AAVVRAGTGE TIMGHHTETV IQDGDHIIFF VSRRRIINEL
301 EKLIQVKMGF FG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 197>:

a047.seq

```

1 ATGGTCATCA TACAGGCGCG GCGCGGCGGA CTGCTTGTCTG GACGCAGCAT

```

```

51  TGCCGACATC  GCGCAAGATT  TGCCCGACGG  GGCCGACTGC  CAAATCTGCG
101 CCGTTTACCG  CAACAACCGC  CTCATCGTCC  CCGCGCCGCA  AACCGTCATC
151 ATCGAAGGCG  ACGAAATCCT  ATTTGCCGCG  GCCGCCGAAA  ACATCGGCGC
201 GGTCATACCC  GAATTGCGCC  CCAAAGAAAC  CAGCACCCGC  CGCATCATGA
251 TTGCCGCGCG  CGGCAACATC  GGCTACCGTC  TCGCCAAGCA  GCTCGAACAC
301 GCATACAACG  TCAAAATCAT  CGAATGCCGG  CCGCGCCGTG  CCGAATGGAT
351 AGCCGAAAAC  CTCGACAACA  CCCTCGTCCT  GCAAGGTTCT  GCAACCGACG
401 AAACCCTGCT  CGACAACGAA  TACATCGACG  AAATCGACGT  ATTCTGCGCC
451 CTGACCAACG  ACGACGAAAG  CAACATTATG  TCCGCCCTTT  TGGCGAAAAA
501 CCTCGGCGCG  AAGCGCGTCA  TCGGCATCGT  CAACCGCTCA  AGCTACGTCG
551 ATTTGCTCGA  AGGCAACAAA  ATCGACATCG  TCGTCTCCCC  CCACCTCATC
601 ACCATCGGCT  CGATACTCGC  CCACATCCGG  CGCGCGGACA  TCGTTGCCGT
651 CCACCCCATC  CGGCGCGGCA  CGGCGGAAGC  CATCGAAGTC  GTCGCACACG
701 GCGACAAAAA  AACTTCGCGC  ATCATCGGCA  GGCGCATCAG  CGGCATCAAA
751 TGGCCCGAAG  GCTGCCACAT  TGCCGCCGTC  GTCCGCGCCG  GAACCGGCGA
801 AACCATTATG  GGACACCATA  CCGAAACCGT  CATCCAAGAC  GGCGACCACA
851 TCATCTTTTT  CGTCTCGCGC  CGGCGCATCC  TGAACGAACT  GGAAAAACTC
901 ATCCAAGTCA  AAATGGGCTT  TTTCGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 198; ORF 047.a>:

```

a047.pep
1  MVIIQARRGG  LLVGRSIADI  AQDLDPGADC  QICAVYRNNR  LIVPAPQTVI
51  IEGDEILFAA  AAENIGAVIP  ELRPKETSTR  RIMIAGGGNI  GYRLAKQLEH
101 AYNVKIIECR  PRRAEWIAEN  LDNTLVLQGS  ATDETLLDNE  YIDEIDVFCA
151 LTNDDESNIM  SALLAKNLGA  KRIVIGVNR  SYVDLLEGNK  IDIVVSPHLI
201 TIGSILAHIR  RGDIVAVHPI  RRGTAEAEIV  VAHGDKKTS  IIGRRISGIK
251 WPEGCHIAAV  VRAGTGETIM  GHHTETVIQD  GDHIIFFVSR  RRILNELEKL
301 IQVKMGFFG*

```

m047/a047 96.5% identity over a 312 aa overlap

```

              10      20      30      40      50      60
m047.pep      MVIIQARXXGXLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA
              |||||  |  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a047           MVIIQARRGGLLVGRSIADIAQDLDPGADCQICAVYRNNRLIVPAPQTVIIIEGDEILFAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m047.pep      AAENIGAVIPELRPKETQRNPXXIMIXGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a047           AAENIGAVIPELRPKETSTR---IMIAGGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI
              70      80      90      100     110

              130     140     150     160     170     180
m047.pep      AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a047           AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNIMSALLAKNLGAKRVIGIV
              120     130     140     150     160     170

              190     200     210     220     230     240
m047.pep      NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a047           NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK
              180     190     200     210     220     230

              250     260     270     280     290     300
m047.pep      TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a047           TSAIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRRILNEL
              240     250     260     270     280     290

              310
m047.pep      EKLIQVKMGFFGX
              |||||  |||||

```



248

a047 EKLIQVKMGFFGX  
300 310

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 047 shows 96.2% identity over a 312 aa overlap with a predicted ORF (ORF 047.ng) from *N. gonorrhoeae*:

m047/g045

m047.pep	MVIIQARXXGXLVGRSIADIAQDLPGADCQICAVYRNRLIVPAPQTVIIEGDEILFAA	60
g047	MVIIQARRGGLLVGRSIADIAQDLPGADCQICAVYRNRLIVPAPQTVIIEGDEILFAA	60
m047.pep	AAENIGAVIPELRPKETQRNPXXIMIXGGNIGYRLAKQLEHAYNVKIIIECRPRRAEWI	120
g047	AAENIGAVIPELRPKETSTRR---IMIAGGGNICYRLAKQLEHAYNVKIIIECRPRRAEWI	117
m047.pep	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNISSALLAKNLGAKRVIGIV	180
g047	AENLDNTLVLQGSATDETLLDNEYIDEIDVFCALTNDDESNISSALLAKNLGAKRVIGIV	177
m047.pep	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK	240
g047	NRSSYVDLLEGNKIDIVVSPHLITIGSILAHIRRGDIVAVHPIRRGTAEAEIVVAHGDKK	237
m047.pep	TSIIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRLNEL	300
g047	TSIIIGRRISGIKWPEGCHIAAVVRAGTGETIMGHHTETVIQDGDHIIFFVSRRLNEL	297
m047.pep	EKLIQVKMGFFGX	313
g047	EKLIQVKMGFFGX	310

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 199>:

g048.seq

1	ATGCTCGACA AAGGCGAGGA GTTGCCCGTC GATTTCACCA ACCGCCTGAT
51	TTACTACGTC ggcCCcgTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG
101	CAGGTCCGAC CACAGCCACC CGCATGGACA AATTACCCG CCAAATGCTC
151	AAACAAACCG GCCTCTTGGG CATGATCGGC AAATCCGagc gcgGcgcggc
201	cacctGCGAA GCcatCGCCG ACAACAAGGC CGTGTACCTC ATGGCAGTCG
251	GCGGCGCGGC ATACCTCGTG GCAAAAGCCA TCAAATCTTC CAAAGTCTTG
301	GCGTCCCCG AATTGGGTAT GGAAGCCGTT TACGAATTG AAGTCAAAGA
351	TATGCCCGTA ACCGTCGCCG TGGACAGCAA AGGCGAATCC ATCCACGCCA
401	CCGCCCCGCG CAAATGGCAG GCGAAAATCG GCATCATCCC CGTCGAGTCT
451	TGA

This corresponds to the amino acid sequence <SEQ ID 200; ORF 048.ng>:

g048.pep

1	MLDKGEELPV DFTNRLIYYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51	KQTGLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101	AFPELGMEAV YEFVKKMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151	*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 201>:

m048.seq

1	ATGCTCAACA AAGGCGAAGA ATTGCCCGTC GATTTCACCA ACCGCCTGAT
51	TTACTACGTC GGCCCCGTCG ATCCGGTCGG CGATGAAGTC GTCGGTCCCG

м048. пер

```

1 MLNKGEELPV DFTNRLIIYV GPVDPVGDEV VGPAGPTTAT RMDKFTRQML
51 EQTDLLGMIG KSERGVATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 APPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPRKWQ AKIGIIPVES
151 *

```

a048.seq

1	ATGCTCGACA	AAGGCGAAGA	ATTGCCCGTC	GATTTCACCA	ACCGCCTGAT
51	TTACTACGTC	GGCCCCGTCG	ATCCGGTCGG	CGACGAAATC	GTGGGCCCAG
101	CAGGTCGCCAG	CACCGCCACG	CGCATGGACA	AATTCAACCG	CCAAATGCTC
151	GAACAAACCG	ACCTCTTGGG	CATGATCGGC	AAATCCGAGC	GCGGCGCGGC
201	CACCTGCGAA	CGCATCGCCG	ACAAACAAAGC	CGGTACTCTC	ATGGCAGTCG
251	GCGGCGCGGC	GTATCTCGTG	GCAAAAGCCA	TCAATCTTTC	CAAAGTCTTG
301	GCGTTCCCG	AATTGGGCAT	GGAAGCCATT	TACGAATTTG	AAGTCAAAGA
351	CATGCCCCGA	ACCGTCGCGG	TAGACAGCAA	AGGCGAATCC	ATCCAGGCCA
401	CCGCCCCGCC	CCAATGGCAG	GCGAAAATCG	GCATCATCCC	CGTCAAATCT
451	TGA				

a048.pep

```

1  MLDKGEELPV DFTNRLIYYV GPVDPVGDEI VGPAGPTTAT RMDKFTRQML
51  EQTDLLGMIG KSERGAATCE AIADNKAVYL MAVGGAAYLV AKAIKSSKVL
101 AFPELGMEAI YEFEVKDMPV TVAVDSKGES IHATAPPQWQ AKIGIIPVKS
151 *

```

	10	20	30	40	50	60
m048.pep	MLNKG	EELPVD	FTNRLI	YYVGP	VDVPG	DEVVGPAGPTTAT
	:					
a048	MLDKG	EELPVD	FTNRLI	YYVGP	VDVPG	DEIVGPAGPTTAT
	10	20	30	40	50	60
	70	80	90	100	110	120
m048.pep	KSERGV	ATCEAI	ADNKAV	YILMAV	GGAAYL	VAKAIKSSKVLAF
	:					
a048	KSERGA	ATCEAI	ADNKAV	YILMAV	GGAAYL	VAKAIKSSKVLAF
	70	80	90	100	110	120
	130	140	150			
m048.pep	TVAVDS	KGESIH	ATAPRK	WQAKIG	IIPVES	XX
a048	TVAVDS	KGESIH	ATAPPQ	WQAKIG	IIPVKS	XX
	130	140	150			

ORF 048 shows 96.4% identity over a 150 aa overlap with a predicted ORF (ORF 048.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 205>:

This corresponds to the amino acid sequence <SEQ ID 206; ORF 049.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 207>:

This corresponds to the amino acid sequence <SEQ ID 208; ORF 049>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 209>:

a049.seq

a049.pcp

**m049/a049** 90.6% identity over a 139 aa overlap

m049/g049

	10	20	30	40	50	60
m049.pep	MRAQAFDQPFQGQLLFGQAEHFAPVDGFRVQDIDLDLGHQRFFRIVFPVFNRRLIRAGFCL					
	:     :     :					
g049	MRAQAFDQPFQGQLLFGQAEHFAPVDGFRVQDIDLDLGHQRLEFRTAFVFRNPVCRRGTGFCR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m049.pep	VGVFFAPFNLSGFKFDTVFFGIGKPDSPPRFDVFFRNRLHQSLRVEPVFLKDDHRVGFDFL					
	:     :     :     :     :     :					
g049	IGVFFPALNLCGFKFGTVFFGIEPDSPPRFDVFFRNRLHQSLRVEPVFLKDDHRVGFDFL					
	70	80	90	100	110	120
	130	139				
m049.pep	AAIGNGGIVFLLPFFQIRL					
	:     :					
g049	AAIGNGAVVFFLPFLQIRLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 211>:

## g050.seq

```

1 atgggCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGg
51 cagccccGAA AAAGccgtgt TGATGGcaaA AGAATCCCTG ATGAGCCACA
101 TCGAcatCca aGaATTGCAG GAAAAAGCCG CGTccggggc ggaattgtcc
151 accaccgaAG ccCTGCGCCT cGAACTCTTT GAAAAGGTCA ACGCGCTGGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAT GCCGCCTCCA AACCGATTGC CATGATTCCC
301 AACTGTGCcg ccacCCGcca cgtcgAATTT GAATTGgACG GCTCAGGtcc
351 TGTCGAactc acgccGCcgc gtgtCGAAGA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 212; ORF 050.ng>:

## g050.pep

```

1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATHRVEF ELDGSGPVEL TPRVED*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 213>:

## m050.seq

```

1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGTATCG GCATCGGCGG
51 C..agCCgAA AAAGCCGTGC TGATGGCAAA AGAGTCCCTG ATGAGCCACA
101 TCGACATTCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GgAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTGGG
201 CATCGGCGCA CAAGGCTTGG GCGGACTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA TCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA TGGCCCGATT TGA

```

This corresponds to the amino acid sequence <SEQ ID 214; ORF 050>:

## m050.pep

```

1 MGAGWCPPGI LGIGIGGXAE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATHRVEF ELDGSGPVEL TPRVEDGPI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 215>:

## a050.seq

```

1 ATGGGCGCGG GCTGGTGTCC TCCCGGCATC TTGGGCATCG GCATCGGCGG
51 TACGCCCGAA AAAGCCGTGT TGATGGCGAA AGAATCCCTG ATGAGCCACA
101 TCGACATCCA AGAATTGCAG GAAAAGGCCG CGTCCGGCGC GGAATTGTCC
151 ACCACCGAAG CCCTGCGCCT CGAACTCTTT GAAAAGTCA ACGCGCTAGG
201 CATCGGCGCG CAAGGCTTGG GCGGTCTGAC CACCGTGTG GACGTGAAAA
251 TCCTCGATTA CCCGACCCAC GCCGCCTCCA AACCGATTGC CATGATTCCG
301 AACTGCGCCG CCACCCGCCA CGTCGAATTT GAATTGGACG GCTCAGGCCC
351 TGTCGAACTC ACGCCGCCGC GCGTCGAAGA CTGGCCC

```

This corresponds to the amino acid sequence <SEQ ID 216; ORF 050.a>:

## a050.pep

```

1 MGAGWCPPGI LGIGIGGTPE KAVLMAKESL MSHIDIQELQ EKAASGAELS
51 TTEALRLELF EKVNALGIGA QGLGGLTTVL DVKILDYPH AASKPIAMIP
101 NCAATHRVEF ELDGSGPVEL TPRVEDWP

```

m050/a050 97.7% identity over a 129 aa overlap

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESLS	MSHIDIQELQ	EKAASGAELST	TTEALRLELF		
a050	MGAGWCPPGILGIGIGGTPEKAVLMAKESLS	MSHIDIQELQ	EKAASGAELST	TTEALRLELF		

253

	10	20	30	40	50	60
m050.pep	70	80	90	100	110	120
	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
a050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
a050	TPPRVEDWP					

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 050 shows 98.4% identity over a 127 aa overlap with a predicted ORF (ORF 050.ng) from *N. gonorrhoeae*:

m050/g050

	10	20	30	40	50	60
m050.pep	MGAGWCPPGILGIGIGGXAEKAVLMAKESIMSHIDIQELQEKAASGAELSTTEALRLELF					
g050	MGAGWCPPGILGIGIGGTPEKAVLMAKESIMSHIDIQELQEKAASGAELSTTEALRLELF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m050.pep	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
g050	EKVNALGIGAQGLGGLTTVLDVKILDYPHTAASKPIAMIPNCAATRHVEFELDGSGPVEL					
	70	80	90	100	110	120
	130					
m050.pep	TPPRVEDGPIX					
g050	TPPRVEDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 217>:

g050-1.seq

```

1  ATGACCGTTA TCAAGCAAGA AGACTTTATT CAAAGTATCT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCAAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCCGCCG CCAAAGACGC GATGACGCG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCCGAA AACACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCTCAA AGTCGGTATG GATGTGCAAT
251 GGGATGCCGA CATGAGCGTG GAAAAGATGG TTAACGAAGG CGTACGCCGC
301 GCCTACACTT GGAAGGCCAA CACCCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCCAAAACA CCAAAGACAA CACCCCGCCG GTCATCCACA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGC GGCTCTG AAAACAAATC CAAACTCGCT ATGCTCAACC CTTCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACGATGGGC GCGGGCTGTT
551 GTCTCCCGG CATCTTGGGC ATCGGCATCG GCGGCAGcC CGAAAAGCC
601 GTGTGATGG cgaAAGAATC CCTGATGAGC CACATCGACA TCCAAGAATT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAG GTCAACGCGC TGGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGACGTG AAAATCCTCG ATTACCCGAC
801 CCATGCCGCC TCCAAACCGA TTGCCATGAT TCCCAACTGT GCCGCCACCC
851 GCCACGTGCA ATTTGAATTG GACGGCTCAG GTCCTGTGCA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGACC CGATCTGACT TACAGCCCCG ACAACGCCAA
951 ACGCGTCGAT GTCGATAAGC TGACCAAAGA AGAAGTGGCA AGCTGAAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCGG CCGCGATGCC
1051 GCGCACAAAC GCCTCGTCAA TATGCTCGAC AAAGCGAGG AGTTGCCCGT
1101 CGATTTACCC AACCGCCTGA TTTACTACGT CGGCCCGTGC GATCCGGTCG
1151 GCGATGAAGT CGTCGGTCCC GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTTACCC GCCAAATGCT CAAACAAACC GGCCTCTTGG GCATGATCGG

```

```

1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAACAAGG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CATACCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGGTTCCCG GAATTGGGTA TGGGAAGCCGT
1401 TTACGAATTT GAAGTCAAAG ATATGCCCGT AACCGTCGCC GTGGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG GCAAATGGCA GCGGAAAATC
1501 GGCATCATCC CCGTCGAGTC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 218; ORF 050-1.ng>:

g050-1.pep

```

1  MTFVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVG M DVQWDADMSV EKMVNEGVRR
101 AYTWEGNTR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCRAKG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMKESLMS HIDIQELQEK AASGAELST EALRLELF EK VNALGIGAQQ
251 LGGLTTVL DV KILDYPTHA A SKPIAMIPNC AATRHVEF EL DSGSPVELTP
301 PRVED*PDLT YSPDNGKRV DDKLTKEE VA SWKTGDVLL NGKILTGRDA
351 AHKRLVNMLD KGEELPVDF T NRIIYVGPV DPVGDEVV GP AGPTTATRMD
401 KETRQMLKQT GLLGMIGK SE RGAATCEA IA DNKAVYLM AV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAVY EF EVKDMPTV TA VDSKGESI HA TAPRKWQAKI
501 GIIPVES*

```

g050-1/p14407

```

sp|P14407|FUMB_ECOLI FUMARATE HYDRATASE CLASS I, ANAEROBIC (FUMARASE)
>gi|280063|pir|B44511 fumarate hydratase (EC 4.2.1.2) fumB, iron-dependent - Escherichia coli
>gi|146048 (M27058) anaerobic class I fumarase (EC 4.2.1.2) [Escherichia coli] Length = 548
Score = 172 bits (432), Expect = 4e-42
Identities = 138/488 (28%), Positives = 216/488 (43%), Gaps = 22/488 (4%)

```

```

Query: 11 QSIDAFQFISYHHPKDYIDALYKAWQKEENPAKDAMTQILVNSRMCAENNRPICQDTG 70
Q+ DA + H K L+ E + K Q L NS + A+ P CQDTG
Sbjct: 53 QAFHDAFMLRPAHQQVAAILHDPEASEND---KYVALQFLRNSEIAAKGVLPCTCQDTG 109

```

```

Query: 71 IATVFLKVGMDVQWDADMSVEKMVNEGVRRAYTWEGNTRASVLADPAGKRQNTKDNTPA 130
A + K G V W E+ +++GV Y E N + A K NT N PA
Sbjct: 110 TAIIVGKKQQRV-WTGGGD-EETLSKGVNTYI-EDNLRYSQNAALDMYKEVNTGTNLPA 166

```

```

Query: 131 VIHMSIVPGGKVEVTCRAKGGGSENKSKL-----AMNPSDNIVDWVLKTIPTMGAGWCP 185
I + V G + + C AKGGGS NK+ L A+L P + +++++ + T+G CP
Sbjct: 167 QIDLYAVDGDGEYKFLCVAKGGGSANKTYLYQETKALLTPG-KLKNFLVEKMRTLGTAAAC 225

```

```

Query: 186 PXXXXXXXXXTPEKAVLMKESLMSHIDIQELQEKAAAGELSTTEALRLELFKVNXXX 245
P T + L + +H EL + + L EL E+
Sbjct: 226 PYHIAFVIGGTS AETNLKTVKLASAHY-YDELPTGEGNEHQAFRDVQLEQELLEEAQKLG 284

```

```

Query: 246 XXXXXXXXXXXXTVLDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGGSG----PVELTPP 301
D++++ P H AS P+ M +C+A R+++ +++ G +E P
Sbjct: 285 LGAQFGGKYFAH-DIRVIRLPRHGASCPVGMGVSCSADRNIKAKINREGIWIIEKLEHNPG 343

```

```

Query: 302 RVEDXPDLTYSPDNGKRVVDKLTKE---EVA SWKTGDVLLNGKILTGRDAAHKRLVNM 358
+ +VD+++ KE +++ + L L G I+ GRD AH +L +
Sbjct: 344 QYIPQELRQAGEGEAVKVDLNRPMKEILAQLSQYPVSTRLSLTGTIIIVGRDIAHAKLKL 403

```

```

Query: 359 LDKGEELPVDFNRIIYXXXXXXXXXXXXXXXXXXTTATRMDKFTQMLKQTGLLGMIGK 418
+D G+ELP + IYY TTA RMD + + G + M+ K
Sbjct: 404 IDAGKELPQYIKDHPYIYAGPAKTPAGYPSGLPPTAGRMDSYVDLLQSHGGSMIMLAK 463

```

```

Query: 419 SERGAATCEAIADNKAVYLMVAVGG-AAYLVAKAIKSSKVLAPFELGMEAVYEFVVKMPV 477
R +A + YL ++GG AA L ++IK + +A+PELGMEA+++ EV+D P
Sbjct: 464 GNRSQQVTDACHKHGGFYLGSIIGGPAAVLAQQSIKHLECVAYPELGMEAIWKIEVEDFPA 523

```

```

Query: 478 TVAVDSKG 485
+ VD KG
Sbjct: 524 FILVDDKG 531

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 219>:

m050-1.seq

```

1  ATGACCGTCA TCAAACAGGA AGACTTTATC CAAAGCATTT GCGATGCCTT
51  CCAATTCAATC AGCTACTATC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AATCCTGCCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGTAT GTGTGCGGAA AACACCGCC CCATCTGCCA
201 AGACACAGGT ATCGCAACCG TCTTCCTCAA AGTCGGTATG AACGTCCAAT
251 GGGATGCGGA CATGAGCGTG GAAGAGATGG TTAACGAAGG CGTACGCCCG

```

```
301 GCCTACACTT GGAAGGCAA TACGCTGCGC GCTTCCGTCC TCGCCGATCC
351 GGCCGGCAAA CGCAAAACA CCAAGACAA CACCCCGCC GTCATCCATA
401 TGAGCATCGT GCCGGGCGGT AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GGCGGCTCTG AAAACAAATC CAACTCGCC ATGCTCAATC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATCCC GACCATGGGC GCGGGCTGGT
551 GTCTCTCCCG CATCTTGGGT ATCGGCATCG GCGGCACGCC CGAAAAAGCC
601 GTGTGATGG CAAAAGAGTC CCTGATGAGC CACATCGACA TTCAAGAATT
651 GCAGGAAAG GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTGAAAAA GTCAACGCGC TGGGCATCGG CGCACAAGGC
751 TTGGGCGGAC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTATCCGAC
801 CCACGCGGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTCGA ACTCAGCCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGC ACAACGCCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAGA AGAAGTGCCA AGCTGGAATA
1001 CCGCGGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCAAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTCACC AACCGCTCGA TTTACTACGT CGGCCCGGTC GATCCGGTGC
1151 GCGATGAAGT CGTCGGTCCG GCAGGTCCGA CCACAGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGTGG CCACCTGCGA AGCCATCGCC GACAACAAAG
1301 CCGTGACCT CATGGCAGTC GCGGCGCGG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GCGCTTCCCC GAATTGGGCA TGAAGCCAT
1401 TTACGAATTG GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGATAGCA
1451 AAGGCGAATC CATCCAGGCC ACCGCCCGC GCAATGGCA GCGGAAATC
1501 GGCATCATCC CCGTCGAATC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 220; ORF 050-1>:

m050-1.pep

```
1 MTVIKQEDFI QSIDAFQFI SYHHPKDYID ALYKAWQKEE NPAAKDAMTQ
51 ILVNSRMCAE NNRPICQDTG IATVFLKVG M NVQWDADMSV EEMVNEGVRR
101 AYTWEQNTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGG KVEVTCAAKG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMKESLMS HIDIQELQEK AASGAELST EALRLELFEK VNALGIGAQG
251 LGGLTTVLVD KILDYPHTAA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRV DKLTKEEVA SWKTGDVLL NGKILTRDA
351 AHKRLVMDLN KGEELPVDF NRIYYVGPV DPVGEVVG PPTATRMD
401 KFTROMLEQT LLGMIGKSE RGVATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKMPVTV VDSKGESHA TAPRKWQAKI
501 GIIPVES*
```

m050-1/g050-1 98.2% identity in 507 aa overlap

m050-1.pep	10	20	30	40	50	60
m050-1.pep	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
g050-1	MTVIKQEDFIQSIDAFQFISYHHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE					
m050-1.pep	70	80	90	100	110	120
m050-1.pep	NNRPICQDTGIATVFLKVG M NVQWDADMSV EEMVNEGVRRAYTWEQNTLRASVLADPAGK					
g050-1	NNRPICQDTGIATVFLKVG M NVQWDADMSV EEMVNEGVRRAYTWEQNTLRASVLADPAGK					
m050-1.pep	130	140	150	160	170	180
m050-1.pep	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSENKSKLMLNPSDNIVDWVLKTIPTMG					
g050-1	RQNTKDNTPAVIHMSIVPGGKVEVTCAAKGGSENKSKLMLNPSDNIVDWVLKTIPTMG					
m050-1.pep	190	200	210	220	230	240
m050-1.pep	AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEK AASGAELSTTEALRLELFEK					
g050-1	AGWCPPGILGIGIGGTPEKAVLMKESLMSHIDIQELQEK AASGAELSTTEALRLELFEK					
m050-1.pep	250	260	270	280	290	300
m050-1.pep	VNALGIGAQGLGGLTTVLVDKILDYPHTAASKPIAMIPNC AATRHVEFELDSGSPVELTP					
g050-1	VNALGIGAQGLGGLTTVLVDKILDYPHTAASKPIAMIPNC AATRHVEFELDSGSPVELTP					



```

          310      320      330      340      350      360
m050-1.pep PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g050-1      PRVEDXPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVNMLD
          310      320      330      340      350      360

          370      380      390      400      410      420
m050-1.pep KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTROMLEQTDLLGMIGKSE
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g050-1      KGEELPVDFTNRLIYYVGPVDPVGDEVVGPAGPTTATRMDKFTROMLKQTGLLMIGKSE
          370      380      390      400      410      420

          430      440      450      460      470      480
m050-1.pep RGVATCEAIADNKAVYLMVGGAAYLVAKAISKSKVLAFPELGMEAIYEFVKDMPVTVA
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g050-1      RGAATCEAIADNKAVYLMVGGAAYLVAKAISKSKVLAFPELGMEAVYEFVKDMPVTVA
          430      440      450      460      470      480

          490      500
m050-1.pep VDSKGESIHATA PRKWQAKIGIIPVESX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g050-1      VDSKGESIHATA PRKWQAKIGIIPVESX
          490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 221>:

```

a050-1.seq
1  ATGACCGTCA TCRAACAGGA AGACTTTATC CAAAGCATT GCGATGCCTT
51  CCAATTCATC AGCTACTACC ATCCCAAAGA CTACATCGAC GCGCTTTATA
101 AGGCGTGGCA GAAGGAAGAA AACCCCGCG CCAAAGACGC GATGACGCAG
151 ATTTTGGTCA ACAGCCGCAT GTGTGCCGAA AACAACCGCC CCATCTGCCA
201 AGATACCGGT ATCGCGACCG TGTTTTGAAG AGTCGGTATG GATGTGCAAT
251 GGGATGCAGA CATGAGCGTC GAAGAGATGG TTAACGAAGG CGTGCGCCGC
301 GCCTACACTT GGAAGGCCAA TACGCTGCGC GCTTCCGTTT TCGCCGACCC
351 CGCCGGCAAA CGCCAAAATA CCAAAGACAA CACGCCCGCC GTCATCCATA
401 TGAGCATCGT GCCGGCGGAC AAAGTCGAAG TAACCTGCGC GGCAAAAGGC
451 GCGGTTCTGT AAAACAAATC CAAACTCGCC ATGCTCAACC CTTCCGACAA
501 CATCGTCGAT TGGGTATTGA AAACCATTC GACCATGGGC GCGGGCTGGT
551 GTCCTCCCGG CATCTTGGGC ATCGGCATCG GCGGTACGCC CGAAAAGCC
601 GTGTTGATGG CGAAGAATC CCTGATGAGC CACATCGACA TCCAAGAAAT
651 GCAGGAAAAA GCCGCGTCCG GCGCGGAATT GTCCACCACC GAAGCCCTGC
701 GCCTCGAACT CTTTGAAAAA GTCAACGCGC TAGGCATCGG CGCGCAAGGC
751 TTGGGCGGTC TGACCACCGT GTTGGACGTG AAAATCCTCG ATTACCCGAC
801 CCACGCCGCC TCCAAACCGA TTGCCATGAT TCCGAAGTGC GCCGCCACCC
851 GCCACGTCGA ATTTGAATTG GACGGCTCAG GCCCTGTGCA ACTCACGCCG
901 CCGCGCGTCG AAGACTGGCC CGATTTGACT TACAGCCCGC ACAACGGCAA
951 ACGCGTCGAT GTCGACAAGC TGACCAAAGA AGAAGTGGCA AGCTGGAAAA
1001 CCGGCGACGT ATTGCTGTTG AACGGCAAAA TCCTCACCAG CCGCGATGCC
1051 GCACACAAAC GCCTCGTCGA TATGCTCGAC AAAGGCGAAG AATTGCCCGT
1101 CGATTTTACC AACCGCCTGA TTACTACGT CGGCCCGGTC GATCCGGTCG
1151 GCGACGAAAT CGTCGGCCCA GCAGTCCGA CCACGCCAC CCGCATGGAC
1201 AAATTCACCC GCCAAATGCT CGAACAAACC GACCTCTTGG GCATGATCGG
1251 CAAATCCGAG CGCGGCGCGG CCACCTGCGA AGCCATCGCC GACAAACAAG
1301 CCGTGTACCT CATGGCAGTC GCGGCGCGCG CGTATCTCGT GGCAAAAGCC
1351 ATCAAATCTT CCAAAGTCTT GGCGTTCCCC GAATTGGGCA TGGAAAGCCAT
1401 TTACGAATTT GAAGTCAAAG ACATGCCCGT AACCGTCGCC GTAGACAGCA
1451 AAGGCGAATC CATCCACGCC ACCGCCCGCG CCCAATGGCA GGCGAAAATC
1501 GGCATCATCC CCGTCAAATC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 222; ORF 050-1.a>:

```

a050-1.pep
1  MTVIKQEDFI QSIDAFQFI SYHPKDYID ALYKAWQKEE NPAAKDAMTQ
51  ILVNSRMCAE NNRPICQDTG IATVFLKVM DVQWDADMSV EEMVNEGVR
101 AYTWEQNTLR ASVLADPAGK RQNTKDNTPA VIHMSIVPGD KVEVTCAARG
151 GGSENKSKLA MLNPSDNIVD WVLKTIPTMG AGWCPPGILG IGIGGTPEKA
201 VLMAKESLMS HIDIQELOEK AASGAELSTT EALRLELFEK VNALGIGAQQ
251 LGGLTTVLDV KILDYPTHAA SKPIAMIPNC AATRHVEFEL DSGSPVELTP
301 PRVEDWPDLT YSPDNGKRVD VDKLTKEEVA SWKTGDVLLL NGKILTGRDA
351 AHKRLVDMLD KGEELPVDFN NRIYYVGPV DPVGDEIVGP AGPTTATRMD
401 KFTROMLEQT DLLGMIGKSE RGAATCEAIA DNKAVYLMV GGAAYLVAKA
451 IKSSKVLAFP ELGMEAIYEF EVKDMPVTVA VDSKGESIHA TAPPQWQAKI
501 GIIPVK*

```

a050-1/m050-1 98.4% identity in 507 aa overlap

a050-1.pep	10	20	30	40	50	60
MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE						
m050-1	10	20	30	40	50	60
MTVIKQEDFIQSICDAFQFISYYHPKDYIDALYKAWQKEENPAAKDAMTQILVNSRMCAE						
a050-1.pep	70	80	90	100	110	120
NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK						
m050-1	70	80	90	100	110	120
NNRPICQDTGIATVFLKVGMDVQWDADMSVEEMVNEGVRRAITWEGNTLRASVLADPAGK						
a050-1.pep	130	140	150	160	170	180
RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG						
m050-1	130	140	150	160	170	180
RQNTKDNTPAVIHMSIVPGDKVEVTCAAKGGGSENKSKLAMLNPSDNIVDWVLKTIPTMG						
a050-1.pep	190	200	210	220	230	240
AGWCPPGILGIGIGGTPEKAVLMAKESLMASHIDIQELQEKAASGAELSTTEALRLLEFEK						
m050-1	190	200	210	220	230	240
AGWCPPGILGIGIGGTPEKAVLMAKESLMASHIDIQELQEKAASGAELSTTEALRLLEFEK						
a050-1.pep	250	260	270	280	290	300
VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP						
m050-1	250	260	270	280	290	300
VNALGIGAQGLGGLTTVLVDVKILDYPTHAASKPIAMIPNCAATRHVEFELDGSGPVELTP						
a050-1.pep	310	320	330	340	350	360
PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLD						
m050-1	310	320	330	340	350	360
PRVEDWPDLTYS PDNGKRVDVDKLTKEEVASWKTGDVLLNGKILTGRDAAHKRLVDMLN						
a050-1.pep	370	380	390	400	410	420
KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDFKFTROMLEQTDLLGMIGKSE						
m050-1	370	380	390	400	410	420
KGEELPVDFTNRLIYYVGPVDPVGDEIVGPAGPTTATRMDFKFTROMLEQTDLLGMIGKSE						
a050-1.pep	430	440	450	460	470	480
RGAAATCEAIADNKAVYLMVAGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA						
m050-1	430	440	450	460	470	480
RGVATCEAIADNKAVYLMVAGGAAYLVAKAIKSSKVLAFPELGMEAIYEFVVKDMPVTVA						
a050-1.pep	490	500				
VDSKGESIHATAPPQWQAKIGIIPVKSX						
m050-1	490	500				
VDSKGESIHATAPRKWQAKIGIIPVESX						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 223>:

g052.seq

```

1  ATGGCTTTGG TGGCGGAGGA AACGGAATA TCCGCGCCGT GTTTCAAAGG
51  CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC
101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC
151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC
201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA
251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC
301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA
351 CGCCGCCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 224; ORF 052.ng&gt;:

g052.pep

1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP  
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN  
 101 RLRLETTWSP ACRKVKNA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 225>:

m052.seq  
 1 ATGGCTTTGG TGGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG  
 51 CTGCGAGCCG ACGGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC  
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCGCCC  
 151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC  
 201 GGCGGCTTTC CATTCAATTA TATCAGTCGG CGACACGCGG CTCACTCCGA  
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC  
 301 AGGCTGCGGC TGGAAACCAC ATGGTCGCCC GCCTGCAGGA AGGTGAAAAA  
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 226; ORF 052>:

m052.pep  
 1 MALVAEETEI SAPCFKGCEP TGDSRLLSTT KSAPMPCANS AKASKSATSP  
 51 KGLDGVSKNS SLVLALTAAF HSFISVGDTR LTPMPNLVTM LLIKPTVVPN  
 101 RLRLETTWSP ACRKVKNA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 227>:

a052.seq  
 1 ATGGCTTTGG TCGCGGAGGA AACGGAAATA TCCGCGCCGT GTTTCAAAGG  
 51 CTGAGAGCCG ACAGGCGACA GCAGGCTGTT GTCCACCACC AAGAGCGCGC  
 101 CGATGCCGTG CGCCAATTCC GCCAAGGCTT CCAAGTCGGC CACTTCTCCC  
 151 AAGGGGTTGG ACGGCGTTTC CAAAAACAGC AGTTTGGTGT TGGCTTTGAC  
 201 GGCGGCTTTC CATTGCTTTA TATCAGTCGG CGACACGTGA CTCACTTCGA  
 251 TGCCGAATTT GGTAACGATG TTATTGATAA AGCCGACGGT CGTGCCGAAC  
 301 AGGCTGCGGC TGGAAATCAC ATGGTCGCCC GCCTGCAAAA AGGTGAAAAA  
 351 CGCCGCCTGA

This corresponds to the amino acid sequence <SEQ ID 228; ORF 052.a>:

a052.pep  
 1 MALVAEETEI SAPCFKG\*EP TGDSRLLSTT KSAPMPCANS AKASKSATSP  
 51 KGLDGVSKNS SLVLALTAAF HSFISVGD\* LTSMPNLVTM LLIKPTVVPN  
 101 RLRLEITWSP ACKKVKNA\*

m052/a052 95.8% identity over a 119 aa overlap

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
a052	MALVAEETEI SAPCFKGXEP TGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					
	10	20	30	40	50	60
m052.pep	SLVLALTAAFHSFISVGDTRLTPMPNLVTMLLIKPTVVPNRLRLETTWSPACRKKVNAAX					
a052	SLVLALTAAFHSFISVGDXTLSMPNLVTMLLIKPTVVPNRLRLEITWSPACKKVKNAAX					
	70	80	90	100	110	120

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 052 shows 95.8% identity over a 119 aa overlap with a predicted ORF (ORF 052.ng) from *N. gonorrhoeae*:

m052/g052

	10	20	30	40	50	60
m052.pep	MALVAEETEI SAPCFKGCEPTGDSRLLSTTKSAPMPCANS AKASKSATSPKGLDGVSKNS					

```

g052      MALVAEETEISAPCFKGCEPTGDSRLLSTTKSAPMPCANSASAKSKSATSPKGLDGVSKNS
           10      20      30      40      50      60
           70      80      90      100     110     120
m052.pep  SLVLALTAAFHSFISVGDWTLSMPNLATMLLIKPTVVPNRLRLLEITWSPACKVKVNAAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g052      SLVLALTAAFHSFISVGDTRLTPMNLVTMLLIKPTVVPNRLRLLETTWSPACRKVKVNAAX
           70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 229>:

```

g073.seq
1  ATGTGTATGC CATACGCAAT AAGGGTTTCA GACGGCATCT GCCGCATTTT
51 TCCGCCGATG CCGTCTGAAA CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AGTCCGGGGC GGatacCGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT TGGTGATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAAGAGT TCCACGACTT TCCACGCGGC TGCTTGGTCG
301 GCGACTTCAA AACCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCTCCGCC TCGGATGGT CGGGCAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 230; ORF 073.ng>:

```

g073.pep
1  MCMPIAIRVS DGICRIFPPM PSETRNQRAS ACFKSSIKSP TYSKPTDRRT
51 SPGRIPAASF SSGCILPCVV VHGLVMVERT SPRLAVREKS STTFHAAAWS
101 ATSKPMTMPP PFCCLRISSA CGWSGNPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 231>:

```

m073.seq
1  ATGTGTATGC CATATAAGAT AAGGGTTTCA GACGGCATCT GCTGTCCAAT
51 GCGGTCTGAA ACACGCAATC AGCGTGCGAG TGCTGTTTTC AAATCGTCAA
101 TCAAATCGCC AACATATTCC AAACCGACCG ACAGGCGCAC CAATCCGGGG
151 CGGATGTTGG CCGCGAGTTT TTCTTCGGGC TGCATCCTGC CGTGCGTGGT
201 TGTCCACGGG TGGGTAATGG TCGAGCGCAC GTCACCGAGG TTGGCGGTGC
251 GGGAAAAGAG TTCCACGCCG TCCACAATT TCCACGCCGC TTCTTGATCG
301 GCAACTTCAA AGCCGATGAC GATGCCGCCG CCGTTTTGCT GTTTGCGGAT
351 AAGCGCCGCC TGAGGATGGT CGGACAATCC GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 232; ORF 073>:

```

m073.pep
1  MCMPIKIRVS DGICCPMPSE TRNQRASACF KSSIKSPTYS KPTDRRTNPG
51 RMLAASFSSG CILPCVVHVG WVMVERTSPR LAVREKSSTP STTFHAASXS
101 ATSKPMTMPP PFCCLRISAA XGWSNDPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 233>:

```

a073.seq
1  ACGTGTATGT CATATAAGAT AAGGGTTTCA GACGGCATTT GCGGTGTTTT
51 TCCGCCGATG CCGTCTGAA. CACGCAATCA GCGCGCGAGT GCCTGTTTCA
101 AATCGTCAAT CAAATCGCCA ACATATTCCA AACCGACCGA CAGGCGCACC
151 AATCCGGGGC GGATGTTGGC GCGAGTTTTT TCTTCGGGCT GCATCCTGCC
201 GTGCGTGGTT GTCCACGGAT GGGTAATGGT CGAGCGCACG TCGCCGAGGT
251 TGGCGGTACG GGAGAAAAGT TCGACGCCGT CCACGACTTT CCACGCGGCT
301 GCTTGGTCGG CCACTTCAA GCGGATGACG ATGCCGCCGC CGTTTTGCTG
351 TTTGCGGATA AGCTCCGCCT GAGGATGGTC GGGTAATCCG GTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 234; ORF 073.a>:

```

a073.pep
1  TCMSYKIRVS DGICGVFPPM PSEXNRQRAS ACFKSSIKSP TYSKPTDRRT
51 NPGRMLAASF SSGCILPCVV VHGWVMVERT SPRLAVREKS STPSTTFHAA
101 AWSATSKPMT MPPPFCLRI SSA*GWSGNP V*

```

m073/a073 92.3% identity over a 130 aa overlap

260

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
a073	TCMSYKIRVSDGICGVFPMPSEXRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKEPMTMPPFPCLRLI				
a073	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAAWSATSKEPMTMPPFPCLRLI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
a073	SSAXGWSGNPVX				
		130			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 073 shows 87.0% identity over a 131 aa overlap with a predicted ORF (ORF 073.ng) from *N. gonorrhoeae*:

m073/g073

	10	20	30	40	50
m073.pep	MCMPIKIRVSDGICC---PMPSETRNQRASACFKSSIKSPTYSKPTDRRTNPGRMMLAASF				
g073	MCMPIAIRVSDGICRIFFPMPSETRNQRASACFKSSIKSPTYSKPTDRRTSPGRIPAASF				
	10	20	30	40	50
	60	70	80	90	100
m073.pep	SSGCILPCVVVHGWVVERTSPRLAVREKSSTPSTTFHAASXSATSKEPMTMPPFPCLRLI				
g073	SSGCILPCVVVHGLVMVERTSPRLAVREKSST---TFHAAWSATSKEPMTMPPFPCLRLI				
	70	80	90	100	110
	120	129			
m073.pep	SAAXGWSNDNPVX				
g073	SSACGWSGNPVX				
		120			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 235>:

g075.seq

```

1  ATGCCGCTT ACTTCATCAC CCTCTTAACG ATGGAAAATA CAAAAAGCGC
51  GGCGAAAACG CCCACTACAA TCCAACCGGC TTCCATACCG TCCGCTTTTG
101 CGGCTTCCAA AGCGTTTTTT GCGGTTTCGG GCAACGCTGC GTTTGCCTGT
151 GCCGCCAAG CCAGCGGGGC GGCTGTTACA ACAGCCAGTT TTGCGCCGTA
201 TTACGGCAG GTGTTAATAA ATTTTCATGAT ATTTTCCTTT ACGAAATTTT
251 TAAAAAATG TGTTCGCGG CTTTGTGAAG GTTTAGAGA CCGCTGCCG
301 GGCCTCTTAA ACTTAATCTT CTTTTCGTA GAATCCGAAA ATTACAAATT
351 CCCCGCTAT CTCTCCAAT GCCGAGCTAA AAGCGTCTTC ATAGCTGTCA
401 TATTACCGG CTGA

```

This corresponds to the amino acid sequence <SEQ ID 236; ORF 075.ng>:

g075.pep

```

1  MPPYFITLLT MENTKSAKT PTTIQPASIP SAFAASKAFF AVSGNAAFAC
51  AAKASGAAVT TASFAPYLRQ VLINFMIFSF TKFLKKCVCV LCEGFRDRLP
101 GLNLNLIFFV ESENYKFPAY LFQCRKSVF IAVIFTG*

```

```

1   ATGCCGTCTT  ACTTCATCAC  TCTCTTAACG  ATGGAAAATA  CAAAAGCGC
51  GCGGAAATG   CCCACTACAA  TCCAACCGGC  TTCCATACCG  TCCGCTTTTG
101 CGGCTTCCAA  AGCGTTTTTT  GCCGTATCGG  GCAACGTTGC  ATTTGCATGT
151 GCGGCCAAAG  CCAGGGGAGC  AGCTGTTACA  ACAGCCAGTT  TTGCGCCGTA
201 TTACGGCAG  GTGTTAATAA  ATTTCATGAT  ATTTTCCTTC  AAAAAGTGTT
251 TGGCGGTAAT  GGATGGAGCG  TTTTTCAGAC  GACCGCGGAA  CATCCGAAAA
301 TCAGTCTTTT  AAAAATCCGA  ATACGACAAA  TTCGTATTGG  TTGCCGATTT
351 CTTCCAAACC  TCGGTTAATC  GCTTCTTCGA  AGTCGTAGAA  ATAATCGGCA
401 TTGGTGATTA  A

```

m075 - pep

1 MPSYFITLLT MENTKSAAKM PTTIQPASIP SAFAASKAFF AVSGNVAFAC  
51 AAKARGAAVT TASFAPYLQR VLINFMIFSF KKCLAVMDGA FFRPPNIRK  
101 SVFOKSEYDK FVLVADFFQT CVNRFFEVE IIGIGD\*

Homology with a predicted ORF from *N. gonorrhoeae*

m075/g075

```

      10      20      30      40      50      60
m075 . pep  MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT
             |||||||||||||||||||||||||||||||||||||||:|||||
g075        MPPYFITLLTMENTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNAAFACAAKASGAAVT
             10      20      30      40      50      60

      70      80      90      100     110
m075 . pep  TASFAPYLRQVLINFMIFSF----KKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVAD
             ||||||||||||||||| |||: : :| |::: :| |::: :|
g075        TASFAPYLRQVLINFMIFSFTKFLKKVCVGLCEGFRDLPLGLNLIFFFVESENYKFPAY
             70      80      90      100     110     120

      120     130
m075 . pep  FFQTCVNRFFEVEIIGIDX
             :|| :| :| :|
g075        LFQCRAKSVFIAVIFTGX
             130

```

**a075.seq**

1	ATGCCGTCTT	ACTTCATCAC	TCTCTTAAACG	ATGGAAAAGA	CAAAAAGCGC
51	GGCGAAAACG	CCCACTACAA	TCCAACCGGC	TTCCATACCG	TCCGCTTTTG
101	CGGCTTCCAA	AGCGTTTTTT	GCTGTATCGG	GCAACGTTGC	ATTTGCATGT
151	CGGGCCAAAG	CCAGGGGAGC	AGCTTGTACA	ACAGCCAGTT	TTGCGCCGTA
201	TTTACGGCAG	GTGTTAATAA	ATTTTCATGAT	ATTTTCCTTC	AAAAAGTGTT
251	TGGCGGTAAT	GGATGGAGCG	TTTTTCAGAC	GACCGCCGAA	CATCCGAAAA
301	TCAGTCTTTT	AAAAATCCGA	ATACGACAAA	TTCGTATTGG	TTGCCGATTT
351	CTTCCAAACC	TGCGTTAATC	GCTTCTTCGA	AGTCGTAGAA	ATAATCGGCA
401	TTGGTGATTA	A			

**a075.pcp**

1 MPSYFITLLT MEKTKSAKT PTTIQPASIP SAFAASKAFF AVSGNVAFAC  
51 AAKARGAAVT TASFAPYLRQ VLINFMIFSF KKCLAVMDGA FFRRPPNIRK  
101 SVFQKSEYDK FVLVADFFQT CVNRFFEVEV IIGIGD\*

m075/a075 98.5% identity over a 136 aa overlap

	10	20	30	40	50	60
m075.pep	MPSYFITLLTMENTKSAAKMPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	:					
a075	MPSYFITLLTMEKTKSAAKTPTTIQPASIPSAFAASKAFFAVSGNVAFACAAKARGAAVT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m075.pep	TASFAPYLQVLFNFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
a075	TASFAPYLQVLFNFMIFSFKKCLAVMDGAFFRRPPNIRKSVFQKSEYDKFVLVADFFQT					
	70	80	90	100	110	120
	130					
m075.pep	CVNRFFEVEIIGIGDX					
a075	CVNRFFEVEIIGIGDX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 241>:

g080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGGCATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAAGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCCGA	TACGGTTGAG
301	GTCGTCCTGA	CCGAGCGCAA	GCCGGTTGCA	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAA	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACgAGA	TGAAACGCCT	CCgGCTTTTT
601	ACcgAAGCGT	GGCAGCATCT	gttgcGTAAG	AATAAAATC	GGTTATCCTA
651	TGTGGATATG	Aggtataagg	acggatttTC	agtcccccat	gctCCCGACG
701	GTTTACCCGA	AAAAGAAATcc	gAAGAAATatt	gggaacaggt	ttgggacata
751	ttacggcctg	gcgtcggaaa	cggttcgacg	caaatttcaa	tcagttatAA
801	GGGCAGacga	acaatggaac	AGcagtaa		

This corresponds to the amino acid sequence <SEQ ID 242; ORF 080.ng>:

g080.pep

1	MWDNAEAMER	LTRWLLVMMMA	MLLAASGLVW	FYNSNHLPVK	QVSLKGNLVY
51	SDKKALGSLA	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDIVE
101	VVLTERKPVA	RWGDHALVDG	EGNVFEARLD	RPGMPVFRGA	EGTSAEMLRR
151	YDEFSTVLAK	QGLGIKEMTY	TARSAWNVVL	DNGITVRLGR	ENEMKRLRLF
201	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVPH	APDGLPEKES	EEYWEQVWDI
251	LRPGVGNGST	QISISYKGRR	TMEQQ*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 243>:

m080.seq

1	ATGTGGGATA	ATGCCGAAGC	GATGGAACGG	CTGACGCGCT	GGCTGCTTGT
51	CATGATGGCG	ATGCTGCTTG	CTGCGTCCGG	GCTGGTTTGG	TTTTACAATT
101	CGAATCATCT	GCCCGTCAAG	CAGGTGTCGC	TGAAGGGCAA	CCTGGTTTAT
151	TCCGATAAGA	AGACATTGGG	CAGTTTGGCG	AAAGAATACA	TCCATGGGAA
201	TATTTTGAGG	ACGGACATCA	ATGGCGCACA	GGAGGCCTAC	CGCCGGTATC
251	CGTGGATTGC	GTCGGTCATG	GTGCGCCGCC	GTTTTCCCGA	CACGGTTGAG
301	GTCGTCCTGA	CCGAGCGCAA	GCCGGTCGCG	CGTTGGGGCG	ACCATGCCTT
351	GGTGGACGGC	GAAGGCAATG	TTTTTGAAGC	CCGCTTGGAC	AGACCCGGAA
401	TGCCGGTATT	CAGAGGCGCG	GAAGGAACGT	CTGCCGAAAT	GCTCCGCCGT
451	TATGACGAAT	TTTCGACTGT	TTTGGCAAAA	CAGGGTTTGG	GCATCAAAGA
501	GATGACCTAT	ACGGCACGTT	CGGCGTGGAT	TGTCGTTTTG	GACAACGGCA
551	TCACCGTCAG	GCTCGGACGG	GAAAACGAGA	TGAAACGCCT	CCGGCTTTTT

601 ACCGAAGCGT GGCAGCATCT GTTGCCTAAA AATAAAATC GGTTATCCTA  
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTTCCGACG  
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 2441; ORF 080>:

m080.pep  
 1 MWDNAEAMER LTRWLLVMM MLLAASGLVW FYNSNHLPVK QVSLKGNLVY  
 51 SDKKTLGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE  
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR  
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF  
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES EE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 080 shows 97.9% identity over a 242 aa overlap with a predicted ORF (ORF 080.ng) from *N. gonorrhoeae*:

m080/g080

m080.pep	10	20	30	40	50	60
	MWDNAEAMERL LTRWLLVMM MLLAASGLVW FYNSNHLPVK QVSLKGNLVY SDKKTLGSLA					
080	MWDNAEAMERL LTRWLLVMM MLLAASGLVW FYNSNHLPVK QVSLKGNLVY SDKKALGSLA					
	10	20	30	40	50	60
m080.pep	70	80	90	100	110	120
	KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE VVLTERKPVARWGDHALVDG					
080	KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDTVE VVLTERKPVARWGDHALVDG					
	70	80	90	100	110	120
m080.pep	130	140	150	160	170	180
	EGNVFEARLD RPGMPVFRGA EGTSAEMLRRYDEFSTVLAK QGLGIKEMTY TARSAWIVVL					
080	EGNVFEARLD RPGMPVFRGA EGTSAEMLRRYDEFSTVLAK QGLGIKEMTY TARSAWNVL					
	130	140	150	160	170	180
m080.pep	190	200	210	220	230	240
	DNGITVRLGRE NEMKRLRLF TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY ASDGLPEKES					
080	DNGITVRLGRE NEMKRLRLF TEAWQHLLRK NKNRLSYVDM RYKDGFSVPHAPDGLPEKES					
	190	200	210	220	230	240
m080.pep	EEX					
080	EEYWEQVWDILRPGVGNSTQISISYKGRRTMEQQX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 245>:

a080.seq  
 1 ATGTGGGATA ATGCCGAAGC GATGGAACGG CTGACGCGCT GGCTGCTTGT  
 51 CATGATGGCG ATGCTGCTTG CTGCGTCCGG GCTGGTTTGG TTTTACAATT  
 101 CGAATCATCT GCCCGTCAAG CAGGTGTCGC TGAAGGGCAA CCTAGTTTAT  
 151 TCCGATAAGA AAGCATTGGG CAGTTTGGCG AAAGAATACA TCCATGGGAA  
 201 TATTTTGAGG ACGGACATCA ATGGCGCACA GGAGGCCTAC CGCCGGTATC  
 251 CGTGGATTGC GTCGGTCA TGCGCGCGCC GTTTTCCCGA CACGGTTGAG  
 301 GTCGTCCTGA CCGAGCGCAA GCCGGTCGCG CGTTGGGGCG ACCATGCCTT  
 351 GGTGGACGGC GAAGGCAATG TTTTGAAGC CCGTTTGGAC AGACCCGGAA  
 401 TGCCGGTATT CAGAGGCGCG GAAGGAACGT CTGCCGAAAT GCTCCGCCGT  
 451 TATGACGAAT TTTGACTGT TTTGGCAAAA CAGGGTTTGG GCATCAAAGA  
 501 GATGACCTAT ACGGCACGTT CGGCGTGGAT TGTCGTTTGG GACAACGGCA



264

551 TCACCGTCAG GCTCGGACGG GAAAACGAGA TGAAACGCCT CCGGCTTTTT  
 601 ACCGAAGCGT GGCAACATCT GTTGCCTAAA AATAAAAATC GGTTATCCTA  
 651 TGTGGATATG AGGTATAAGG ACGGATTTTC AGTCCGCTAT GCTCCCGACG  
 701 GTTTACCCGA AAAAGAATCC GAAGAATAG

This corresponds to the amino acid sequence <SEQ ID 246; ORF 080.a>:

a080.pep

1 MWDNAEAMER LTRWLLVMA MLLAASGLVW FYNNSHLPVK QVSLKGNLVY  
 51 SDKKALGSLA KEYIHGNILR TDINGAQEAY RRYPWIASVM VRRRFPDVE  
 101 VVLTERKPVA RWGDHALVDG EGNVFEARLD RPGMPVFRGA EGTSAEMLRR  
 151 YDEFSTVLAK QGLGIKEMTY TARSAWIVVL DNGITVRLGR ENEMKRLRLF  
 201 TEAWQHLLRK NKNRLSYVDM RYKDGFSVRY APDGLPEKES EE\*

m080/a080 99.2% identity over a 242 aa overlap

	10	20	30	40	50	60
m080.pep	MWDNAEAMER	LTRWLLVMA	MLLAASGLVW	FYNNSHLPVK	QVSLKGNLVY	SDKKTLGSLA
a080	MWDNAEAMER	LTRWLLVMA	MLLAASGLVW	FYNNSHLPVK	QVSLKGNLVY	SDKKALGSLA
	70	80	90	100	110	120
m080.pep	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDVE	VVLTERKPVA	RWGDHALVDG
a080	KEYIHGNILR	TDINGAQEAY	RRYPWIASVM	VRRRFPDVE	VVLTERKPVA	RWGDHALVDG
	130	140	150	160	170	180
m080.pep	EGNVFEARLD	RPGMPVFRGA	EGTSAEMLRR	YDEFSTVLAK	QGLGIKEMTY	TARSAWIVVL
a080	EGNVFEARLD	RPGMPVFRGA	EGTSAEMLRR	YDEFSTVLAK	QGLGIKEMTY	TARSAWIVVL
	190	200	210	220	230	240
m080.pep	DNGITVRLGR	ENEMKRLRLF	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVRY	ASDGLPEKES
a080	DNGITVRLGR	ENEMKRLRLF	TEAWQHLLRK	NKNRLSYVDM	RYKDGFSVRY	APDGLPEKES
m080.pep	EEX					
a080	EEX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 247>:

g081.seq

1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTCCGAT  
 51 GCCGTCTGAA AACAAACCCG TGTCGCGCAT CGTAACCGAC AGCCGCGATA  
 101 TTCGGGAAGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGACGCG  
 151 CATGATTTTG TTGGAGGCGT ATTGTCTGCG GGCGCGGGCG CGGTGTGGT  
 201 TTCGCGCGAA GATTGCGCGG CTTTGGGCGG CGCGTTGAAA GTCGATGACA  
 251 CGCTTGCCGC GTTGCAAACG TTGGCGAAGG CGTGGCGCGA TAATGTGAAC  
 301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA  
 351 GATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTTTCGG  
 401 CGACGCGAGG CAACTTCAAC AACCACatcg gaTTGCCGCT GACTTTATTG  
 451 AAATtaacAcg aAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA  
 501 TTTTGGcgaa ctggcggtTt taacgcaaaT CGCCAAACCC GATGCCGCTT  
 551 TGGtcaACAA CGCCCTGCGC GCCCATGTGCG GATGCGGTTt cgacggagtg  
 601 GCGGATATTG CCAAAGcgaa aagcGAGATT TatgcagGct tATGTTcAGA  
 651 CGGCATGGCA CTGATTCTCT AAGAAGATGC CAATATGGCT GTCTTCAAAA  
 701 CGGCAACGTT TAATTTGAAT ACGTGCACTT TCGGCGTCGA TAGCGGCGAT  
 751 GTCCGCGCGG AAAATATCGT GCTGAAACCT TTGTCGTGCG AATTTGATT

```

801 GGTGTGCGGC GACGAGCGCA CTGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG CAAGGCTTCA GCAACATCAA
951 AGGCCGTCTG AACGTCAAAG CCGGCATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAATCCC GACAGTATGA AAGCCGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCCGCCGC CATTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAGGAc gaAGCCGCCG CCATGCACGC CGAagtgcGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGcggaAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGAGCC ACGATTGGCC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTG GCGCTTTATG CAGatggaAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTga

```

This corresponds to the amino acid sequence <SEQ ID 248; ORF 081.ng>:

```

g081.pep
1 MKPLDLNFIC QALKLPMPSE NKPVSRIVTD SRDIREGDVF FALAGGRFDA
51 HDFVGGVLSA GAAAVVVSRE DCAALGGALK VDDTLAALQT LAKAWRDNVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFDD AVSATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTQIAKP DAALVNNALR AHVCGGFDGV
201 GDIKAKSEI YAGLCSDGMA LIPQEDANMA VFKTATFNLN TCTFGVDSGD
251 VRAENIVLKP LSCEFDLVCG DERTAVVLPV PGRHNHVNAA AAAALALAG
301 LSLNDVAEGL QGFSNIKGRL NVKAGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFV MGDMSGELGED EAAAMHAEVG AYARDQGIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLSHDLPERA TVLVKGSFRM QMEEVVEALE
451 DK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 249>:

```

m081.seq
1 ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51 GCCGTCTGAA AGCAAACCCG TGTCCGCGAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGAGCG GTTTGACGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCT GGTGCGGCGG CGGTTGTGGT
201 TTCGCGCGAA GATTGTGCTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTGCCGC ATTGCAAACG CTGGCAAAGG CGTGGCGTGA AAATGTGAAT
301 CCGTTTGTGT TCGGCATTAC CGGTTCCGGC GGCAAGACGA CGGTGAAGGA
351 AATGCTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATGAT GCCGTGTTGG
401 CGACGCGAGG CAACCTCAAC AACCATATCG GATTGCCGCT GACTTTGTTG
451 AAGTTAAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GCATGAACCA
501 TTTCGCGGAA CTGGCGGTTT TAACGCAMAT CGCCAAACCA AATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GGCGATATTG CCAAAGCGAA AAGCGAGATT TACCAAGGTT TATGTTTACA
651 CGGCATTGCA CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTGAAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTTCACGCGG AAAATATTGT GCTGAAACCG TTGTCGTGCG AATTGTATT
801 GGTGTGCGGC GATGAGCGCG CCGCCGTGGT GCTGCCTGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCTGCCGCCG CGCTGGCTTT GGCTGCCGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TGCGAACCCT GACAGCATGA AAGCTGCGAT TGACGTGTTG
1051 GCGCGTATGC CTGCCGCCGC TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGCGAACTG GCGGAGGACG AAGCCGCCGC TATGCACGCC GAAGTCGGCG
1151 CGTATGCCCG CGACCAAGGC ATCGAAGCGG CTTATTTTGT CGGCGACAAC
1201 AGCGTCGAAG CGGCGGAAAA ATTTGCGCGG GACGGTTTGT GGTTCGCCCG
1251 CAAAGACCCG TTGATTCAAG TGTTGCGCCA CGATTTGCCC GAACGCGCCA
1301 CCGTGTGGT GAAAGGTTTCG CGCTTTATGC AGATGGAAGA AGTGGTCGAG
1351 GCATTGGAGG ATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 250; ORF 081>:

```

m081.pep
1 MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGERFDA
51 HDFVEDVLA GAAAVVVSRE DCAAMDGALK VDDTLAALQT LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFDD AVLATAGNFN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFE LAVLTXIAKP NAALVNNAMR AHVCGGFDGV

```

201 GDIKAKSEI YQGLCSDGIA LIPQEDANMA VFKTATLNLN TRTFGIDSGD  
 251 VHAENIVLKP LSCEFDLVCG DERAADVLPV PGRHNVHNA AAAALALAAG  
 301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAIDVL  
 351 ARMPAPRIFV MGD MGELGEL GEDEAAAMHA EVGAYARDQG IEAAYFVGDN  
 401 SVEAAEKFGA DGLWFAAKDP LIQVLRHDL PERATVLVKGS RFMQMEEVVE  
 451 ALEDK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 081 shows 94.1% identity over a 455 aa overlap with a predicted ORF (ORF 081.ng)

from *N. gonorrhoeae*:

m081/g081

m081.pep	10	20	30	40	50	60
	MKPLDLNFI CQALKLPMPSESKPVSRIVTDSRDIRAGDVFFALAGERFDAHDFVEDVLAA					
g081	MKPLDLNFI CQALKLPMPSENKPVSRIVTDSRDI REGDVFFALAGGRFDAHDFVGGVLSA					
	10	20	30	40	50	60
m081.pep	70	80	90	100	110	120
	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
g081	GAAAVVVSREDCAALGGALKVDDTLAALQTLAKAWRDNVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	130	140	150	160	170	180
	AVLRRRFGD DAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTXIAKP					
g081	AVLRRRFGD DAVSATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					
	130	140	150	160	170	180
m081.pep	190	200	210	220	230	240
	NAALVNNAMRAHVGCGFDGVGDIKAKSEI YQGLCSDGIALIPQEDANMA VFKTATLNLN					
g081	DAALVNNALRAHVGCGFDGVGDIKAKSEI YAGLCSDGMALIPQEDANMA VFKTATFNLN					
	190	200	210	220	230	240
m081.pep	250	260	270	280	290	300
	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVLPVPGRHNVHNA AAAALALAAG					
g081	TCTFGVDSGDVRAENIVLKPLSCEFDLVCGDERTAVVLPVPGRHNVHNA AAAALALAAG					
	250	260	270	280	290	300
m081.pep	310	320	330	340	350	360
	LSLNDVAEGLKGFSNIKGR LNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
g081	LSLNDVAEGLQGFSNIKGR LNVKAGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
m081.pep	370	380	390	400	410	420
	MGDMGELGELGEDEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
g081	MGDMGELGE ---DEAAAMHA EVGAYARDQGEAAYFVGDN SVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
m081.pep	430	440	450			
	LIQVLRHDL PERATVLVKGS RFMQMEEVVE ALEDKX					
g081	LIQVLSHDL PERATVLVKGS RFMQMEEVVE ALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 251>:

a081.seq

```

1  ATGAAACCAC TGGACCTAAA TTTCATCTGC CAAGCCCTCA AGCTTCCGAT
51  GCCGTCTGAA AGCAAACCCG TGTGCGCAT CGTAACCGAC AGCCGCGACA
101 TCCGCGCGGG CGATGTGTTT TTCGCATTGG CGGGCGGGCG GTTTGATGCG
151 CATGATTTTG TTGAAGACGT ATTGGCTGCG GGTGCGGGCG CGGTTGTGGT
201 TTCGCGCGAA GATTGCGTTG CAATGGATGG CGCGTTGAAA GTCGATGACA
251 CGCTTACCGC GTTGCAAATG TTGGCGAAGG CGTGGCGCGA GAATGTGAAC
301 CCGTTTGTGT TCGGTATTAC CGGCTCGGGC GGCAAGACGA CGGTGAAGGA
351 AATGTTGGCT GCGGTATTGC GCCGCCGTTT CGGCGATAAT GCCGTTTGG
401 CGACGGCAGG CAACTTCAAC AACCACATCG GATTGCCGTT GACTTTGTTG
451 AAATTAACG AAAAACACCG CTATGCCGTG ATTGAAATGG GTATGAACCA
501 TTTTGGCGAA CTGGCGGTTT TGACACAAAT CGCCAAACCC GATGCCGCAT
551 TGGTCAACAA CGCCATGCGC GCCCATGTCG GCTGCGGTTT CGACGGAGTG
601 GCGGATATTG CCAAAGCGAA AAGCGAGATT TATCAAGGCT TATGTTTCAGA
651 CGGCATGGCG CTGATTCCTC AAGAAGATGC CAATATGGCT GTCTTCAAAA
701 CGGCAACGCT TAATTTGAAT ACGCGCACTT TCGGCATCGA TAGCGGCGAT
751 GTCCACGCGG AAAATATCGT GCTGAAACCG TTGTCGTGCG AATTTGATTT
801 GGTGTGCGGC AACGAGTGGC CAGCCGTGGT TCTGCCCGTT CCCGGCCGCC
851 ACAATGTCCA CAACGCCGCC GCCGCCGCCG CGCTGTCTTT GGCTGCAGGT
901 TTGAGTTTGA ACGATGTGGC GGAAGGTTTG AAAGGCTTCA GCAATATCAA
951 AGGCCGTCTG AACGTCAAAT CCGGAATCAA GGGCGCAACC CTGATTGACG
1001 ATACTTATAA TCGGAACCCCT GACAGCATGA AAGCTGCGGT TGACGTGTTG
1051 GCGCGTATGC CTGCGCCGCG TATTTTCGTG ATGGGCGATA TGGGCGAACT
1101 GGGTGAGGAC GAAGCCGCGC CCATGCACGC CGAAGTCGGC GCGTACGCCC
1151 GCGACCAAGG CATCGAAGCG GCTTATTTTG TCGGCGACAA CAGCGTCGAA
1201 GCGGCGGAAA AATTTGGCGC GGACGGTTTG TGGTTCGCCG CCAAAGACCC
1251 GTTGATTCAA GTGTTGCGCC ACGATTGACC CGAACGCGCC ACCGTGTTGG
1301 TGAAAGGTTT GCGCTTTATG CAGATGGAAG AAGTGGTCGA GGCATTGGAG
1351 GATAAGTGA

```

This corresponds to the amino acid sequence <SEQ ID 252; ORF 081.a>:

a081.pep

```

1  MKPLDLNFIC QALKLPMPSE SKPVSRIVTD SRDIRAGDVF FALAGGRFDA
51  HDFVEDVLAA GAAAVVVSRE DCVAMDGALK VDDTLTALQM LAKAWRENVN
101 PFVFGITGSG GKTTVKEMLA AVLRRRFGDN AVLATAGNEN NHIGLPLTLL
151 KLNEKHRYAV IEMGMNHFGE LAVLTQIAKP DAALVNNAMR AHVCGFDGV
201 GDIKAKAKSEI YQGLCSGMA LIPQEDANMA VFKTATLNLN TRTFGIDSGD
251 VHAENIVLKP LSCEFVLVCG NECAAVVLPV PGRHNVHNA AALSLAAG
301 LSLNDVAEGL KGFSNIKGR LNVKSGIKGAT LIDDTYNANP DSMKAAVDVL
351 ARMPAPRIFF MGDMLGELG EAAAMHAEVG AYARDQIEA AYFVGDNVSE
401 AAEKFGADGL WFAAKDPLIQ VLRHDLPERA TVLVKGSREM QMEEVVEALE
451 DK*

```

m081/a081 96.7% identity over a 455 aa overlap

	10	20	30	40	50	60
m081.pep	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGERFDAHDFVEDVLAA					
a081	MKPLDLNFICQALKLPMPSESKPVSRIVTDSDIRAGDVFFALAGGRFDAHDFVEDVLAA					
	10	20	30	40	50	60
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCVAMDGALKVDDTLALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	70	80	90	100	110	120
m081.pep	GAAAVVVSREDCAAMDGALKVDDTLAALQTLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
a081	GAAAVVVSREDCVAMDGALKVDDTLALQMLAKAWRENVNPFVFGITGSGGKTTVKEMLA					
	130	140	150	160	170	180
m081.pep	AVLRRRFGDDAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					
a081	AVLRRRFGDNAVLATAGNFNNHIGLPLTLLKLNEKHRYAVIEMGMNHFGE LAVLTQIAKP					

268

	130	140	150	160	170	180
	190	200	210	220	230	240
m081.pep	NAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGIALIPQEDANMAVFKTATLNLN					
a081	DAALVNNAMRAHVGCDFGVGDIKAKSEIYQGLCSGDMALIPQEDANMAVFKTATLNLN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m081.pep	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGDERAAVLPVPGRHNHVNAAAAAALALAAG					
a081	TRTFGIDSGDVHAENIVLKPLSCEFDLVCGNECAAVLPVPGRHNHVNAAAAAALSLAAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m081.pep	LSLNDVAEGLKGFNSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAIDVLARMPAPRIFV					
a081	LSLNDVAEGLKGFNSNIKGRNLNVKSGIKGATLIDDTYNANPDSMKAAVDVLARMPAPRIFV					
	310	320	330	340	350	360
	370	380	390	400	410	420
m081.pep	MGDMGELGELGEDEAAAMHAEVGAAYARDQGIEAAYFVGDNVVEAAEKFGADGLWFAAKDP					
a081	MGDMGELGE---DEAAAMHAEVGAAYARDQGIEAAYFVGDNVVEAAEKFGADGLWFAAKDP					
	370	380	390	400	410	
	430	440	450			
m081.pep	LIQVLRHDLPERATVLVKGSRFQMEEVVEALEDKX					
a081	LIQVLRHDLPERATVLVKGSRFQMEEVVEALEDKX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 253>:

```

g082.seq
1  aTGTGGTTGT TGAAGTTGCC TGCCGTCGCC GAAACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATCTC CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAACCGGT TCACATTATC GCGCCACGCC
151 TCGCCAACG TTTGCAACGC GGCAAGCGTG TCATCGACTT TCAACGCGCC
201 GCCCAAAGCC GCGCAATCTT CGCGCGAAAC CACAACGCC GCGCGCCCG
251 CAGACAATAC GCCTCCAACA AAATCATGCG CGTCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC TTCCCGAATA TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTGTGTTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTCATAT TTGCTTTCGT TAATATTCCG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAACACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTT TAGACGTATT TTAGCCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGAAT GTCTGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCGGCAC ATCGGGGACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 254; ORF 082.ng>:

```

g082.pep
1  MWLLKLPAPA ETASSPKRRR NTAASISFTV VLPPEVMPN TNGFTLSRHA
51  FANVCNAASV SSTFNAPPKA AQSSRETTA AAPADNTPPT KSCASNRPAA
101 NAKNTSPSRI SRLSVTMRDT GLPSDGIGSL RAWQMKFRSS GFIFAFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGLSVD KGKVIAPARH IGDIPPKIIA VIGQLVGFDI RPTAESA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 255>:

```

m082.seq
1  ATGnnGTTGT TGAAGTTGCC TGCCGTCGCC AACACGGCAT CATCGCCGAA
51  ACGGCGGCGC AATACCGCAG CCAGCATTTT CTTACCGTC GTCTTGCCGC
101 CCGAACCGGT AATGCCGAAC ACAACGGAT TCACATTTTC ACGCCACGCC
151 TTTGCCACG TTTGCAATGC GGCAAGCGTG TCATCGACTT TCAACGCGCC

```

```

201 ATCCATTGCA GCACAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCAG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CGTCAAACCG CTCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTACTTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGsATTT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTTC CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCTGCAC ATCGGGAACA TTCCCCAAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAAC TG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 256; ORF 082>:

```

m082.pep
  1 MXLLKLPAVA NTASSPKRRR NTAASISFTV VLPPEPVMPN TNGFTFSRHA
 51 FASVCNAASV SSTFNAPSIA AQSSRETTTA AAPAANTSST KSCASNRSFA
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSXF FLYVSFFRRI PSRFAFSRIP
201 RRGVVQSVD KGKVIAFALH IGNIPPKIIA VIGQLVGFD TPTAESAX

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 082 shows 92.7% identity over a 247 aa overlap with a predicted ORF (ORF 082.ng) from *N. gonorrhoeae*:

m082/g082

```

              10      20      30      40      50      60
m082.pep    MXLLKLPAVANTASSPKRRRNTAASISFTVLPPEPVMPNTNGFTFSRHAFASVCNAASV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082         MWLLKLPAVAETASSPKRRRNTAASISFTVLPPEPVMPNTNGFTLSRHAFANVCNAASV
              10      20      30      40      50      60

              70      80      90     100     110     120
m082.pep    SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRSFANAKNTSPARMSRLSVTMRDT
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082         SSTFNAPPKAAQSSRETTTAAAPADNTPPTKSCASNRPANAKNTSPSRISRLSVTMRDT
              70      80      90     100     110     120

              130     140     150     160     170     180
m082.pep    GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082         GLFSDGIGSLRAWQMKFRSSGFIFAFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF
              130     140     150     160     170     180

              190     200     210     220     230     240
m082.pep    FLYVSFFRRIFSRFAFSRIPRRGVVQSVDKGKVIAFALHIGNIPPKIIAVIGQLVGFD
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g082         FLYVSFFRRIFSRFAFSRIPRRGVVGLSVDKGKVIAFARHIGDIPPKIIAVIGQLVGFD
              190     200     210     220     230     240

m082.pep    RPTAESAX
              | | | | |
g082         RPTAESAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 257>:

a082.seq

```

  1 ATGTGTTGT TGAAGTTGCC TGCCGTCGCC AAAACGGCAT TATCGCCGAA
 51 ACGGCGGCGC AATACCGCAG CCAACATTTC CTTCACCGTC GTCTTGCCGC

```

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```

101 CCGAGCCGGT AATACCGAAC ACAAACGGGT TCACATTCTC GCGCCACGCC
151 TTCGCCAACA TTTGCAACGC GGTAAGCGTG TCATCGACTT TCAACGCGCC
201 ATCCATTGCA ACGCAATCTT CGCGCGAAAC CACAACCGCC GCCGCACCCG
251 CAGCCAATAC GTCTTCAACA AAATCATGCG CATCAAACCG CCCGCCCGCC
301 AATGCGAAAA ACACATCGCC CGCGCGGATG TCGCGGCTGT CGGTTACGAT
351 GCGCGACACG GGTTCGCTTT CAGACGGCAT CGGAAGCTTG AGGGCTTGGC
401 AGATGAAATT TAGGTCCAGT GGTTTCATAT TTAATTTCGT TAATATTCGG
451 GCGGCGGACA CATCGGTAGC GGCTGATTTT TTTATCGCCT GTTTTGCTGT
501 GGTAAACAC AGATTATTTT CCCATTCTCA TTCGGCATT TTTCTGTACG
551 TATCATTTTT TAGACGTATT TTTAGTCGAT TTGCCTTTT CCGCATACCA
601 CGGCGCGGGG TCGTCGGGCA GTCCGTCGAT AAAGGCAAGG TTATTGCCTT
651 CGCCCTGCAC ATCGGGAACA TTCCCCCAA AATCATAGCC GTCATCGGGC
701 AACTCGTCGG TTTCGATACC CGTCCAACG CCGAATCCGC GTAA

```

This corresponds to the amino acid sequence <SEQ ID 258; ORF 082.a>:

```

a082.pep
1 MWLLKLPAVA KTALSPKRRR NTAANISFTV VLPPEPVIPN TNGFTFSRHA
51 FANICNAVSV SSTFNAPSIA TQSSRETTA AAPAANTSST KSCASNRP
101 NAKNTSPARM SRLSVTMRDT GLLSDGIGSL RAWQMKFRSS GFIFTFVNIR
151 AADTSVAADF FIACFAVVKH RLFSHSHSAF FLYVSFFRRI FSRFAFSRIP
201 RRGVVGQSV DKGKVI AFALH IGNIPKIIA VIGQLVGFD TPTAES*

```

m082/a082 95.5% identity over a 247 aa overlap

	10	20	30	40	50	60
m082.pep	MXLLKLPAVANTASSPKRRRNTAASISFTVVLPPEPVMPNTNGFTFSRHAFASVCNAASV					
a082	MWLLKLPAVAKTALSPKRRRNTAANISFTVVLPPEPVIPNTNGFTFSRHAFANICNAVSV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m082.pep	SSTFNAPSIAAQSSRETTTAAAPAANTSSTKSCASNRS PANAKNTSPARMSRLSVTMRDT					
a082	SSTFNAPSIAATQSSRETTTAAAPAANTSSTKSCASNRP PANAKNTSPARMSRLSVTMRDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m082.pep	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSXF					
a082	GLLSDGIGSLRAWQMKFRSSGFIFTFVNIRAADTSVAADFFIACFAVVKHRLFSHSHSAF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m082.pep	FLYVSFFRRIFSRFAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPKIIA VIGQLVGFD					
a082	FLYVSFFRRIFSRFAFSRIPRRGVVGQSV DKGKVI AFALHIGNIPKIIA VIGQLVGFD					
	190	200	210	220	230	240
m082.pep	RPTAESAX					
a082	RPTAESAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 259>:

```

g084.seq
1 ATGAAacaAT CCGcccgaat aAAAAATATG GATCAGACAT TAAAAAATAC
51 attgggcatt tGCGCGcttt tagcctTTTG TTTTggcgCg gccatCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGC
151 GCTTTGGCTT CGGTGTGATT TTTATTATTA TTGGCACGCG GCTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCTT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC
351 CGGTCGCTT TATTTTGTGC AGGCATTATT TTTCATTTTT GGCTTGACAG

```

401 TTTGAAATA TTGTGTATCT GTGGGGGTAT TTGCTGACGT AAAAACTAT  
 451 AAACGTCGCA GCAAAATATG GCTGACCATA TTATTGACTT TGATTTTGTC  
 501 CTGCGCGGTG ATGGAGAAAA TCGccggcgca taaAGATTGG CGAGaacctg  
 551 atgcccgcct gttgttgaat ATTTTCgacc tgtattaCga cttggctttc  
 601 cgcgcgggca CAATATGCCG CCAAGCGCGC CCacattttg gaagCagcaa  
 651 aaaaagcgtC AACATGGCAt atccgccaac ttgcgccccaa gTataa

This corresponds to the amino acid sequence <SEQ ID 260; ORF 084.ng>:

g084.pep

1 MKQSARIKNM DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSAVG  
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS  
 101 ILESNPPEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS VGVFADVKNY  
 151 KRRSKIWLTI LLTLILSCAV MEKIAGDKDW REPDAGLLLN IFDLYYDLAF  
 201 RAGTICRQAR PHFGSSKKS SV NMAPPTCAQ V\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 261>:

m084.seq

1 ATGAAACAAT CCGCCCGAAT AAAA.ATATG AATCAGACAT TACTTTATAC  
 51 ATTGGGCATT TGCGCGCTTT TAACCTTTnn nnnnnnnnnnn nnnnnnnnnnn  
 101 nnnnnTATCA CCCnGAATAT GAATACGGCT ACCGTTATTC TGCCGTGGGT  
 151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTCCCGCG  
 201 CGTTTCTTCA GTTGTTTTAC TGATTACGT CGGCACAACC GCCCTATATT  
 251 TGCCGGTCGG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTTCG  
 301 ATATTGGAAA GCAATCCTGC CGAGGCGCGT GAATTTGTCG GCAATCTTCC  
 351 CGGGTCGCTT TATTTTGTGC AGGCATTATT TTTCAATTTT GGCTTGACAG  
 401 TTTGAAATA TTGTGTATCG GGGGGGTAT TTGCTGACGT AAAAACTAT  
 451 AAACGCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC  
 501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTG CGAGAACCTG  
 551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCT.TC  
 601 CGCGCCGGCA CAATATGCCG CCAAGCGCGC CCACATTTTG GAAGCAGCAA  
 651 AAAAAAGCTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

This corresponds to the amino acid sequence <SEQ ID 262; ORF 084>:

m084.pep

1 MKQSARIKXM NOTLLYTLGI CALLTFXXXX XXXXXYHPEY EYGYRYSAVG  
 51 ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS  
 101 ILESNPPEAR EFVGNLPGSL YFVQALFFIF GLTVWKYCVS GGVFADVKNY  
 151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLLN IFDLYYDLAX  
 201 RAGTICRQAR PHFGSSKKS SV NMAPSCCAQ V\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 084 shows 90.5% identity over a 231 aa overlap with a predicted ORF (ORF 084.ng) from *N. gonorrhoeae*:

m084/g084

	10	20	30	40	50
m084.pep	MKQSARIKXMNQTLTYTLGICALLTF-----YHPEY EYGYRYSAVGALASVVFLLL				
	:          :				
g084	MKQSARIKNMDQTLKNTLGLICALLAFCFGAAIASGYHLEYEYGYRYSAVGALASVVFLLL				
	10	20	30	40	50
	60	70	80	90	100
m084.pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPPEARFVGNLPGSL				
g084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILESNPPEARFVGNLPGSL				
	70	80	90	100	110
	120	130	140	150	160
m084.pep	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL				
g084	YFVQALFFIFGLTVWKYCVSGGVFADVKNYKRRSKIWLTI LLTLILSCAVMEKIAGDKDW				
	130	140	150	160	170
	130	140	150	160	180



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	180	190	200	210	220
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX				
g084	REPDAGLLLNIFDLYYDLAFRAGTICRQARPHFGSSKKSVMAYPPTCAQVX				
	190	200	210	220	230

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 263>:

a084 . seq

```

1  ATGAAACAAT CCGCCGAAT AAAAAATATG GATCAGACAT TAAAAAATAC
51  ATTGGGCATT TGC GCGCTTT TAGCCTTTTG TTTTGGCGCG GCCATCGCAT
101 CAGGTTATCA CTTGGAATAT GAATACGGCT ACCGTATTTC TGCCGTGGGT
151 GCTTTGGCTT CGGTTGTATT TTTATTATTA TTGGCACGCG GTTTCCCGCG
201 CGTTTCTTCA GTTGTTTTAC TGATTTACGT CGGCACAACC GCCCTATATT
251 TGCCGGTCCG CTGGCTGTAT GGTGCGCCGT CTTATCAGAT AGTCGGTTCG
301 ATATTGAAA GCAATCCTGC CGAGGCGCGT GAATTGTGCG GCAATCTTCC
351 CGGGTCGCTT TATTTGTGC AGGCATTATT TTTCATTTT GCCTTGACAG
401 TTTGGAGATA TTGTGTATCG GGGGGGGTAT TTGCTGACGT AAAAACTAT
451 AAACGCCGCA GCAAAATATG GCTGACTATA TTATTGACTT TGATTTTGTC
501 CTGCGCGGTG ATGGATAAAA TCGCCAGCGA TAAAGATTTC CGAGAACCTG
551 ATGCCGGCCT GTTGTGAAT ATTTTCGACC TGTATTACGA TTTGGCTTCC
601 .GCGCCGCCA CAATATGCCG CCAAGCGCGC CCACATTTTG GAAGCAGCAA
651 AAAAAGCGTC AACATGGCAT ATCCGTCATG TTGCGCCCAA GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 264; ORF 084.a>:

a084 . pep

```

1  MKQSARIKMN DQTLKNTLGI CALLAFCFGA AIASGYHLEY EYGYRYSVAVG
51  ALASVVFLLL LARGFPRVSS VLLIYVGT ALYLPVGWLY GAPSYQIVGS
101 ILESNPAEAR EFGVNLPGSL YFVQALFFIF GLTVWRYCVS GGVFADVKNY
151 KRRSKIWLTI LLTLILSCAV MDKIASDKDL REPDAGLLN IFDLYYDLAS
201 XAGTICRQAR PHFGSSKKSVMAYPSCCAQ V*

```

m084/a084 92.2% identity over a 231 aa overlap

	10	20	30	40	50	60
m084 . pep	MKQSARIKXMNQTLTYLIGICALLTFXXXXXXXHYPEYGYRYSVAVGALASVVFLLL					
	:         :					
a084	MKQSARIKNMDQTLKNTLIGICALLAFCFGAIAISGYHLEYEYGYRYSVAVGALASVVFLLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m084 . pep	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAREFVGNLPGSL					
a084	LARGFPRVSSVLLIYVGTALYLPVGWLYGAPSYQIVGSILES NPAEAREFVGNLPGSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m084 . pep	YFVQALFFIFGLTVWKYCVS GGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
a084	YFVQALFFIFGLTVWRYCVS GGVFADVKNYKRRSKIWLTI LLTLILSCAVMDKIASDKDL					
	130	140	150	160	170	180
	190	200	210	220	230	
m084 . pep	REPDAGLLLNIFDLYYDLAXRAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
a084	REPDAGLLLNIFDLYYDLASXAGTICRQARPHFGSSKKSVMAYPSCCAQVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 265>:

g085 . seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCCTG CGCGACCGT TGAAAGATAA

```

```

51  GGCAAAAGGC GTGTTCTGA TCGGCGTCGA TCGCGCCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AACCTGACCG ACTGCGTCAC TTTGGAAGAG
151 GCGGTTTCTG CCGCATACGC CCAAGCCGAA GCGGGCGATA TTGTCTTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT tatCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 266; ORF 085.ng>:

g085.pep

```

1  MGKGQDFTPL RDALKDKAKG VFLIGVDAPO IRRDLGCGL NLTDCVTL EE
51  AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 267>:

m085.seq

```

1  ATGGGTAAAG GGCAGGACTT CACGCCCTG CGCGATGCAC TGGTAGGCAA
51  GGCAAAAGGC GTGTTCTGA TTGGTGTGCA TCGCGCCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGGCTTG AATATGACCG ACTGCGCCAC TTTGGGAGAA
151 GCCGTTTCTG CCGCATATGC CCAAGCCGAA GCAGGCGATA TTGTGTTGCT
201 CAGCCCCGCC TCGCGGAGCT TTGATATGTT CAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGAAGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 268; ORF 085>:

m085.pep

```

1  MGKGQDFTPL RDALVGKAKG VFLIGVDAPO IRRDLGCGL NMTDCATLGE
51  AVQTAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 085 shows 94.7% identity over a 94 aa overlap with a predicted ORF (ORF 085.ng) from *N. gonorrhoeae*:

m085/g085

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGLNMTDCATLGEAVQTAYAQA E					
g085	MGKGQDFTPLRDALKDKAKGVFLIGVDAPOIRRDLGCGLNLTDCTVTL EEAVQTAYAQA E					
	10	20	30	40	50	60
	70	80	90			
m085.pep	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
g085	AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX					
	70	80	90			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 269>:

a085.seq

```

1  ATGGGCAAAG GGCAGGACTT CACGCCCTG CGGACGCGC TTGCCGCAA
51  GGCAAAAGGC GTGTTCTGA TCGGTGTGCA TCGCGCCGCAA ATCCGCCGCG
101 ATTTGGACGG CTGCGATCTG AATATGACCG ACTGCGCCAC TTTGGAAGAA
151 GCGGTTTCTG AGGCATATGC CCAAGCCGAA GCGGGCGATA TCGTGCTGCT
201 CAGCCCCGCC TCGCGGAGTT TCGATATGTT TAAAGGCTAC GCGCACCGTT
251 CGGAAGTGTT TATCGGGGCG TTTAAGGCTT TGTGA

```

This corresponds to the amino acid sequence <SEQ ID 270; ORF 085.a>:

a085.pep

```

1  MGKGQDFTPL RDALAGKAKG VFLIGVDAPO IRRDLGCDL NMTDCATLEE
51  AVQKAYAQA E AGDIVLLSPA CASFDMFKGY AHRSEVFIEA FKAL*

```

m085/a085 94.7% identity over a 94 aa overlap

	10	20	30	40	50	60
m085.pep	MGKGQDFTPLRDALVGKAKGVFLIGVDAPOIRRDLGCGLNMTDCATLGEAVQTAYAQA E					

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```

|||||
a085  MGKGQDFTPLRDALAGKAKGVFLIGVDAPQIRRDLDGCDLNMDCATLEEAVQKAYAQAEE
      10      20      30      40      50      60

      70      80      90
m085.pep AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
|||||
a085  AGDIVLLSPACASFDMFKGYAHRSEVFIEAFKALX
      70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 271>:

```

g086.seq
1   ATGGTGGTGC TGATGACGGC GTTCGGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCGAAGG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GGCAGGCGGG GTTCGTCGTT GCCGGCCTTA TAGCGAGCGG TTTTATATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CTTATCCGGC CTGTTGCTGG TAGCCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCAGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCAGGGGAC GGCCAACCTG ATTATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAAACAT TAGAAATGTA CGGCGGTTTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTCC
551 GTTCGTTTGT CGTCATTACC GTCATTACCG TTGGAATGCT GTTCTGGCA
601 GGATTGCCGT GGAAATATTT TTTTGTCTCG GTAGGCAGCG TCTTGGGTGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CCGGTAGTGG
701 CATTTTTGGA CCCGTGAAA GACCCGACAG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGTTTCGGTA TGGGTTTGGG
801 TCGAGATTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCTGAA GAATTCGGCT TCTTCGGGAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTTCCA TCGGCAAGCA
951 GLTCGCGCAT TTGGGtttgA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAAGGTCT GACGctgCcg tTGATGTCCT ATGGcggTTC
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTTG CGTATCGATT
1151 ATGAAAACCG CCAGAAAATG CGCGGTTACC GGGTGGAGTA AA

```

This corresponds to the amino acid sequence <SEQ ID 272; ORF 086.ng>:

```

g086.pep
1   MVVLMTAFGL LMIYSASVYL ASKEGGDQFF YLTRQAGFVV AGLIASGFLW
51  FLCRMRTWRR LVPWIFALSG LLLVAVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTREE VLRSMESLW QSIWRGTANL IMSATNPQAR
151 RETLEMYGRF RAILPIMLV AFGLVLIMVQ PDFGSFVVIT VITVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDLPWK DPQGAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGWLVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGIQ SFFNIGVNIG
351 ALPTKGLTLP LMSYGGSSVF FMLISMMLL RIDYENRQKM RGYRVE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 273>:

```

m086.seq
1   ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATTT ATTCGGCTTC
51  TGTGTATTTG GCATCAAAAG AAGGCGGCGA TCAGTTTTTC TATTTGACCA
101 GACAGGCGGG GTTCGTCGTT GCCGGCTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTGC
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CGTTGAATTT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGCAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGcGCA GCATGGAAAG TTTGGGTTGG CAGTCGATTT
401 GGCAGGGGAC GGCCAATCTG ATCATGTCCG CCACCAATCC GCAGrCACGT
451 CGTGAAaACAT TAGAAATGTA CGGCGGTWTC CGGGCGATCA TCCTGCCGAT
501 TATGCTGGTG GCGTTCGGTT TGGTGCTGAT AATGGTACAG CCGGATTTCC

```

```

551 GTTCGTTTGT CGTCATTACC GTCATTGCCG TTGAATGCT GTTTTGGCA
601 GGATTGCCGT GGAAATATTT TTTCGTCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTGCTG ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCCGTGAAA GACCCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTGGG
801 TCGGAGTTG AGCAAACGCG GCTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGGCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGCTGGCT GGTGGTGCGG GCGTTTCCA TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGkTCCAA AGTTTCTTCA ATATCGGTGT GAACATCGGT
1051 GCTTTGCCGA mCAAAGyCT GACGCyGCCG Tg.AtGTCCw ATGGCGGTTT
1101 GTCAGTCTTT TTCATGCTGA TCAGCATGAT GCTGCTGTkG CGTATAGATT
1151 ATGAAAACCG CCGGAAAATG CGCGGTTATC GGGTGGAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 274; ORF 086>:

m086.pep

```

1  MVVLMTAFSL LMIYSASVYL ASKEGGDOFF YLTRQAGFVV AGLIASGLLW
51  FLCRMRTWRR LVPWIFALSG LLLVVVLIAG REINGATRWI PLGPLNFQPT
101 ELFKLAVILY LASLFTREE VLRSMESLGW QSIWRGTANL IMSATNPQXR
151 RETLEMYGRX RAIILPIMLV AFGLVLIMVQ PDFGSFVVIT VIAVGMLFLA
201 GLPWKYFFVL VGSVLGGMVL MITAAPYRVQ RVVAFDPWK DPQAGYQLT
251 HSLMAIGRGE WFGMGLGASL SKRGFLPEAH TDFIFAIIE EFGFFGMCVL
301 IFCYGLVVR AFSIGKQSRD LGLTFNAYIA SGIGIWIGXQ SFFNIGVNIC
351 ALPKKGLTXP XMSXGSSVF FMLISMMLLX RIDYENRRKM RGYRVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 086 shows 96.7% identity over a 396 aa overlap with a predicted ORF (ORF 086.ng) from *N. gonorrhoeae*:

m086/g086

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLMIYSASVYLASKEGGDOFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
g086	MVVLMTAFGLLMIYSASVYLASKEGGDOFFYLTRQAGFVVAGLIASGLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTREE					
g086	LVPWIFALSGLLLVAVLIAGREINGATRWIPLGPLNFQPTLFLKAVILYLASLFTREE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m086.pep	VLRSMESLGWQSIWRGTANLIMSATNPQXRRETLEMYGRXRRAIILPIMLVAFGLVLIMVQ					
g086	VLRSMESLGWQSIWRGTANLIMSATNPQARRETLEMYGRFRAIILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m086.pep	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQVVAFDPWK					
g086	PDFGSFVVITVITVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQVVAFDPWK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m086.pep	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
g086	DPQAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIEEFGFFGMCVL					
	250	260	270	280	290	300
	310	320	330	340	350	360

```

a086.seq
1 ATGGTGGTGC TGATGACGGC GTTCAGCCTG CTGATGATT ATTCCGGCTTC
51 TGTGTATTG GCATCAAAAG AAGCGCGCGA TCAGTTTTTC TATTTGACCA
101 GACAGCGGG GTTCGTCGTT GCCGCGTTGA TAGCGAGCGG TTTGTTATGG
151 TTTCTTTGCA GGATGAGGAC ATGGCGGCGG CTTGTGCCGT GGATTTTTCG
201 CCTATCCGGC CTGTTGCTGG TAGTCGTATT GATTGCCGGG CGCGAAATCA
251 ATGGCGCGAC CCGTTGGATA CCTTTGGGTC CTTTGAATT CCAGCCGACC
301 GAGCTGTTCA AGCTGGCGGT CATCCTTTAT TTGGGAAGCC TGTTCACGCG
351 CCGTGAAGAA GTGTTGCGCA GCATGGAAG TTTGGGTTGG CAGTCGATTT
401 GCGGGGGGAC GGCCAATCTA ATCATGTCCG CCACCAATCC GCAGGCACGT
451 CGTGAACAT TAGAAATGTA CGGCCGTTTC CAGGCGATAT TCCTGCCGAT
501 TATGCTGGTG GCGTTGCGTT TGGTGCTGAT AATGCTACAG CCGGATTTTC
551 GTTCGTTTGT CGTCATTACC GTCAATTGCCG TTGGAATGCT GTTTTTGGCA
601 GGATTGCCGT GGAATATATT TTTTCGTCCTG GTAGGCAGCG TCTTGGGCGG
651 GATGGTCTGT ATGATTACCG CCGCTCCCTA CCGTGTGCAG CGGGTAGTGG
701 CATTTTGGGA CCGGTGGAAG GACCGCAGG GTGCCGGCTA CCAGCTTACC
751 CACTCTCTGA TGGCAATCGG GCGCGGAGAG TGGTTCGGTA TGGGTTTGGG
801 TGCAGATTTG AGCAAACGCG GCTTTCTGCC GGAAGCGCAT ACCGATTTTA
851 TTTTGTCCAT CATCGCCGAA GAATTCGGTT TCTTCGGTAT GTGCGTGCTG
901 ATATTCTGTT ACGGTCGGCT GGTGGTGCGG GCGTTTTCCT TCGGCAAGCA
951 GTCGCGCGAT TTGGGTTTGA CTTTCAACGC CTATATCGCT TCGGGTATCG
1001 GCATTTGGAT CGGTATCCAA AGTTTCTTCA ATATCCGTGT GAACATCGGT
1051 GCTTTGCCGA CCAAGGTCTA GACGCTGCCG TTGATGTCTT ATGGCGGTTT
1101 GTCAGTCCCT TTCATGCTGT TACAGCATGAT GCTGTGTGTT CGTATAGATT
1151 ATGAAAACCT CCGGAAAATG CGCGGTTACC GGGTGGAGTA A

```

a086.pap

1	MVVLMTAFSL	LMIYSASVYL	ASKEGGDQFF	YLTRQAGFVV	AGLIASGLLW
51	FLCRMRTWRL	LVPWIFALSG	LLLVVVLIAG	REINGATRWI	PLGPLNFQPT
101	ELFKLAVLYL	LASLFTTRREE	VLRSMESLGW	QSIWRGTANL	IMSATNPQAR
151	RETLEMYGRF	RAILPIMLV	AFGLVLLIMVQ	PDFGSFVVIT	VIAVGMFLFA
201	GLPWKYFFVL	VGSVLGGMVL	MITAAPYRVQ	RVVAFELDPWK	DPQAGYQLT
251	HSLMAIGRGE	WFGMGLGASL	SKRGFLPEAH	TDGIFAIIE	EFGFFGMCVL
301	IFCYGILVVR	AFSGTKQSRD	LGLTFNAYIA	SGGIVGAGI	FFFNIGVNIG
351	ALPTKGLTLP	LMSYGGSSVF	FMLISMMLLL	RIDYENRRKM	RGYRVE*

	10	20	30	40	50	60
m086.pep	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
a086	MVVLMTAFSLLMIYSASVYLASKEGGDQFFYLTRQAGFVVAGLIASGLLWFLCRMRTWRR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m086.pep	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASLFTREE					
a086	LVPWIFALSGLLLVVVLIAGREINGATRWIPLGPLNFQPTLEFKLAVILYLASLFTREE					

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	70	80	90	100	110	120
m086.pep	130	140	150	160	170	180
	VLRSMESLQSIWRGTANLIMSATNPQXRRETLEMYGRXRAILPIMLVAFGLVLIMVQ					
a086	VLRSMESLQSIWRGTANLIMSATNPQARRETLEMYGRFRAILPIMLVAFGLVLIMVQ					
	130	140	150	160	170	180
m086.pep	190	200	210	220	230	240
	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
a086	PDFGSFVVITVIAVGMLFLAGLPWKYFFVLVGSVLGGMVLMITAAPYRVQRVVAFLDPWK					
	190	200	210	220	230	240
m086.pep	250	260	270	280	290	300
	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
a086	DPQGAGYQLTHSLMAIGRGEWFGMGLGASLSKRGFLPEAHTDFIFAIIAEEFGFFGMCVL					
	250	260	270	280	290	300
m086.pep	310	320	330	340	350	360
	IFCYGWLVRFAFSIGKQSRDLGLTFNAYIASGIGIWIGXQSFFNIGVNIGALPXKGLTXP					
a086	IFCYGWLVRFAFSIGKQSRDLGLTFNAYIASGIGIWIGIQSFFNIGVNIGALPTKGLTLP					
	310	320	330	340	350	360
m086.pep	370	380	390			
	XMSXGGSSVFFMLISMMLLXRIDYENRRKMRGYRVEX					
a086	LMSYGGSSVFFMLISMMLLLRIDYENRRKMRGYRVEX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 277>:

g087.seq

```

1  ATGGGCGGTA AAACCTTTAT GCTGATGGCG GCGGGAACGG GCGGACACAT
51  TTTCCAGCT CTGGCTGTGG CGGATTCATT GCGCGTGGCG GGTCATCATG
101 TAATTTGGCT GGGCAGCAAG GATTTCGATG AAGAGCGCAT CGTGCCGCAA
151 TACGGCATA GCTTGGAAC GCTGGCGATT AAAGGAATAC GCGGCAACGG
201 CATCAAACGC AAGCTGATGC TTCCGTTTAC TCTGTACAAA ACCGTCCGCG
251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGCCT CATCGGCTTC
301 GGGGTTTTG TTACCTTTCC CGGCGTCTG GCGGCGAAAC TCTTGGCGGT
351 GCCGATTGTG ATTCACGAGC AAAACGCCGT GGCAGGCTTG TCCAACGCC
401 AccTGTCGCG ctGGGCGAAA CGGGTGTGTG ACGCTTTTCC GAAAGCGTTC
451 AGCCACGAAG GCGGTTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA
501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGCGAAGGC CGTCTGAAAA
551 TTTTGGTGGT CGGCGGCAGT TTGGGTGCGG ACGTTTGA CAAAACCGTA
601 CCGCAGGCGT TGGCACTGCT GCCTGAAGAG GTGCGCCCGC AGATGTACCA
651 CCAGTCGGGG CGTAACAAGC TGGGCAATCT TCAGGCGGAT TATGACGCGT
701 TGGGCGTGAA AGCGGAATGC GTGGAATTTA TTACCGACAT GGTGTCCGCC
751 TACCGTGATG CCGATTGGT GATTTGCCGT GCCGCGCGCG TGACGATTGC
801 CGAGTTGACG GCGGCGGGG TGGGCGCGTT GTTAGTGCCG TATCCTCAGC
851 CCGTTGATGA CCATCAAACC GCCAACGCGC GTTTCATGGT GCAGGCAGAA
901 GCGGGGCTGC TGTGCGGCA AACCCAGTTG ACGGCGGAAA AACTCGCCGA
951 AATCCTCGGC AGCCTCAACC GCGAAAAATG CCTCAAATGG GCGGAAAACG
1001 CCCGTACGTT GGCATTGCCG CACAGCGCGG ATGACGTTGC CGAAGCCGCG
1051 ATTGCGTGTG CGGCGTAAA

```

This corresponds to the amino acid sequence <SEQ ID 278; ORF 087.ng>:

g087.pep

```

1  MGGKTFMLMA GGTGGHIFPA LAVADSLRVR GHVVIWLGSK DSMEERIVPO
51  YGIRLETLAI KGIRNGIKR KLMLPFTLYK TVREAQRIIR KHRVECVIGF
101 GGFVTFPGGL AAKLLGVPIV IHEQNAVAGL SNRHLSRWAK RVLVAFPKAF
151 SHEGGLVGNP VRADISNLPV PAERFQGREG RLKILVVGGS LGADVLNKTV

```

201 PQALALLPEE VRPQMYHQSG RNKLGNLQAD YDALGVKAEC VEFITDMVSA  
 251 YRDADLVICR AGALTIAELT AAGLGALLVP YPHAVDDHQT ANARFMVQAE  
 301 AGLLLPQTQL TAEKLAEILG SLNREKCLKW AENARTLALP HSADDVAEAA  
 351 IACAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 279>:

m087.seq  
 1 ATGGGCGGTA AAACCTTTAT GCTGawkkCG GCGGGAACGG GCGGACATAT  
 51 TTTCCCCGCG CTGGCGGTGG CCGATTTCATT GCGCGCGCGC GGCCATCATG  
 101 TGATTTCGCT GGGCAGCAAG GATTCGATGG AAGAGCGTAT CGTGCCGCAA  
 151 TACGGCATACT GCTTGGAAC GCTGGCGATT AAAGGCGTGC GCGGCAACGG  
 201 CATCAAACGC AAACCTGATGC TGCCGGTTAC TTTGTATCAA ACCGTCCGCG  
 251 AAGCGCAGCG GATTATCCGC AAACACCGTG TCGAGTGGCT CATCGGCTTC  
 301 GCGGCTTCG TTACCTTCCC GGGCGGTTTG GCGGCGAAGC TATTATGCGT  
 351 GCCGATTGTG ATTACAGAGC AAAACGCCGT GGCAGGTTTG TCCAACCGCC  
 401 ACCTGTTCGCG CTGGGCGAAG CGGGTGTTGT ACGCTTTTCC GAAAGCGTTC  
 451 AGCCACGAAG GCGGCTTGGT CGGCAACCCC GTCCGCGCCG ATATTAGCAA  
 501 CCTGCCCGTG CCTGCCGAAC GCTTCCAAGG GCGTGAAGGC CGTCTGAAAA  
 551 TTTTGGTGGT CCGCGGCAGT TTGGGCGCGG ACGTTTTGAA CAAAACCGTA  
 601 CCGCATGCAT TGGCTTTGCT GCGCGACAAT GCGCGTCCGC ATATGTACCA  
 651 CCAATCGGGA CCGGGCAAGC TGGGCATCTT GCAGGCGnnn nnnnnnnnnn  
 701 nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn  
 751 nnnGCGGGAT TGGGTGCGTT GTTAGTGCCG TATCCTCACG CCGTTGACGA  
 801 TCACCAAACC GCCAACGCGC GTTTTATGGT GCAGGCGGAG GCGGATTGCG  
 851 TGTTGCCGCA AACCAGTTG ACGGCGGAAA AACTCGCCGA GATTCTCGGC  
 901 GGCTTAAACC GCGAAAAATG CCTCAAATGG GCAGAAAACG CCCGTACGTT  
 951 GGCAGTCCG CACAGTCCG ACGACGTGGC GGAAGCCGCG ATTGCGTGTG  
 1001 CGGCGTAA

This corresponds to the amino acid sequence <SEQ ID 280; ORF 087>:

m087.pep  
 1 MGGKTFMLXX GGTGGHIFPA LAVADSLRAR GHVWLGLSK DSMEERIVPO  
 51 YGIRLETIAI KGVNGIKR KLMLPVTLYQ TVREAQRIIR KHRVECVIGF  
 101 GGFVTFPGL AAKLLXVPIV IHEQNAVAGL SNRHLRWAK RVLVAFPKAF  
 151 SHEGGLVGNP VRADISNLPV PAERFQREG RLKILVVGGS LGADVLNKTV  
 201 PHALALLPDN ARPHMYHQSG RGKLGILQAX XXXXXXXXXX XXXXXXXXXX  
 251 XAGLGALLVP YPHAVDDHQT ANARFMVQAE AGLLLPQTQL TAEKLAEILG  
 301 GLNREKCLKW AENARTLALP HSADDVAEAA IACAA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 087 shows 83.9% identity over a 355 aa overlap with a predicted ORF (ORF 087.ng) from *N. gonorrhoeae*:

m087/g087

	10	20	30	40	50	60
m087.pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVWLGLSKDSMEERIVPQYGIRLETIAI					
g087	MGGKTFMLMAGGTGGHIFPALAVADSLRVGRHHVWLGLSKDSMEERIVPQYGIRLETIAI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m087.pep	KGVNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGLAALKLVPIV					
g087	KGIRNGIKRKLMLPFTLYKTVEAQRIIRKHRVECVIGFGGFVTFPGLAALKLVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
g087	IHEQNAVAGLSNRHLRWAKRVLVAFPKAFSHEGGLVGNPVRADISNLPVPAERFQREG					
	130	140	150	160	170	180

279

	190	200	210	220	229
m087 . pep	RLKILVVGGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGKLGILQA-----				
g087	RLKILVVGGSLGADVLNKTVPQALALLPEEVRPQMYHQSGRNKLGNLQADYDALGVKAEC				
	190	200	210	220	230
			230	240	250
m087 . pep	-----AGLGALLVPYPHAVDDHQTANARFMVQAE				
g087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE				
	250	260	270	280	290
	260	270	280	290	300
m087 . pep	AGLLLPQTQLTAEKLAEILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX				
g087	AGLLLPQTQLTAEKLAEILGSLNREKCLKWAENARTLALPHSADDVAEAAIACAAX				
	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 281>:

a087 . seq

```

1  ATGGGCGGTA  AAACCTTTAT  GCTGATGGCG  GCGGGAACGG  GCGGACATAT
51  TTTCCCCGCG  CTGGCGGTGG  CGGATTCATT  GCGCGCGCGC  GGCCATCATG
101 TAATTTGGCT  GGGCAGCAAG  GATTTCGATG  AAGAGCGCAT  CGTGCCGCAA
151 TACGACATCC  TGCTCGAAAC  GCTGGCGATT  AAAGGCGTGC  GCGGCAACGG
201 CATCAAACGC  AAGCTGATGC  TGCCGTTTAC  TTTGTATCAA  ACTGTCCGCG
251 AAGCGCAGCA  GATTATCCGC  AAACACCGTG  TCGAGTGGCT  CATCGGCTTC
301 GCGGCTTCG  TTACCTTTCC  CGGCGGTTG  GCGGCGAAGT  TATTAGCGCT
351 GCCGATTGTG  ATTCACGAGC  AAAACGCCGT  GGCAGGTTTG  TCCAACGCC
401 ACCTGTCGCG  CTGGGCGAAG  CGGGTGTGT  ACGCTTTTCC  GAAAGCGTTC
451 AGCCACGAAG  GCGGCTTGGT  CGGCAACCCC  GTCCGCGCCG  ATATTAGCAA
501 CCTGCCCGTG  CCTGCCGAAC  GCTTCCAAGG  GCGTGAAGGC  CGTCTGAAAA
551 TTTTGGTGGT  CGGCGGCAGT  TTGGGCGCGG  ACGTTTGGAA  CAAAACCGTA
601 CCGCAGGCAT  TGGCTTTGCT  GCCCGACAAT  GCGCGTCCGC  AGATGTACCA
651 CCAATCGGGA  CGGGGCAAGC  TGGGCAGCTT  GCAGGCGGAT  TACGACGCGC
701 TGGGCGTGCA  AGCGGAATGC  GTGGAATTTA  TTACCGATAT  GGTGTCCGCC
751 TACGCGCATG  CCGATTGGT  GATTTGCCGT  GCCGCGCGCG  TGACGATTGC
801 CGAGTTGACG  GCGGCGGGAT  TGGGTGCGTT  GTTAGTGCCG  TATCCTCAGC
851 CCGTTGATGA  CCATCAAACC  GCCAACGCGC  GTTTATGGT  GCAGGCGGAG
901 CGCGGATTGC  TGTGCGCGCA  AACCCAGTTG  ACGGCGGAAA  AACTCGCGCA
951 GATTCTCGGC  GGCTTAAACC  GCGAAAAATG  CCTCAAATGG  GCAGAAAACG
1001 CCGTACGTT  GGCAGTCCG  CACAGTGCGG  ACGACGTTGC  CGAAGCCGCG
1051 ATTGCGTGTG  CGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 282; ORF 087.a>:

a087 . pep

```

1  MGGKTFMLMA  GGTGGHIFPA  LAVADSLRAR  GHVIVLWLSK  DSMEERIVPQ
51  YDILLETLAI  KGVNRNGIKR  KLMLPFTLYQ  TVREAQQIIR  KHRVECVIGF
101 GGFVTFPGGL  AAKLLGVPIV  IHEQNAVAGL  SNRHLSRWAK  RVLVYAFPKAF
151 SHEGGLVGNP  VRADISNLPV  PAERFQREG  RLKILVVGGS  LGADVLNKTVP
201 QALALLPDN  ARPQMYHQSG  RGKLGSLQAD  YDALGVQAE  VEFITDMVSA
251 YRDADLVICR  AGALTIAELT  AAGLGALLVP  YPHAVDDHOT  ANARFMVQAE
301 AGLLLPQTQL  TAEKLAEILG  GLNREKCLKW  AENARTLALP  HSADDVAEAA
351 IACAA*

```

m087/a087 85.4% identity over a 355 aa overlap

	10	20	30	40	50	60
m087 . pep	MGGKTFMLXXGGTGGHIFPALAVADSLRARGHHVIVLWLSKDSMEERIVPQYGIRLETIAI					
a087	MGGKTFMLMAGGTGGHIFPALAVADSLRARGHHVIVLWLSKDSMEERIVPQYDILLETIAI					
	10	20	30	40	50	60



280

	70	80	90	100	110	120
m087.pep	KGVRRNGIKRKLMLPVTLYQTVREAQRIIRKHRVECVIGFGGFVTFPGGLAAKLLXVPIV					
a087	KGVRRNGIKRKLMLPFTLYQTVREAQQIIRKHRVECVIGFGGFVTFPGGLAAKLLGVPIV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m087.pep	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
a087	IHEQNAVAGLSNRHLSRWAKRVLYAFPKAFSHEGGLVGNPVRADISNLPVPAERFQGREG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m087.pep	RLKILVVGSLGADVLNKTVPHALALLPDNARPHMYHQSGRGLGILQAXXXXXXXXXXX					
a087	RLKILVVGSLGADVLNKTVPQALALLPDNARPMYHQSGRGLGSLQADYDALGVQAE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m087.pep	XX-----XXXXXXXXXAGLGALLVPYPHAVDDHQTANARFMVQAE					
a087	VEFITDMVSAYRDADLVICRAGALTIAELTAAGLGALLVPYPHAVDDHQTANARFMVQAE					
	250	260	270	280	290	300
	290	300	310	320	330	
m087.pep	AGLLLPQTQLTAEKLAIEILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
a087	AGLLLPQTQLTAEKLAIEILGGLNREKCLKWAENARTLALPHSADDVAEAAIACAAX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 283>:

```

g088.seq
1  ATGTTTATAT  GGCTCGCACA  TTTTCAGCAAC  TGGTTAACCG  GTCTGAATAT
51  TTTTCAATAC  ACCACATTCC  GCGCCGTTAT  GCGCGCGTTG  ACCGCCTTGG
101 CGTTTTCCTT  GATGTTTCGG  CCGTGGACGA  TACGCAGGCT  GACCGCGCTC
151 AAATGCGGGC  AGGCAGTGGC  TACCGACGGC  CCGCAAACCC  ACCTCGTCAA
201 AAACGGCAGC  CCGACGATGG  GCGGTTTCGG  GATTCTGACC  GCCATTACCG
251 TGTCCACCCT  GTTGTGGGGC  AACTGGGCGA  ACCGATATAT  CTGGATTCTC
301 TTGGGCGTAC  TGCTTGCCAC  CGGTGCGCTC  GGTTTTACG  ACGACTGGCG
351 CAAAGTCGTT  TATAAAGACC  CCAACGGCGT  GTCCGCCAAA  TTCAAATGG
401 TGTGGCAGTC  AAGCGTTGCC  GTTatcgCG  GTttggcATT  GTTTTACctt
451 gCcgCcaATT  CCGCCAACAA  TATTTTGATT  GTCCCGtttT  TCAAACAAAT
501 CGCCCTGCGG  CTGGGCGTGG  TCGGCTtttt  gGtggtgtCT  TACCTGACCA
551 TCGTCGGCAC  ATCCAACGCC  GTCAACCTCA  CcgaCGGCTT  GGACGCGCTT
601 GCCGCcttcc  cgttcgctct  cgttgcgcC  GGGCTCGCCA  ttttcgcctA
651 CGTCAGCGGA  CACTACCAAT  TTTCCAATA  CCTCCAGCTT  CCCTATGTCG
701 CCGGCGCGAA  CGAAGTCGCT  ATATTCTGCA  CCGCCATGTG  CGGCGCGTGC
751 CTCGGATTTT  TGTGGTTCAA  CGCCTATCCC  GCGCAAGTCT  TTATGGGCGA
801 TGTCGGCGCG  CTGGCATTGG  GTGCCGCGCT  CCGTaccGtt  gCCGTcaTcg
851 tCCGCCAAGA  ATTTGTcttc  gtcattatGG  GCGGTCTGTT  cgtcgtagaa
901 gccgtgTCCG  TTATGCTTca  tgtcggCTGG  TACAAGAAAA  Ccaaaaaacg
951 CATCTTcCTg  acgGcaccga  ttcataacca  ttaCCaactt  cgatgCTGga
1001 aagaaaacgca  agtcgctcgtc  CGTTtCTGGA  TTAtTaccat  cgtcgtgggt
1051 tTgatagggt  tGagtaccct  caAAattcgc  ggaaactatg  ccgTCCGAAC
1101 ACCTTTCAGA  CGGCATTGA  ACGCGCAATA  A

```

This corresponds to the amino acid sequence <SEQ ID 284; ORF 088.ng>:

```

g088.pep
1  MFLWLAHFSN  WLTGLNIFQY  TTFRAVMAAL  TALAFSLMFG  PWTIRRLTAL
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSLILT  AITVSTLLWG  NWANPYIWL
101 LGVLLATGAL  GFYDWRKV  YKDPNGVSAK  FKMVWQSSVA  VIAGLALFYL
151 AANSANNILI  VPFFKQIALP  LGVVGFLVLS  YLTIVGTSNA  VNLTGDLGL

```

201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC  
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE  
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV  
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 285>:

m088.seq  
 1 ATGTTTTTAT GGCTCGCACA TTTCAGCAnC TGGTTAACCG GTCTGAATnn  
 51 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 101 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 151 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 201 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 251 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 301 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 351 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 401 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 451 nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn nnnnnnnnnnnn  
 501 nnnnnnnnnnnn nnnGGCGTGG TCGGCTTTT GGTGTTGTCT TACCTGACCA  
 551 TCGTCGGCAC ATCCAATGCC GTCAACCTCA CCGACGGCTT GGACGGCCTT  
 601 GCGACCTTCC CCGTCGTCTT CGTTGCCGCC GGCCTCGCCA TCTTCGCCTA  
 651 TGCCAGCGGC CACTCACAAT TTGCCCAATA CCTGCAATTA CTTTACGTTG  
 701 CCGGCGCAAA CGAAGTGGTG ATTTTCTGTA CCGCCATGTG CCGGCGGTGC  
 751 CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGCGA  
 801 TGTCGGTGCA TTGGCATTGG GTGCCGCGCT CGGTACCGTC GCCGTTATCG  
 851 TCCGCCAAGA GTTTGTCCTC GTCATTATGG GCGGATTATT TGTCGTAGAA  
 901 GCCGTATCCG TTATGCTTCA GGTGGGCTGG TATAAGAAAA CCAAAAAACG  
 951 CATCTTCCTG ATGGCGCCCA TCCATACCA CTACGAACAA AAAGGCTGGA  
 1001 AAGAAACCCA AGTCGTCGTC CGCTTTTGA TTATTACCAT CGTCTTGGTG  
 1051 TTGATCGGTT TGAGTACCCT CAAAATCCGC TGAACCTATG CCGTCTGAAC  
 1101 ATCTTTTCTA CGGCATTGA ACGCGCAATA A

1 MFLWLAHFSN WLTGLNIFQY TTFRAVMAAL TALAFSLMFG PWTIRRLTAL  
 51 KCGQAVRTDG PQTHLVKNGT PTMGGSLILT AITVSTLLWG NWANPYIWIL  
 101 LGVLLATGAL GFYDDWRKVV YKDPNGVSAK FKMVWQSSVA VIAGLALFYL  
 151 AANSANNILI VPFFKQIALP LGVVGFLVLS YLTIVGTSNA VNLTDGLDGL  
 201 AAFPFVLVAA GLAIFAYVSG HYQFSQYLQL PYVAGANEVA IFCTAMCGAC  
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE  
 301 AVSVMLHVGW YKKTKKRIFL TAPIHHHYQL RCWKETQVVV RFWIITIVVV  
 351 LIGLSTLKIR GNYAVRTPFR RHLNAQ\*

This corresponds to the amino acid sequence <SEQ ID 286; ORF 088>:

m088.pep  
 1 MFLWLAHFSX WLTGLNXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX  
 51 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX  
 101 XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX XXXXXXXXXXX  
 151 XXXXXXXXXXX XXXXXXXXXXX XGVVGFLVLS YLTIVGTSNA VNLTDGLDGL  
 201 ATFPVVLVAA GLAIFAYASG HSQFAQYLQL PYVAGANEVV IFCTAMCGAC  
 251 LGFLWFNAYP AQVFMGDVGA LALGAALGTV AVIVRQEFVL VIMGGFLVVE  
 301 AVSVMLQVGW YKKTKKRIFL MAPIHHHYEQ KGWKETQVVV RFWIITIVLV  
 351 LIGLSTLKIR XTYAVXTSFR RHLNAQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 088 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 088.ng) from *N. gonorrhoeae*:

m088/g088

m088.pep  
 10 20 30  
 GVVVGFLVLSYLTIVGTSNAVNLTDGLDGLA  
 |||||  
 g088 IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTDGLDGLA  
 150 160 170 180 190 200

	40	50	60	70	80	90
m088.pep	TFPVVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVIFCTAMCGACLGFLWFNAYPA					
	:                    :          :          :					
g088	AFPFLVLAAGLAIFAYVSGHYQFSQYLQLPYVAGANEVAIFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	100	110	120	130	140	150
m088.pep	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
	:					
g088	QVFMGDVGALALGAALGTVAIVIRQEFVLVIMGGLFVVEAVSVMLHVGWYKTKKRIFLT					
	270	280	290	300	310	320
	160	170	180	190	200	
m088.pep	APIHHHYEQKGWKETQVVVRFWIIITIVLVLIGLSTLTKIRXTYAVXTSFRRHNLNAQX					
	:           :           :					
g088	APIHHHYQLRCWKETQVVVRFWIIITIVVVLIGLSTLTKIRGNYAVRTPFRRHNLNAQX					
	330	340	350	360	370	

```

a088.seq
1      ATGTTTTTTAT GGCTCGCACA TTTCAGCAAC TGGTTAACCG GTCTGAATAT
51     TTTTCAATAC ACCACATTCC GCGCCGTCAT GGC CGCGCTTG ACCGCGCTGG
101    CGTTTTCCTT GATGTTTCGG CCGTGGACGA TACGCAGGCT GACCCGCGCT
151    AAATGCGGGC AGGCAGTGCG TACCGACGGT CCGCAAACCC ACCTCGTCAA
201    AAACGGCAGC CCGACGATGG GCGGTTTCGT GATTCTGACC GCCATTACCG
251    TGTCCACCCT GTTGTGGGGC AACTGGGCAA ACCCGTATAT CTGGAATTCTC
301    TTGGGCGTAT TGCTCGCCAC GGGCGCACTC GGTTTTTACG ACGATGCGCG
351    CAAAGTCGTC TATAAAGACC CCAACGGCGT GTCCGCCAAA TTCAAATGG
401    TGTGGCAGTC AAGCGTTGCC ATTATCGCCG GTTTGGCATT GTTTTACCTT
451    GCCGCCAATT CCGCCAACAA TATTTTGATT GTCCCGTTCT TCAAACAAAT
501    CGCCCTGCGC CTGGGCGTGG TCGGCTTTTT GGTGTTGTCT TACCTGACCA
551    TCGTCGGCAC ATCCAATTGC GTCAACCTCA CGACGGGCTT GGACCGCGCTT
601    GCGACCTTCC CCGTCGTCTT GTTGTCCGCC GGCCTCGCCA TCTTCGCGTA
651    TGCCAGCGGC CACTCACAAT TTGCCCAATA CCTGCAATTA CTTTACGTTG
701    CGGCGCAGAA CGAAGTGGTG ATTTTCTGTA CCGCATGTG CGGCGCGTGC
751    CTCGGTTTCT TGTGGTTTAA CGCCTATCCC GCGCAAGTCT TTATGGGGCA
801    TGTCCGTTGA TTGGCATTGG GTCCCGCGCT CGGTACCGTC CCGCTCATCG
851    TCCGCCAAGA GTTTGTCTTC GTCAATTATG GCGGATTATT TGTCGTAGAA
901    GCCGTATCCG TTATGCTTCA GGTCCGCTGG TATAAGAAAA CCAAAAAACG
951    CATCTTCCCT ATGGCGCCCA TCCATCACCA CTACGAACAA AAAGGCTGGA
1001   AAGAAACCCA AGTCGTCGTC CGCTTTTGGA TTATTACCAT CGTCTTGGTG
1051   TTGATCGGTT TGAGTACCCT CAAATCCGC TGAACCTATG CCGTCTGAAC
1101   ACCTTTCAGA CGGCATTGTA ACGCGCAATA A

```

```
a088.pep
  1  MFLWLAHFSN  WLTGLNIFQY  TTFRAVMAAL  TALAFLMFG  PWTIRRLTAL
51  KCGQAVRTDG  PQTHLVKNGT  PTMGGSLLIT  AITVSTLLWG  NWANPYYIWL
101 LGVLLATGAL  GFYDLWRKVV  YKDPNGVSAK  FKMVQSSVA  ILAGLALFYL
151 AANSANNILI  VPFQKIALP  LGVVGFVLVS  YLTIVGTSNA  VNLTGDLGL
201 ATFPVVLVAA  GLAIFAYASG  HSQFAQYLQL  PYVAGANEV  IFCTAMCGAC
251 LGFLWFNAYP  AQVEMGDVGA  LALGAALGT  AVIVRQEFVL  VIMGGFLVVE
301 AVSVMLQKWR  YKTKKRIFL  MAPIHHHYEQ  KGWKETQVVV  RFWIITIVLV
351 LIGLSTLKR  *TYAV*TPFR  RHLNAQ*
```

	150	160	170	180	190	200
m088.pep	XXXXXXXXXXXXXXXXXXXXXXXXXXXXXGVVGFLVLSYLTIVGTSNAVNLTGDLGLA					
a088	IAGLALFYLAANSANNILIVPFFKQIALPLGVVGFLVLSYLTIVGTSNAVNLTGDLGLA					

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	150	160	170	180	190	200
	210	220	230	240	250	260
m088.pep	TFPVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
a088	TFPVLVAAGLAIFAYASGHSQFAQYLQLPYVAGANEVVFCTAMCGACLGFLWFNAYPA					
	210	220	230	240	250	260
	270	280	290	300	310	320
m088.pep	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
a088	QVFMGDVGALALGAALGTVAIVRQEFVLVIMGGLFVVEAVSVMLQVGWYKTKKRIFLM					
	270	280	290	300	310	320
	330	340	350	360	370	
m088.pep	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
a088	APIHHHYEQKGWKETQVVVRFWIITIVLVLIGLSTLKIRXTYAVXTSFRRLHNAQX					
	330	340	350	360	370	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 289>:

g089.seq

```

1  ATGCCGCCCA AAATCAGCAA GAGCGGGTTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATG AATACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACACGGT GCGGCAAGCC TTGGAAGGTT
151 TTGACGTGTT CCAGCAATGC TTCGCGCGGC AAACCGACGG CCTCGCACAA
201 AGCCACGGCA GCCATAACGT TGGCGGCGTT GTGCAAACCT TGCAGCGGGA
251 TGTCTTGCGT AGAAATCAAA TCTTCATTGC CTTGTTTAA ACAGCCCGTC
301 CCGCGTTCCA ACCAAAAATC GGTTCGTGT TCCAAGGAAA ACCGTTTCAC
351 TTCACGCCCT GCCCGTTTCA TGGCGCGGCA GAACACGTCG TCCGCATTCA
401 AAACCTGCAC TCCATCGCCA CGGAAATCT CGGCTTTGGT ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 290; ORF 089.ng>:

g089.pep

```

1  MPPKITKSGF CKPAIAAAVA PTFVPLLSSM NTTPFFSPIF STRCGKPWKV
51  LTCSSNASRG KPTASHKATA AITLAALCKP CSGMSCVEIK SSLPCFKQPV
101 PRSNQKSASC SKENRFTSRP ARFMARQNTS SAFKTCTPSP RKISALVCA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 291>:

m089.seq

```

1  ATGCCGCCCA AAATCACKAw GAGCGGATTT TGCAAACCGG CAATCGCGGC
51  GGCAGTCGCG CCGACATTCG TGCCTTTGCT GTCGTCGATA AACACCACGC
101 CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC TTGGAAGGTT
151 TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG CCTCACACAA
201 AGCCACKGCA GCCATGACGT TAGCGGCGTT GTGCAKACCT TGCAACGGwA
251 TGTCTTGCGT GACAATCAAA TCTTCATTGC CTTGTTTCAG GCGGCCTGTC
301 TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA ACCATTTTAC
351 CTCGCGCCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG TCCGCATTCA
401 AAACCTGCAC GCCGTCGCCA CGGAAATCT TGGCTTTGGT ATGCGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 292; ORF 089>:

m089.pep

```

1  MPPKITXSGF CKPAIAAAVA PTFVPLLSSI NTTPFFSPIF STRCGRPWKV
51  LTCSSNASRD KPMASHKATA AMTLAALCXP CNGMSCVTIK SSLPCFRRPV
101 SRSNQKSASC SNENHFTSRP ARFIARQNAS SAFKTCTPSP RKILALVCA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 089 shows 88.6% identity over a 149 aa overlap with a predicted ORF (ORF 089.ng)

from *N. gonorrhoeae*:

m089/g089

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	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	:         :					
g089	MPPKITXSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	:            :               : :            :    :					
g089	KPTASHKATAAITLAALCKPCSGMSCVEIKSSLPCFKQFVPRSNQKSASCSKENRFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	:      :					
g089	ARFMARQNTSSAFKTCTPSPRKISALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 293>:

a089.seq

```

1  ATGCCGCTA  AAATCACGAA  GAGCGGATTT  TGCAAACCGG  CAATCGCGGC
51  GCGCGTCGCA  CCGACGTTTC  TGCCTTTGCT  GTCGTCGATG  AACACCACGC
101  CATTTTCTC  GCCGATTTT  TCCACGCGGT  GCGGCAGGCC  TTGAAAGGTT
151  TTGACGTGTT  CGAGCAATGC  TTCGCGCGGC  AAACCGACGG  CTTGCGACAA
201  GGCAACGGCA  GCCATCACGT  TAGTGGCGTT  GTGCAAGCCT  TGCAGCGGAA
251  TATCTTGCGT  GGCAATCAAA  TCTTCATTGC  CTTGTTTCAG  GCGACCTGTC
301  TCACGTTCCA  ACCAAAAATC  GGCTTCGTAT  TCCAACGAAA  ACCATTTCAC
351  CTCGCGCCCG  GCGCGCTTCA  TCGCACGACA  GAACGCATCG  TCCGCATTCA
401  AAACCTGCAC  ACCGTCGCCA  CGGAAAATCT  TGGCTTTGGT  ATGCGCGTAG

```

This corresponds to the amino acid sequence <SEQ ID 294; ORF 089.a>:

a089.pep

```

1  MPPKITKSGF  CKPAIAAAVA  PTFVPLLSSM  NTTPFFSPIF  STRCGRP*KV
51  LTCSSNASRG  KPTASHKATA  AITLVALCKP  CSGISCVAIK  SSLPCFRRPV
101  SRSNQKSASY  SNENHFTSRP  ARFIARQNAS  SAFKTCTPSP  RKILALVCA*

```

m089/a089 91.9% identity over a 149 aa overlap

	10	20	30	40	50	60
m089.pep	MPPKITXSGFCKPAIAAAVAPT FVPLLSSINTT PFFSPIFSTRCGRPWKVLTCSSNASRD					
	:         :					
a089	MPPKITKSGFCKPAIAAAVAPT FVPLLSSMNTT PFFSPIFSTRCGRPWKVLTCSSNASRG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m089.pep	KPMASHKATAAMTLAALCXPCNGMSCVTIKSSLPCFRRPVSRSNQKSASCSNENHFTSRP					
	:    :       :               : :            :    :					
a089	KPTASHKATAAITLVALCKPCSGISCVAIKSSLPCFRRPVSRSNQKSASYSNENHFTSRP					
	70	80	90	100	110	120
	130	140	150			
m089.pep	ARFIARQNASSAFKTCTPSPRKILALVCAX					
a089	ARFIARQNASSAFKTCTPSPRKILALVCAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 295>:

g090.seq

```

1  ATGCGCGTAG  TCGAGCAAAT  CGTCGTAGCG  GTCGAGATGG  TCTTCGGAAT

```

q090.pap

1 MRVVEQIVVA VEMVFGNVHH RRRSRAQAFG VFQLEAGKLP HPHVRLFAFA  
51 LQFCLQDGR TDIARNDGIQP ALDAEIAQQA GYRGFAVAAG NRNHLVAAAV  
101 HNVROQLDVA XHAXRRFA\*

m090.seq

Seq	1	ATGCGCATAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
	51	TGTTTCAGCAC	CGTCGCCGCA	GTCGGACGCA	GGCTTTCGGT	GTTTTCAGT
	101	TGGAAGCTGG	AAAGCTCCAA	CACCCACACG	TCCGCTTTT	TGCCTTCGCG
	151	CTGCCATTCC	GCCTCAAAA	CCGGCGTGCC	GATATTGCC	GCGATAACGG
	201	TATCCAGCCC	GCACTTGATA	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
	251	GTTTTCGGCT	TGCTGCCGGT	AATCGCAATT	ACCTTGTCTG	CCCGCGGGT
	301	CACAATTGTC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	.CCGCCGTTT
	351	TGCTTGA				

1090. пер

```

1 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA
51 LPFRLQNRRA DIARDNGIQP ALDTEIADQA RYRGFAVAAG NARNYLVPVAV
101 HNVROOFDVA OHAXRRFA*

```

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 090 shows 83.9% identity over a 118 aa overlap with a predicted ORF (ORF 090.ng) from *N. gonorrhoeae*:

m090/g090

	10	20	30	40	50	60
m090.pep	MRIVEQVVAVEMVFGNVQHRRRSRTQA	FGVFQLEAGKLQHPHVLFAFALPFR	LQNRA			
	:     :	:	:	:	:	:   :
g090	MRVVEQIVVAVEMVFGNVHHRRRSRAQAF	GVFQLEAGKLPHPHVLFAFALQFC	LQDGR			
	10	20	30	40	50	60
	70	80	90	100	110	119
m090.pep	DIARDNGIQPALDTEIADQARYRGFAVAAGNRN	YLVVPVAVHNVRQQFDVAQHAXRRFAX				
	:   :	:	:	:	:	:
g090	DIARNDGIQPALDAEIAHQGYRGFAVAAGNRNHL	VAAAHVNVRQLDVAXHAXRRFAX				
	70	80	90	100	110	

a090.seq

seq	ATGCGCGTAG	TCGAGCAAGT	CGTCGTAGCG	GTCGAGATGG	TCTTCGGA
51	TGTTCCAGCAC	TGTCGCCGCA	GTCGGGCGCA	GGCTTTCCGT	GTTTTCCAGT
101	TGGAACCTGG	AAAGCTCCAA	CACCCACACG	TCCGCCTTTT	TGCCTTCGCG
151	CTGCAATTCC	GCCTCCAAAA	CCGGCGCGCC	GATATTGCC	GCGATAACGG
201	TATCCAGCCC	ACACTTGATG	CAGAGATAGC	CGACCAGGCT	CGTTACCGTG
251	GTTTTCGCGT	TGCTGCCGGT	AATCGCAATC	ACCTTGTCGC	CGCGGCGGTT
301	CACAATTGTC	GCCAGCAATT	CGATGTCGCC	CAACACGCGT	C.CGCCGTTT
351	CGCTTAA				

This corresponds to the amino acid sequence <SEQ ID 300; ORF 090.a>:

## a090.pep

1 MRVVEQVVVA VEMVFGNVQH CRRSRAQAFG VFQLETGKLQ HPHVRLFAFA  
 51 LQFRLQNRRA DIARDNGIQP TLDAEIAQDA RYRGFAVAAG NRNHLVAAA  
 101 HNVRRQFDVA QHAXRRFA\*

m09/a090 91.5% identity over a 117 aa overlap

	10	20	30	40	50	60
m090.pep	MRIVEQVVVA	VEMVFGNVQH	RRRSRTQAFG	VFQLEAGKLQ	HPHVRLFA	FALPFRQLQNRRA
a090	MRVVEQVVVA	VEMVFGNVQH	CRRSRAQAFG	VFQLETGKLQ	HPHVRLFA	FALQFRLQNRRA
	10	20	30	40	50	60

	70	80	90	100	110	119
m090.pep	DIARDNGIQP	ALDTEIAQDA	RYRGFAVAAG	NRNHLVVP	PAVHNVRRQ	QFDVAQHAXRRFAX
a090	DIARDNGIQP	TLDAEIAQDA	RYRGFAVAAG	NRNHLVAAA	VHNVRRQ	QFDVAQHAXRRFAX
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae*

g090-1.seq This sequence contains multiple stop codons (not shown)

This corresponds to the amino acid sequence < ORF 090-1.ng>:

g090-1.pep (not shown)

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2>:

## m090-1.seq

1 ATGACGGCGT TTGCATTTC A GACGGCATCA CAAAGCCTTA AACGCTTCGA  
 51 TAAACACTTC CGAACGGTGC GCGTAGCCTT TGAACATATC AAAGCTCGCG  
 101 CAGGCGGGGC TGAGCAACAC AATATCGCCT GCTTCGGCTT GGGCATATGC  
 151 CGTCTGAACG GCTTCTCCCA AAGTGGCGCA GTCGGTCATA TTCAAGCCGC  
 201 AGCCGTCCTA ATCGCGGCGG ATTTGCGGCG CATCGACACC AATCAAGAAC  
 251 ACGCCTTTTG CTTTGCCTAC CAGTGCATCG CGCAGGGGCG TGAAGTCTCG  
 301 CCCTTTACCC ATGCGGCCCA AAATCACGAA GAGCGGATTT TGCAAACCGG  
 351 CAATCGCGGC GGCAGTCGCG CCGACATTTC TGCCTTTGCT GTCGTCGATA  
 401 AACACCAACG CGTTTTTCTC GCCGATTTT TCCACGCGGT GCGGCAGGCC  
 451 TTGGAAGGTT TTGACGTGTT CGAGCAATGC TTCGCGCGAC AAACCGATGG  
 501 CCTCACACAA AGCCACGGCA GCCATGACGT TAGCGGCGTT GTGCAGACCT  
 551 TGCAACGGAA TGTCTTGCCT GACAATCAA TCTTCATTGC CTTGTTTCAG  
 601 CGGCGCTTGC TCGCGTTCCA ACCAGAAATC AGCTTCGTGT TCCAACGAAA  
 651 ACCATTTTAC CTGCGCGCCG GCACGCTTCA TCGCGCGGCA GAACGCATCG  
 701 TCCGCATTCA AAACCTGCAC GCCGTCGCCA CGGAAAATCT TGGCTTTGGT  
 751 ATGCGCATAG TCGAGCAAGT CGTCGTAGCG GTCGAGATGG TCTTCGGAAA  
 801 TGTTCAGCAC CGTCGCCGCA GTCGGACGCA GGCTTTCGGT GTTTTCCAGT  
 851 TGGAGGCTGG AAAGTCCAA CACCACACG TCCGCTTTT TGCCTTCGCG  
 901 CTGCCATTCC GCCTCCAAA CCGCGGTGCC GATATTGCC GCGATAACGG  
 951 TATCCAGGCC GCACTTGATA CAGAGATAGC CGACCAGGCT CGTTACCGTG  
 1001 GTTTTGCCGT TGCTGCCGGT AATCGCAATT ACCTTGTCGT CCCGGCGGTT  
 1051 CACAATGTCC GCCAGCAATT CGATGTCGCC CAACACGCGT CCGCCGTTTT  
 1101 GCTTGAACGC CTCAATATCC GGCTGCCGCT CGCTGATGCC GGGACTGAGA  
 1151 GCCAGAATAT CGAAACCGTT GTCCAGCGCA TCTTTCAGAC GGCCCGTGTA  
 1201 AAACACCAAC CCGTCAAACA TCTTACCGAT TTGCGACACG CGTTCCGGCT  
 1251 TCAGCTCCGC ATCATAACGA GCAACCTCCG CGCCGTTTT GCGCAGGTAG  
 1301 GCAATCATGG AAATACCGT ACCGCCGAGT CCGCGACGA GGATTTTTTT  
 1351 GTTTTGAAAA GTCATTTTGG TTTGCTCTAA

This corresponds to the amino acid sequence <SEQ ID 3; ORF 090-1>:

## m090-1.pep

1 MTAFATQAS QSLKRFDKHF RTVRVAFEH KARAGGAEQH NIACFGLGIC  
 51 RLNGFSQSGA VGHIAAAVQ IAADLRRI DT NOEHAFCLAY OCIAQGREVL  
 101 PFTHAAQNHE ERILOGTNRG GSRADIRAF VVDKHHAVFL ADFHFAVRQA  
 151 LEGFDVFEC FARQTDGLTQ SHGSHDVSGV VQTLQNVLR DNQIFIALFO  
 201 AACLAFOPEI SPVFQRKPFY LAPGTLHRAA ERIVRIQNLH AVATENLFGF  
 251 MRIVEQVVVA VEMVFGNVQH RRRSRTQAFG VFQLEAGKLQ HPHVRLFAFA  
 301 LPFRLQNRRA DIARDNGIQP ALDTEIAQDA RYRGFAVAAG NRNHLVVP  
 351 HNVRRQFDVA QHASAVLLER LNIRLPLADA GTESQNIETV VQRIQTARV  
 401 KHQPVKHLTD LRHAFRLQLR IIRSNLRAVF AQVGNHGNTR TAESGDEDFD  
 451 VLKSHFGLS\*

1	ATGGAATAC	CCGTGCCGCC	AAGTCCGGCG	ACGAGGATTT	TTTTGTTTGA
51	AAGTCATTTT	GGTTTTGTCC	TAAAACAAAT	CATATTGGGC	AGGAGACGTC
101	CGCCCTTGCC	CAAGCCGCTT	TCAGACGSCA	TCGCGAGCCG	ATTAATAACC
151	CGCCTTCAGG	CGTTGGTCAT	TGTCGCAGCT	GTTTGGTCT	CCGTTTTGAC
201	AAGCCTTGCC	AAGCCATTGT	TGAGCGAGCG	CAAGGTCTTG	GCGCACGCCG
251	CGTCCATCGT	AATACATCAA	GCCCAAATTG	TATTGGGCTT	GGGCATCCCC
301	TTGTTCTGA				

```

1 MEIPVPPSPA TRIFLFESHF GFVLKQIILG RRRPPLPKPL SDGIASRLIT
51 RLQALVIVAA VLVSVLTSLA KPLLSEKVL AHAASIVIHQ AQIVLGLGIP
101 LF*

```

1	ATGGAATAC	CCGTACCGCC	GAGTCCGGCG	ACGAGGATTT	TTTTGTTTGA
51	AAAGTCATTT	TGGTTTGTCC	TAAAACAAAT	CATATTGAGC	AGGAGATGTC
101	CGCCCCTGCC	CAAGCCGCTT	TCAGACGGCA	TCGCGAGCTG	TTCAATAACC
151	CGCCTTCAGG	CGTTGGTCAT	TGTCGCAGCC	GTCTTGGTCT	CCGTTTTGAC
201	AAGCCTTCGG	AAACCATTCT	TGTGCAAGGG	CGCGGTCTTG	GCGCACGCCG
251	CGCTTTTCGC	CATACATCAC	GCCCAAATTG	TTTTGGGCTT	GGGCTACCCC
301	CTGCGC...				

1 MEIPVPPSPA TRIFLFEKSF WFLVKQIILS RRCPLPKPL SDGIASCSIT  
51 RLQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLGLGYP  
101 LR.

m091/g091

```

                                10      20      30      40      50      60
m091.pep  MEIPVPPSPATRIFLFEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g091      MEIPVPPSPATRIFLFESHFGFVLKQIILGRRRPPLPKPLSDGIASRLITRLQALVIVAA
          10      20      30      40      50      60

                                70      80      90      100
m091.pep  VLVSVLTSIAKPFCKGAVLAHAASFGIHHQAQIVLGLGYPLR
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g091      VLVSVLTSIAKPLLSEKVLHAHAASIVIHQAQIVLGLGIPFLX
          70      80      90      100

```

1 ATGGAATAC CCGTGCCGCG AGTCCGGCG ACAGGATT TTTGTTTTG  
51 GAAATCATTT TGGTTTGTCC TAAACAAAT CATATTGAGC AGGGGATGTC  
101 TGATCCTGCT CAAGCCGCTT TCAGACGGCA TCGCGAGCTG TTCAATAACC  
151 CGCTTTCAGG CGTTGGTCAT TGTGCGAGCT GTCTTGGTAT CCGTTTTGAC  
201 AAGCCTTGCC AAGCCATTCT TGTGCAAGGG CGCGGCTCTG GCGCACGCCG  
251 CGCTTTTCGG CATACTACAC GCCCAAATG TTTTGGGC



This corresponds to the amino acid sequence <SEQ ID 308; ORF 091.a>:

a091.pep

```

1  MEIPVPPSPA TRIFLEWKSF WFLVKQIILS RGCLILLKPL SDGIASCSIT
51  RFQALVIVAA VLVSVLTSLA KPFLCKGAVL AHAASFGIHH AQIVLG

```

m091/a091 93.8% identity over a 96 aa overlap

	10	20	30	40	50	60
m091.pep	MEIPVPPSPATRIFLEKSFWFVLKQIILSRRCPLPKPLSDGIASCSITRLQALVIVAA					
a091	MEIPVPPSPATRIFLEKSFWFVLKQIILSRGCLILLKPLSDGIASCSITRFQALVIVAA					
	10	20	30	40	50	60
	70	80	90	100		
m091.pep	VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQIVLGLGYPLR					
a091	VLVSVLTSLAKPFLCKGAVLAHAASFGIHHQIVLG					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 309>:

g092.seq

```

1  ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGTCCGC
51  AAACGGTCAG ACCTTTAAAA TAACGCCCTT ACGCACTAAA AACCAACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTAA GCAACATCCA TTTTGTCCGT
151 ATCGGCGGCG TCGGCATGAG CGGTATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGTTCCGG ATCAGGCGCG AAATGCCGCT ACCGAGCATT
251 TGAGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC AGAACACGTT
301 AACGGTgcgg ATGTCGTCGT TGCCTCTACC GCCGTCAAGA AAGAAaatcc
351 CGAAGTtgct gcTGCgTTGG AGCGGCAAAT TCCCGTTATT CCGCGCGCCT
401 TGATGCTGGC AGAGCTGATG CGCTTCCGTG ACGgcatcgc cattgccggT
451 ACGCACGGCA AAACCACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTC GACCCCACTT TCGTTATCGG CGGCAAACTC AACGCCGCAG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAATCCGATG CCTCTTTCCT ACATCTGACC CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTTGT GTGTTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGC CGC GCAA TGA AATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGc gtggcGCTgg
1001 aagtcGgCGC ATcggttgAA GCGAtcCAA AaggCTTGCT CGGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATAcggc gacatCAagt tgccaaacgg
1101 cggGaccgCT TTgctGGTGG ACGATTAcgg ACACCACCCC GTCGAAATGG
1151 CGGcaaccct tgccgcTGCA CGCGGCGCGT ATCCGGAAAA acgtTTGGTG
1201 CtgcCCTTCC AGCCGCACCG CTATACCCGC ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTACTCAATA CCGTTGatgC GCTGGTACTG ACCGAAGTTT
1301 AtgccgcccG CGAAGAGCCG GTTGCCGCCG CCGactcCCG CGCCTTGGCG
1351 CGTGCTATCC GCGTATTGGG CAAACTTGAG CCGATTACT GCGAAAatgt
1401 cgccgACCTG CCGCAAATGC TGATGAATGT TTTACAGGAT Gcggatgttg
1451 tgttgAATAT GggTgcggga agcatcaacc gcgttccttc cgcgctgttg
1501 gaattgtcga AACAGAttg A

```

This corresponds to the amino acid sequence <SEQ ID 310; ORF 092.ng>:

g092.pep

```

1  MFFISIRYIF VRKLWCANGQ TFKITPLRTK NQPERNIMMK NRVSNIHFVG
51  IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLSSLGIO VYPGHTAEHV
101 NGADV VAST AVKENPEVV AALERQIPVI PRALMLAELM RFRDGIAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK

```

```

251 AFLCVDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP VAAADSRALA
451 RAIRVLGKLE PIYCENVADL PQMLMNVLQD GDVVLNMGAG SINRVPSALL
501 ELSKQI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 311>:

m092.seq

```

1 ATGTTTTTTTA TTTCAATCCG CTATATATTT GTCAGAAAAC TATGGCGCGC
51 AAACGGTCAG CCCTTTAAAA TAACGCCTTT ACGCATCGAA AATCCACCGG
101 AACGCAACAT TATGATGAAA AATCGAGTTA CCAACATCCA TTTTGTGGT
151 ATCGGCGGCG TCGGCATGAG CGGCATCGCC GAAGTCTTGC ACAATTTGGG
201 CTTTAAAGTT TCCGTTTCGG ATCagGCGCG AAATGCCGCT ACCGAGCATT
251 TGGGCAGCCT GGGCATTCAA GTTTATCCCG GCCATACCGC CGAACACGTT
301 AACGGTGC GG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCGTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGGC
451 ACGCACGCA AAACACGAC CACCAGCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAACTC AACGCCGACG
551 GCACTAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGC GTCGAAAAAC
701 TGCATCAGGC GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAAA
751 GCCTTTTGT GTATTGACAG CGAACACGTC CGCGCGATT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGA CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GCGCGCAAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTT GAAGTCGTGC TGAATATGCC
951 CCGCAGACAC AACGTGCTGA ACGCATTTGG AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CCGCTTTGAA
1051 GCGGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 CGGGACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CCGCGACCTT TCCCGCCGCA CGCGGCGCGT ATCTGAAAAA ACGTTTGGTA
1201 CTCGCCTTCC AGCGGCACCG CTATACCGCG ACGCGCGATT TGTTTGAAGA
1251 CTTTACCAAA GTCCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CCGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTGGG CAAACTCGAG CCGATTACT GCGAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTTGAACGT TTTGCAGGAC GCGGACATCG
1451 TGTTGAATAT GGGCGCGGGA AGCATCAACC GCGTCCCGC CGCGTGCTG
1501 GCATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 312; ORF 092>:

m092.pep

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDGIATAG
151 THGKTTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 GVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLAAA RGAYLEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLLNVLQD GDIVLNMGAG SINRVPAALL
501 ALSKQI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 092 shows 96.6% identity over a 506 aa overlap with a predicted ORF (ORF 092.ng) from *N. gonorrhoeae*:

m092/g092

```

10 20 30 40 50 60
m092.pep MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA

```

a092.seq

85					
1	ATGTTTTTTA	TTTCAATCCG	CTATATATTT	GTCAGAAAAC	TATGGCGCGC
51	AAACGGTCAG	CCCTTTAAAA	TAACGCCTTT	ACGCATCGAA	AATCCACCGG
101	AACGCAACAT	TATGATGAAA	AATCGAGTGA	CCAACATCCA	TTTTGTGGT
151	ATCGGCGGGC	TCGGCATGAG	CGGTATCGCC	GAAGTCTTGC	ACAATTTTGGG
201	TTTTAAAGTT	TCCGTTTCGG	ATCAGGCGCG	AAATGCCGCT	ACCGAGCATT
251	TGGCGACGCT	GGGCATTCAA	GTTTATCCCG	GCCATACCGC	AGAACACGTT

```

301 AACGGTGCGG ATGTCGTCGT TACCTCTACC GCCGTCAAAA AAGAAAATCC
351 CGAAGTTGTC GCTGCGTTGG AGCAGCAAAT TCCCCTTATT CCGCGCGCCC
401 TGATGTTGGC GGAGTTGATG CGCTTCCGTG ACGGCATCGC CATTGCCGCG
451 ACGCAGGCA AAACACGAC CACCAGCCTG ACCGCCTCCA TCCTCGGCGC
501 GGCAGGACTT GACCCGACTT TCGTTATCGG CGGCAAATC AACGCCGCG
551 GCACCAACGC CCGCTTGGGC AAAGGCGAAT ACATCGTTGC CGAAGCCGAC
601 GAGTCGGATG CATCCTTCT GCACCTGACA CCGATTATGT CCGTCGTTAC
651 CAATATCGAC GAAGACCATA TGGATACCTA CGGGCACAGT GTTGAGAAGC
701 TGCATCAGG GTTTATCGAT TTCATCCACC GTATGCCCTT CTACGGCAA
751 GCCTTTTTGT GTATTGACAG CGAACACGTC CGCGCGATTT TGCCCAAAGT
801 GAGCAAACCT TATGCTACTT ACGGTTTGGG CGATACCGCC GACATCTACG
851 CCACCGACAT CGAAAACGTC GGC GCGCAA TGAAATTCAC CGTCCATGTT
901 CAAATGAAAG GACATGAGCA GGGGTCGTTT GAAGTCGTGC TGAATATGCC
951 CGGCAGACAC AACGTGCTGA ACGCATTGGC AGCCATCGGC GTGGCGCTGG
1001 AAGTCGGCGC ATCGGTTGAA GCGATCCAAA AAGGCTTGCT CGGCTTTGAA
1051 GGTGTCGGCC GCCGCTTCCA AAAATACGGC GACATCAAGT TGCCAAACGG
1101 TGAACCGCG CTCTTGGTGG ACGACTACGG ACACCACCCC GTCGAAATGG
1151 CGGCGACCCT TTCCGCCGCA CGCGCGCGT ATCCGGAAAA ACGTTTGGTA
1201 CTCGCTTCC AGCCGCACCG CTATACCGC ACGCGCGATT TGTGGAAGA
1251 CTTTACCAA GTCTCAATA CCGTTGACGC GCTGGTGCTG ACCGAAGTTT
1301 ATGCCGCCGG TGAAGAGCCG ATTGCCGCCG CTGATTCCCG CGCTCTTGCC
1351 CGCGCCATCC GCGTGTTGGG CAAACTCGAG CCGATTACT GCGAAAACGT
1401 TGCCGATCTG CCCGAAATGC TGTGAACGT TTTGCAGGAC GGCGACATCG
1451 TGTGAATAT GGGTGCGGA AGCATCAACC GCGTCCCCG CGCGCTGCTG
1501 GAATTGTCGA AACAGATTG A

```

This corresponds to the amino acid sequence <SEQ ID 314; ORF 092.a>:

**a092.pep**

```

1 MFFISIRYIF VRKLWRANGQ PFKITPLRIE NPPERNIMMK NRVTNIHFGV
51 IGGVMSGIA EVLHNLGFKV SGSDQARNAA TEHLGSLGIQ VYPGHTAEHV
101 NGADVVTST AVKKENPEVV AALEQQIPVI PRALMLAELM RFRDIAIAG
151 THGKTTTSL TASILGAAGL DPTFVIGGKL NAAGTNARLG KGEYIVAEAD
201 ESDASFLHLT PIMSVVTNID EDHMDTYGHS VEKLHQAFID FIHRMPFYGK
251 AFLCIDSEHV RAILPKVSKP YATYGLDDTA DIYATDIENV GAQMKFTVHV
301 QMKGHEQGSF EVVLNMPGRH NVLNALAAIG VALEVGASVE AIQKGLLGFE
351 VVGRRFQKYG DIKLPNGGTA LLVDDYGHHP VEMAATLSAA RGAYPEKRLV
401 LAFQPHRYTR TRDLFEDFTK VLNTVDALVL TEVYAAGEEP IAAADSRALA
451 RAIRVLGKLE PIYCENVADL PEMLNLVQD GDIVLNMGAG SINRVPAALL
501 ELSKQI*

```

**m092/a092** 99.4% identity over a 506 aa overlap

	10	20	30	40	50	60
m092.pep	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA					
a092	MFFISIRYIFVRKLWRANGQPFKITPLRIENPPERNIMMKNRVTNIHFGVIGGVMSGIA					
	10	20	30	40	50	60
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	70	80	90	100	110	120
m092.pep	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
a092	EVLHNLGFKVSGSDQARNAAATEHLGSLGIQVYPGHTAEHVNGADVVTSTAVKKENPEVV					
	130	140	150	160	170	180
m092.pep	AALEQQIPVIPRALMLAELMRFRDIAIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
a092	AALEQQIPVIPRALMLAELMRFRDIAIAGTHGKTTTTSLTASILGAAGLDPTFVIGGKL					
	130	140	150	160	170	180
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
	190	200	210	220	230	240
m092.pep	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					
a092	NAAGTNARLGKGEYIVAEADESDASFLHLTPIMSVVTNIDEDHMDTYGHSVEKLHQAFID					

292

	190	200	210	220	230	240
	250	260	270	280	290	300
m092.pep	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKTIVHV					
a092	FIHRMPFYGKAFLCIDSEHVRAILPKVSKPYATYGLDDTADIYATDIENVGAQMKTIVHV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m092.pep	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
a092	QMKGHEQGSFEVVLNMPGRHNVNLALAAIGVALEV GASVEAIQKGLLGFEVGRRFQKYG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m092.pep	DIKLPNGGTALLVDDYGHHPVEMAATLAAARGAYLEKRLVLA FQPHRYTRTRDLFEDFTK					
a092	DIKLPNGGTALLVDDYGHHPVEMAATLSAARGAYPEKRLVLA FQPHRYTRTRDLFEDFTK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m092.pep	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
a092	VLNTVDALVLTEVYAAGEEPIAAADSRALARAIRVLGKLEPIYCENVADLPEMLLNVLQD					
	430	440	450	460	470	480
	490	500				
m092.pep	GDIVLNMGAGSINRVPAALLALSQIX					
a092	GDIVLNMGAGSINRVPAALLELSQIX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 315>:

```

g093.seq
1  atGCAGAAAtt ttgGCAAAGT ggccgtATTG ATGGGtggtT TTTCCAGCGA
51  ACGAGAAatc tcgctGGACA GcGTACCGC CATTTTGAAC GCCTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGACC CTAAGGAAAC GCCGTATATCC
151 GAACTGAAGG AGCGGGGCTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGCGCAA GACGGGGCTG TTCAGGTGC ATTGGAAC TGGGGCATTC
251 CCTATACCGG CAGCGGTGTC GCCGCCTCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTGGA GGCATTGGGA TTACCCGTT CCGAGTTTCGC
351 CGTACTGTAC GATGATACCG ATTTGATGC CGTCGAAGAA AAATTGGGTC
401 TGCCGATGTT TGTGAAGCCG GCGGCCGAAG GCAGCAGCgt cggcgtggta
451 aaAGTCAAAG AAAaaggccg TCTGAAAAGC GTTtacgaag aatTGAAaCA
501 CCTTcagggg cgaAatcatt gccgAacgTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACGG CAAAGGGCTG CCCGGCATA ACATCATCCC
601 CGCAACCGAG TTTTACGAct acgaagccaa GtacaacCGA GACGAcacca
651 tttatCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTGCGCG CGCACAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 316; ORF 093.ng>:

```

g093.pep
1  MQNFGKVAVL MGFSSEREI SLDsgTAILN ALKSKGIDAY AFDPKETPLS
51  ELKERGFQTA FNILHGTYGE DGAVQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLY DDTDFDAVEE KLGLPMFVKP AAEGSSVGUV
151 KVKEKGRLKS VYEELKHLQG RNHCRTFYRR RRIFLPRPER QRAARHTHP
201 RNRVLRRLRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RTGNRCGLRL
251 ARRFQRYRR QTLVGNQHP ARYDRP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 317>:

m093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CTAAAGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCtAA GACGGGGCGG TTCAGGGTGC ATTGGAAC TGGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTGGCA GGCATTGGGA TTGCCCCTTC CCGAGTTTCG
351 CGTCCTGCAC GACGACACTG ATTTTCGATG CGTCGAAGAA AAATTGGGGC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CCTTCAGGG. CGAAATCATT GCCGAACGTT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCCG TCCTGAACCG CAAAGGGCTG CCCGGCATA ACATCATTCC
601 CGCAACCGAG TTTTACGACT ACGAAGCCAA GTACAACCGC GACGACACCA
651 TTTATCAATG TCCTTCGGAA GATTTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACGG CAAACTCTAT CTGTTGGAAA
801 TCAACACCCT GCCCGGTATG ACGAGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 318; ORF 093>:

```

m093 . pep
1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGX DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AEGSSVGVV
151 KVKGKGR LKS VYEELKHLQX RNHCRTFYRR RRI FLPRPER QRAARHTHHS
201 RNRVLR LRSQ VQPRRHLSM SFGRFDRSRR KPDARTGGS RAGNRCGR LR
251 ARRFQRYRR QTL SVGNQHP ARYDEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 093 shows 96.7% identity over a 276 aa overlap with a predicted ORF (ORF 093.ng) from *N. gonorrhoeae*:

m093/g093

	10	20	30	40	50	60
m093 . pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKAQGFQTA					
g093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPL SELKERGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093 . pep	FNILHGTYGX DGA VQGALELL LGIPYTGSGVA ASAIGMDKYRCKLIWQALGLPVPEFAVLH					
g093	FNILHGTYGEDGA VQGALELL LGIPYTGSGVA ASAIGMDKYRCKLIWQALGLPVPEFAVLY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093 . pep	DDTDFDAVEE KLGLPMFVKPAAEGSSVGVV KVKGKGR LKS VYEELKHLQX RNHCRTFYRR					
g093	DDTDFDAVEE KLGLPMFVKPAAEGSSVGVV KVKEKGR LKS VYEELKHLQGRNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093 . pep	RRI FLPRPERQRAARHTHHSRNRVLR LRSQVQPRRHLSMSFGRFDRSRRKPDARTGGS R					
g093	RRI FLPRPERQRAARHTHHSRNRVLR LRSQVQPRRHLSMSFGRFDRSRRKPDARTGGS R					
	190	200	210	220	230	240
	250	260	270			
m093 . pep	RAGNRCGR LRARRFPQRYRRQ TLSVGNQHPARYDEPX					
g093	RTGNRCGR LRARRFPQRYRRQ TLSVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 319>:

## a093.seq

```

1  ATGCAGAATT TTGGCAAAGT GGCCGTATTG ATGGGCGGTT TTTCCAGCGA
51  ACGAGAAATC TCGCTGGACA GCGGCACCGC CATTTTGAAT GCTTTAAAAA
101 GCAAAGGCAT AGACGCATAC GCCTTCGATC CCAAGGAAAC CCCATTGTCT
151 GAATTGAAGG CACAAGGTTT TCAGACGGCA TTCAACATCC TTCACGGTAC
201 TTACGGCGAA GACGGGGCTG TTCAGGGTGC ATTGGAAC TGGGGCATTG
251 CCTATACCGG CAGCGGTGTC GCCGCATCCG CCATCGGCAT GGACAAATAC
301 CGCTGCAAAC TGATTTGGCA GGCATTGGGA TTGCCCGTTC CCGAGTTCGC
351 CGTCCTGCAC GACGACACTG ATTTGATGCG CGTCGAAGAA AAATTGGGCC
401 TGCCGATGTT TGTGAAACCG GCGGCCGAAG GCAGCAGCGT AGGCGTGGTA
451 AAAGTCAAAG GAAAAGGCCG TCTGAAAAGC GTTTACGAAG AATTGAAACA
501 CTTTCAGGG. CGAAATCATT GCCGAACGGT TTATCGGCGG CGGCGAATAT
551 TCCTGCCCTG TGTGAAACCG CAAAGGCCCTG CCCGGCATAC ACATCATCCC
601 CGCGACCGAG TTTTATGACT ACGAAGCCAA GTACAACCGC AACGACACCA
651 TTTATCAATG TCCTTCGGAA GATCTGACCG AAGCCGAAGA AAGCCTGATG
701 CGCGAACTGG CGGTTTCGGG CGCGCAGGCA ATCGGTGCGG AAGGCTGCGT
751 GCGCGTCGAT TTCCTCAAAG ATACCGACCG CAAACTCTAT CTGTTGAAAA
801 TCAACACCCT GCCCGGTATG ACCGGCCATA G

```

This corresponds to the amino acid sequence <SEQ ID 320; ORF 093.a>:

## a093.pep

```

1  MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLS
51  ELKAQGFQTA FNILHGTYGE DGA VQGALEL LGIPYTGSGV AASAIGMDKY
101 RCKLIWQALG LPVPEFAVLH DDTDFDAVEE KLGLPMFVKP AAEGSSVG VV
151 KVKGKGR LKS VYEELKHFX RNHCRTVYRR RRIFLPCVER QRPARTHHP
201 RDRV L* LRSQ VQPQRHLSM SFGRSDRSRR KPDARTGGS RAGNRCGR LR
251 ARRFQRYRR QTL SVGNQHP ARYDRP*

```

m093/a093 95.7% identity over a 276 aa overlap

	10	20	30	40	50	60
m093.pep	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
a093	MQNFGKVAVL MGGFSSEREI SLDSGTAILN ALKSKGIDAY AFDPKETPLSELKAQGFQTA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m093.pep	FNILHGTYGX DGA VQGALELLG IPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
a093	FNILHGTYGEDGA VQGALELLG IPYTGSGVAASAIGMDKYRCKLIWQALGLPVPEFAVLH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m093.pep	DDTDFDAVEEKLGLPMFVKPAAEGSSVG VVKVGKGR LKSVYEELKHLQXRNHCRTFYRR					
a093	DDTDFDAVEEKLGLPMFVKPAAEGSSVG VVKVGKGR LKSVYEELKHFXRNHCRTFYRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m093.pep	RRIFLPRPERQRAARHTHHSRNRVLR LRSQVQPRRHLSMSFGRFDRSRRKPDARTGGS R					
a093	RRIFLPCVERQRPARTHHPDRVLXLR SQVQPRRHLSMSFGRSDRSRRKPDARTGGS R					
	190	200	210	220	230	240
	250	260	270			
m093.pep	RAGNRCGR LRARRFPQRYRRQTL SVGNQHPARYDEPX					
a093	RAGNRCGR LRARRFPQRYRRQTL SVGNQHPARYDRPX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 321>:

```
g094.seq
  1 ATGTATTCGC CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
 51 GCCGCCGATA ACGAAAGTGG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CCGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTAcggc aatggcgatg
151 cCGTCACGGA AGCGCATCAG CTCTGCCAGC ATCAAGGCGC GCGGAATAAC
201 GGGAAATTGC CGTCCAACG CAgcgacaAC TTCGGgattT TCTTTCTTGA
251 CGGCGGTAGA GGCAACGACG ACATccgcAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 322; ORF 094.ng>:

```
g094.pep
  1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKRISSAS IKARGITGIC RSNAATTSGF SFLTAVEATT TSAPLTCSAV
101 WPG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 323>:

```
m094.seq
  1 ATGTATTCGC CTTTGCCCAA GCGGGCGTTA GTGCCTGCGG CGTTGAGTTT
 51 GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CCGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCGGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 324; ORF 094>:

```
m094.pep
  1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM
 51 PSRKINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV
101 WPG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 094 shows 95.1% identity over a 103 aa overlap with a predicted ORF (ORF 094.ng) from *N. gonorrhoeae*:

```
m094/g094

      10      20      30      40      50      60
m094.pep MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISSAN
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g094     MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVVVLPCVPAMAMPSRKRISSAS
          10      20      30      40      50      60

      70      80      90     100
m094.pep IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g094     IKARGITGICRSNAATTSGFSFLTAVEATTTAPLTCSAVWPGX
          70      80      90     100
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 325>:

```
a094.seq
  1 ATGTATTCGC CTTTGCCCAA GCGGGCGTTG GTGCCTGCGG CGTTGAGTTT
 51 GCCGCCGATA ACGAAAGTCG GGTCAAGTCC TGCCGCGCCG AGGATGGAGG
101 CCGTCAGGCT GGTGGTCGTG GTTTTGCCGT GCGTGCCGGC AATGGCGATG
151 CCGTCACGGA AGCGCATCAA CTCCGCCAAC ATCAGGGCGC GCGGAATAAC
201 GGGAAATTGC TGCTCCAACG CAGCGACAAC TTCGGGATT TCTTTTTTGA
251 CGGCGGTAGA GGTAACGACG ACATCCGCAC CGTTAACGTG TTCTGCGGTA
301 TGGCCGGGAT AA
```

This corresponds to the amino acid sequence <SEQ ID 326; ORF 094.a>:



a094.pep  
 1 MYSPLPKRAL VPAALSLPPI TKVGSSPAAP RMEAVRLVVV VLPCVPAMAM  
 51 PSRKINSAN IRARGITGIC CSNAATTSGF SFLTAVEVTT TSAPLTCSAV  
 101 WPG\*

m094/a094 100.0% identity over a 103 aa overlap

	10	20	30	40	50	60
m094.pep	MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVV VLPCVPAMAMPSRKINSAN					
a094	MYSPLPKRALVPAALSLPPI TKVGSSPAAPRMEAVRLVVV VLPCVPAMAMPSRKINSAN					
	10	20	30	40	50	60
	70	80	90	100		
m094.pep	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX					
a094	IRARGITGICCSNAATTSGFSFLTAVEVTTTSAPLTCSAVWPGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 327>:

g095.seq  
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT  
 51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA  
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC  
 151 AACACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA  
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG  
 251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGGGTCA GTGTAGGAAA  
 301 GAGGCATCGG ATCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG  
 351 CGGGCGTTGG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 328; ORF 095.ng>:

g095.pep  
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV  
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK  
 101 EASDRRLRQR CIRLCPSGRW CLRR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 329>:

m095.seq  
 1 ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTGC GCGCCGACGT  
 51 TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA  
 101 GCATAAGGTT TGCTCACTTT GGGCAAAATC GCGCGGACGT GTTCGCTGTC  
 151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA  
 201 TAAACGCCTG ATGCAGTTTT TCGACGCTGT GCCCGTAGGT ATCCATATGG  
 251 TCTTCGTCGA TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG  
 301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTCGCC TTTGCCCAAG  
 351 CGGGCGTTAG TGCCTGCGGC GTTGA

This corresponds to the amino acid sequence <SEQ ID 330; ORF 095>:

m095.pep  
 1 MSFHLNMDGE FHLRADVFDV GGVDVGGIVQ TVSSIRFAHF GQNRADVFAV  
 51 NTQKGFAVEG HTVDEIDKRL MQFFDAVPVG IHMVFDIGN DGHNRQCQRK  
 101 DASDRRLRQR CIRLCPSGRX CLRR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 095 shows 97.6% identity over a 124 aa overlap with a predicted ORF (ORF 095.ng) from *N. gonorrhoeae*:

m095/g095

	10	20	30	40	50	60
m095.pep	MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG					

297

```

g095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
m095.pep  HTVDEIDKRLMQFFDAVPVGIHMVFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           70      80      90     100     110     120
g095      HTVDEIDKRLMQFFDAVPVGIHMVFVDIGNDGHNRCQCRKEASDRRLRQRCIRLCPSGRW
           70      80      90     100     110     120

m095.pep  CLRRX
           ||||
g095      CLRRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 331>:

```

a095.seq
1  ATGTCCTTTC ATTTGAACAT GGACGGTGAA TTTCATTTCG GCGCCGACGT
51  TTTCGATGTC GGTGGCGTAG ATGTCGGCGG TATCGTCCAA ACCGTAAGTA
101 GCATAAGGTT TGCTCACTTT GGGCAAATC GCGCGGACGT GTTCGCTGTC
151 AATACACAAA AAGGCTTTGC CGTAGAAGGG CATACGGTGG ATGAAATCGA
201 TAAACGCCTG ATGCAGCTTC TCAACACTGT GCCCGTAGGT ATCCATATGG
251 TCTTCGTCTG TATTGGTAAC GACGGACATA ATCGGTGTCA GTGCAGAAAG
301 GATGCATCCG ACCGTCGGCT TCGGCAACGA TGTATTGCC TTTGCCCAAG
351 CGGGCGTTGG TGCTGCGGC GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 332; ORF 095.a>:

```

a095.pep
1  MSFHLNMDGE FHLRADVFDV GGVVDVGGIVQ TVSSIRFAHF GQNRADVFAV
51  NTQKGFAVEG HTVDEIDKRL MQLLNTVPVG IHMVFDIGN DGHNRCQCRK
101 DASDRRLRQR CIRLCPSGRW CLRR*

```

m095/a095 96.0% identity in 124 aa overlap

```

m095.pep  MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60
a095      MSFHLNMDGEFHLRADVFDVGGVDVGGIVQTVSSIRFAHFGQNRADVFAVNTQKGFAVEG
           10      20      30      40      50      60

m095.pep  HTVDEIDKRLMQFFDAVPVGIHMVFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRX
           70      80      90     100     110     120
a095      HTVDEIDKRLMQLLNTVPVGIHMVFVDIGNDGHNRCQCRKDASDRRLRQRCIRLCPSGRW
           70      80      90     100     110     120

m095.pep  CLRRX
           ||||
a095      CLRRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 333>:

```

g096.seq
1  ATGGCCGGTC ATACCGGGCA GGGTGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCGATT
101 GCCTGTGCGC CGCGAACC GCAGTTGCGC ATCAGGCTTT CTTGCGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGataaat ggtgTCGTCT CGGttgtaCt

```

298

```

201  tggcttcgta gTCGTAAAC TCGGTTGCGG GGATGATGTG TATGCCGGGC
251  AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301  AcgtTcggca atgaTTtcgc ccctgAAGGT GttTCAattc ttcgtaAACG
351  CTTTTCAGAc ggccttTTTC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 334; ORF 096.ng>:

**g096.pep**

```

1  MAGHTGQGVDFQOIEFAVGI FEEIDAHAAF RTDCLCAANR QFAHQAFFGF
51  GQIFRRTLIN GVVSVVLGFV VVKLGCGDDV YAGQPFVAVQD GAGIFAAADK
101 TFGNDFAPEG VSILKRFSDFGLFL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 335>:

**m096.seq**

```

1  ATGGCTCGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACCGC CAGTTCGCGC ATCAGGCTTT CTTGCGCTTC
151 GGTCAAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTCG CGGTTGTACT
201 TGGCTTCGTA GTCGTAAAC TCGGTTGCGG GAATGATGTG TATGCCGGGC
251 AGCCCTTTGC CGTTCAGGAC GGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 ACGTTCGGCA ATGATTTCGC CC.TGAAGGT GTTCAATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 336; ORF 096>:

**m096.pep**

```

1  MARHTGQGVDFQOIEFAVGI FEEIDAHAAF RTDCLRAANR QFAHQAFFGF
51  GQIFRRTLIN GVVAVVLGFV VVKLGCGNDV YAGQPFVAVQD GAGIFAAADK
101 TFGNDFAXEG VSILKRFSDFGLFL*

```

m096/g096 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQOIEFAVGI	FEEIDAHAAFRTDCLRAANR	QFAHQAFFGFGQIFRRTLIN			
g096	MAGHTGQGVDFQOIEFAVGI	FEEIDAHAAFRTDCLCAANR	QFAHQAFFGFGQIFRRTLIN			
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDV	YAGQPFVAVQDGAGIFAAADK	TFGNDFAXEGVSILKRFSDFGLFLX			
g096	GVVSVVLGFVVVKLGCGDDV	YAGQPFVAVQDGAGIFAAADK	TFGNDFAPEGVSILKRFSDFGLFLX			
	70	80	90	100	110	120
m096.pep	GLFLX					
g096	GLFLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 337>:

**a096.seq**

```

1  ATGGCCGGTC ATACCGGGCA GGGTGTGAT TTCCAACAGA TAGAGTTTGC
51  CGTCGGTATC TTTGAGGAAA TCGACGCGCA CGCAGCCTTC CGCACCATT
101 GCCTGCGCGC CGCGAACCGC CAGTTCGCGC ATCAGGCTTT CTTGCGCTTC
151 GGTCAATCT TCCGAAGGAC ATTGATAAAT GGTGTCGTCG CGGTTGTACT
201 TGGCTTCGTA GTCATAAAAC TCGGTCGCGG GGATGATGTG TATGCCGGGC
251 AGGCCTTTGC CGTTCAACAC AGGGCAGGAA TATTCGCCGC CGCCGATAAA
301 CCGTTCGGCA ATGATTTCGC CCT.GAAAGT GTTCAATTC TTCGTAAACG
351 CTTTTCAGAC GGCCTTTTCC TTTGA

```

This corresponds to the amino acid sequence <SEQ ID 338; ORF 096.ng>:

**a096.pep**

```

1  MAGHTGQGVDFQOIEFAVGI FEEIDAHAAF RTDCLRAANR QFAHQAFFGF

```

51 GQIFRRTLIN GVVAVVLGFV VIKLGRGDDV YAGQAFVQH RAGIFAAADK  
101 PFGNDFAXES VSILRKRFSD GLFL\*

m096/a096 92.7% identity in 124 aa overlap

	10	20	30	40	50	60
m096.pep	MARHTGQGVDFQQIEFAVGIFEEIDAHAAERTDCLRAANRQFAHQAFFGFGQIFRRTLIN					
a096	MAGHTGQGVDFQQIEFAVGIFEEIDAHAAERTDCLRAANRQFAHQAFFGFGQIFRRTLIN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m096.pep	GVVAVVLGFVVVKLGCGNDVYAGQPFQVQDGAGIFAAADKTFGNDFAEXGVVSILRKRFSD					
a096	GVVAVVLGFVVIKLGCGNDVYAGQAFVQHRAGIFAAADKPFNGNDFAXESVSILRKRFSD					
	70	80	90	100	110	120
m096.pep	GLFLX					
a096	GLFLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 339>:

g097.seq

1	ATGGATATTT	CAAAACAAAC	ATTGCTGGAT	AGGGTTTTTA	ACCTGAAGGC
51	AAACGGTACG	ACGGTACGTA	CCGAGTTGAT	GGCGGGTTTG	ACGACCTTTT
101	TGACGATGTG	CTACATCGTT	ATCGTCAATC	CCCTGATTTT	GGGCGAGACC
151	GGAATGGATA	TGGGGGCGGT	ATTCTGCGCT	ACCTGTATCG	CATCCGCCAT
201	CGGCTGTTTT	GTCATGGGTT	TTATCGGCAA	CTATCCGATT	GCGCTTGCCC
251	CGGGGATGGG	GCTGAATGCC	TATTTACCTT	TGCGCGTCGT	TAAGGGTATG
301	GGCGTGCCCT	GGCAGGTGGC	GTTGGGTGCG	GTGTTTCATT	CCGGTCTGAT
351	TTTCATCCTG	TTCAGCTTTT	TTAAAGTCAG	GGAAATGCTG	GTCAACGCAC
401	TGCCTATGGG	TTTGAAGATG	TCGATTGCCG	CCGGTATCGG	TTTGTTTTTG
451	GCACTGATTT	CCCTGAAAGG	CGCAGGCATT	ATCGTTGCCA	ATCCGGCAAC
501	CTTGGTCCGC	TTGGGCGATA	TTCATCAGCC	CAGCGCACTG	TTGGCATTGT
551	TCGGTTTTGT	CATGGTGGTC	GTATTGGGGT	ATTTCCGCGT	TCAAGGCGCA
601	ATCATCATCA	CCATTCTGAC	GATTACCGTC	ATTGCCAGCC	TGATGGGTTT
651	GAACGAGTTT	CACGGCGTGG	TCCGGCGAAGT	ACCGGGCATT	GCGCCGACCT
701	TTATGCAGAT	GGATTTTAAA	GGTCTGTTTA	CCGTCAGCAT	GGTCAGCGTG
751	ATTTTCGTCT	TCTTCTTGGT	CGATTGTTC	GACAGTACCG	GAACGCTGGT
801	CGGCGTATCC	CACCGTGCCG	GACTGCTGGT	GGACGGTAAG	CTGCCCCGCC
851	TGAAACGCGC	ACTGCTTGCA	GACTCTACCG	CCATTGTGGC	AGGTGCGGCT
901	TTGGGTACTT	CTTCAACCAC	GCCTTATGTG	GAAAGCGCGG	CGGGCGTATC
951	GGCAGGCGGA	CGGACCGGCC	TGACGGCGGT	TACCGTCGGC	GTATTGATGC
1001	TGGCGTGTCT	GATGTTCTCC	CCATTGGCGA	AAAGTGTTC	GGTATTTGCC
1051	ACCGCGCCCG	CACTGCTTTA	TGTCGGCACG	CAGATGCTCC	GCAGTGCGAG
1101	GGACATTGAT	TGGGACGATA	TGACTGAAGC	CGCGCCCGCG	TTCTTGACCA
1151	TGTCTTCAT	GCCGTTTACC	TATTGATTG	CAGACGGCAT	CGCCTTCGGC
1201	TTCATCAGCT	ATGCCGTGGT	CAAACTTTTG	TGTCGCCCGA	CTGGGGACGT
1251	GCCGCCATG	GTATGGGTTG	TTGCCGTATT	GTGGGCATTG	AAATTCTGGT
1301	ATTTGGGCTG	A			

This corresponds to the amino acid sequence <SEQ ID 340; ORF 097.ng>:

g097.pep

1	MDISKQTLDD	RVFNKANGT	TVRTELMAGL	TTFLTMCIYV	IVNPLILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFIGNYPI	ALAPGMGLNA	YFTFAVVKGM
101	GVPWQVALGA	VFISGLIFIL	FSFFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDHQPASL	LALFGFVMV	VLGYFRVQGA
201	IIITILTITV	IASLMGLNEF	HGVVGEVPGI	APTFMQMDFK	GLFTVSMVSV
251	IFVFFLVDF	DSTGTLVGVS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSSSTPYV	ESAAGVSAGG	RTGLTAVTVG	VLMLACLMS	PLAKSVPVFA
351	TAPALLYVGT	QMLRSARDID	WDDMTEAAPA	FLTIVFMPFT	YSIADGIAFG

m097.seq

**This corresponds to the amino acid sequence <SEO ID 342; ORF 097>:**

m097.pcp

1	MDTSQTLLD	GIFLKGANGT	TVRTELMAGL	TFFLTMCYIV	IVNPXILGET
51	GMDMGAVFVA	TCIASAIGCF	VMGFVGNYP	ALAPGMGLNA	YFTFAVVKGM
101	GV <del>PQ</del> VALGA	VFISGLIFIL	<del>FS</del> FFKVREML	VNALPMGLKM	SIAAGIGLFL
151	ALISLKGAGI	IVANPATLVG	LGDIHQPSAL	LALFGFAMV	VLGHFRVQGA
201	<del>II</del> ITILTITV	IASLMGLNEF	HGIIGEVPSI	APTFFQMDFE	GLFTVSMVSV
251	<del>IF</del> VFFFLVDLF	DSTGTLVGIS	HRAGLLVDGK	LPRLKRALLA	DSTAIVAGAA
301	LGTSS <del>TT</del> PPV	ESAAVGSAGD	RTGLTAVTVG	VLMLACLMFS	PLAKSVPAFA
351	TAPALLVYGT	QMLRSARDIG	WDDMTEAAPA	FLTIVLMPFT	YSIADGIAFG
401	FISYAVVKLL	CRRTKDVPMP	VWIVAVLWAL	KFWYLG*	

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 097 shows 96.3% identity over a 436 aa overlap with a predicted ORF (ORF 097.ng) from *N. gonorrhoeae*:

m097/q097

[illegible]

301

m097 . pep	FSFFKVR	EMLVN	ALP	MLK	MSIA	AAGIGL	FLALIS	SLKG	AGII	VAN	PATL	VGL	GDI	HQ	PSAL
g097	FSFFKVR	EMLVN	ALP	MLK	MSIA	AAGIGL	FLALIS	SLKG	AGII	VAN	PATL	VGL	GDI	HQ	PSAL
		130		140		150		160		170		180			
m097 . pep	LALFGF	FAMVV	VLGH	FRVQ	GAII	ITILT	ITVIA	SLMGL	NEFH	GII	GEV	PSI	APT	FMQ	MDFE
g097	LALFGF	FAMVV	VLGH	FRVQ	GAII	ITILT	ITVIA	SLMGL	NEFH	GII	GEV	PSI	APT	FMQ	MDFE
		190		200		210		220		230		240			
m097 . pep	GLFTV	SMVSV	IFVFF	LVDL	FDST	GT	LVG	ISH	RAGL	LV	DGK	L	PRL	K	RALLAD
g097	GLFTV	SMVSV	IFVFF	LVDL	FDST	GT	LVG	ISH	RAGL	LV	DGK	L	PRL	K	RALLAD
		250		260		270		280		290		300			
m097 . pep	LGTSS	STTPY	VESA	AAGV	SAGGR	TGLT	AVTV	GV	ML	ACL	MF	SP	LAKS	V	PAFAT
g097	LGTSS	STTPY	VESA	AAGV	SAGGR	TGLT	AVTV	GV	ML	ACL	MF	SP	LAKS	V	PAFAT
		310		320		330		340		350		360			
m097 . pep	QMLRS	ARDID	WDDM	TEA	APAF	L	TIV	F	MP	FT	YSI	AD	GIA	F	GFI
g097	QMLRS	ARDID	WDDM	TEA	APAF	L	TIV	F	MP	FT	YSI	AD	GIA	F	GFI
		370		380		390		400		410		420			
m097 . pep	VWIV	AVL	WALK	FWY	L	G	X								
g097	VWV	AVL	WALK	FWY	L	G	X								
		430													

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 343>

a097 . seq

```

1  ATGGACACTT CAAAACAAAC ACTGTTGGAC GGGATTTTTA AGCTGAAGGC
51  AAACGGTACG ACGGTGCGTA CCGAGTTGAT GGCGGGTTTG ACAACTTTTT
101 TGACGATGTG CTACATCGTT ATCGTCAACC CTCTGATTTT GGGCGAGACC
151 GGCATGGATA TGGGGGCGGT ATTCGTCGCT ACCTGTATCG CGTCTGCCAT
201 CGGCTGTTTT GTTATGGGTT TTGTCGGCAA CTATCCGATT GCACTCGCAC
251 CGGGGATGGG GCTGAATGCC TATTTACCTT TTGCCGTCGT TAAGGGTATG
301 GGCCTGCCTT GGCAGGTTGC GTTGGGTGCG GTGTTTCATCT CCGGTCTGAT
351 TTTTCATCTG TTCAGCTTTT TTAAAGTCAG GGAAATGCTG GTCAACGCAC
401 TGCCTATGGG TTGAAAATG TCGATTGCTG CCGGTATCGG TTTGTTTTTG
451 GCACTGATTT CCCTGAAAGG CGCAGGCATT ATCGTTGCCA ATCCGGCAAC
501 CTTGGTCGGC TTGGGCGATA TTCATCAGCC GTCCGCGTTG TTGGCACTGT
551 TCGGTTTTGC CATGGTGGTC GTATTGGGAC ATTTCCGCGT TCAAGGCGCA
601 ATCATCATCA CCATTTTGAC GATTACCGTC ATTGCCAGCC TGATGGGTTT
651 GAACGAATTT CACGGCATCA TCGGCGAAGT GCCGAGCATT GCGCCGACTT
701 TTATGCAGAT GGATTTTAAA GGGTTGTTTA CCGTCAGCAT GGTGAGCGTG
751 ATTTTCGTCT TTTTCCTAGT CGATCTGTTC GACAGTACCG GAACACTGGT
801 CCGTGTATCG CATCGTGCCG GACTGCTGGT GGACGGTAAG CTGCCCCGCC
851 TGAAACGCGC ACTGCTTGCA GACTCTACCG CTATTGTGGC AGGTGCGGCT
901 TTGGGTACTT CTTCACCAC GCCTTATGTG GAAAGTGCGG CGGGCGTATC
951 GGCAGGCGGG CGGACAGGTC TGACGGCGGT TACCGTCGGC GTATTGATGC
1001 TCGCCTGCCT GATGTTTTCA CCTTTGGCGA AAAGTGTTCC CGCTTTTGCC
1051 ACCGCGCCCG CCCTGCTTTA TGTGGGCACG CAGATGCTCC GCAGTGCGAG
1101 GGACATCGAT TGGGACGATA TGACGGAAGC CGCACCAGCA TTCCTGACCA
1151 TTGTCTTCAT GCCGTTTACC TATTCGATTG CAGACGGCAT CGCTTTCGGC
1201 TTCATCAGTT ATGCCGTGGT TAAACTTTTA TGCCGCGGCA CCAAAGACGT
1251 TCCGCCTATG GTATGGATTG TTGCCGTATT GTGGGCACTG AAATTCTGGT

```

1301 ATTTGGGCTG A

This corresponds to the amino acid sequence &lt;SEQ ID 344; ORF 097.a&gt;:

a097.pep

```
1  MDTSKQTLDD GIFKLGKANGT TVRTELMAGL TTFLTMCYIV IVNPLILGET
51  GMDMGAVFVA TCIASAIGCF VMGFVGNYP I ALAPGMGLNA YFTFAVV KGM
101 GVPWQVALGA VFISGLIFIL FSFFKVREML VNALPMGLKM SIAAGIG LFL
151 ALISLKGAGI IVANPATLVG LGDIHQPSAL LALFGFAMVV VLGHFRVQGA
201 IIITILTITV IASLMGLNEF HGIIGEVPSI APTFMQDFK GLFTVSMVSV
251 IFVFFLVDLF DSTGTLVGVS HRAGLLVDGK LPRLKRALLA DSTAIVAGAA
301 LGTSSTTPYV ESAAGVSAGG RTGLTAVTVG VLMLACLMFS PLAKSVPAFA
351 TAPALLYVGT QMLRSARDID WDDMTEAAPA FLTIVFMPFT YSIADGIAFG
401 FISYAVVKLL CRRTKDVPPM VWIVAVLWAL KFWYLG*
```

m097/a097 99.3% identity in 436 aa overlap

	10	20	30	40	50	60
m097.pep	MDTSKQTLDDGIFKLGKANGT	TVRTELMAGLTTFLTMCYIV	IVNPLILGET	ETGMDMGAVFVA		
a097	MDTSKQTLDDGIFKLGKANGT	TVRTELMAGLTTFLTMCYIV	IVNPLILGET	ETGMDMGAVFVA		
	70	80	90	100	110	120
m097.pep	TCIASAIGCFVMGFVGNYP	IALAPGMGLNAYFTFAVV	KGMGVPWQVALGAVFISGLIFIL			
a097	TCIASAIGCFVMGFVGNYP	IALAPGMGLNAYFTFAVV	KGMGVPWQVALGAVFISGLIFIL			
	130	140	150	160	170	180
m097.pep	FSFFKVREMLVNALPMGLKMS	SIAAGIGLFLALISLKGAGI	IVANPATLVGLGDIHQPSAL			
a097	FSFFKVREMLVNALPMGLKMS	SIAAGIGLFLALISLKGAGI	IVANPATLVGLGDIHQPSAL			
	190	200	210	220	230	240
m097.pep	LALFGFAMVVVLGHFRVQGA	IIITILTITVIASLMGLNEF	HGIIGEVPSIAPT	FMQDFE		
a097	LALFGFAMVVVLGHFRVQGA	IIITILTITVIASLMGLNEF	HGIIGEVPSIAPT	FMQDFE		
	250	260	270	280	290	300
m097.pep	GLFTVSMVSVIFVFFLVDL	FDSTGTLVGISHRAGLLVDGK	LPRLKRALLAD	STAIVAGAA		
a097	GLFTVSMVSVIFVFFLVDL	FDSTGTLVGISHRAGLLVDGK	LPRLKRALLAD	STAIVAGAA		
	310	320	330	340	350	360
m097.pep	LGTSSSTTPYVESAAAGVS	AGGRGLTAVTVGVLMACLMF	SPLAKSVPAFATAPALLYVGT			
a097	LGTSSSTTPYVESAAAGVS	AGGRGLTAVTVGVLMACLMF	SPLAKSVPAFATAPALLYVGT			
	370	380	390	400	410	420
m097.pep	QMLRSARDIDWDDMTEAAP	AFLTIVFMPFTYSIADGIAFG	FISYAVVKLLCRRTKDVPPM			
a097	QMLRSARDIDWDDMTEAAP	AFLTIVFMPFTYSIADGIAFG	FISYAVVKLLCRRTKDVPPM			
	430					
m097.pep	VWIVAVLWALKFWYLGX					
a097	VWIVAVLWALKFWYLGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 345>:

```
g098.seq
1  ATGACCGCCG ACGGTCTCTT CGTCGCTTTC AACTTCAATA CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAGCAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTCTG CGATGTCGCG CGCTTCGCTG TCGGGATGGC TTTCGCGTTC
151 GGGATGAACG CAGCCGAGCA TGGACACGCC GGTACGCATC ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAAGTG TGCGACTTCT TCAAATCGC
351 ATTTTGTGTC CAAATTAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 346; ORF 098.ng>:

```
g098.pep
1  MTADGLFVAF NFNTFAVVRI LIPVQDAAQ AGDQFVGDDVA RFAVGMFAF
51  GMNAAEHGHA GTHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV CDFPKLAFLC QIRMS*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 347>:

```
m098.seq
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
101 AGTTTGTCTG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTTT
151 AGGATGAACG CAGCCGAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGGACTTCT TCAAATCGC
351 ATTTTGTGTC CAAATCAGAA TGTCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 348; ORF 098>:

```
m098.pep
1  MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51  RMNAAQHGYA GTHVHRMGM CRQAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFPKLAFLC QIRMS*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 098 shows 89.6% identity over a 125 aa overlap with a predicted ORF (ORF 098.ng) from *N. gonorrhoeae*:

m098/g098

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
	:     :     :     :     :     :					
g098	MTADGLFVAFNFNTFAVVRI LIPVQDAAQAGDQFVGDDVARFAVGMFAFAGMNAAEHGHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHVHRMGMCQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
	:     :     :     :     :     :					
g098	GTHVHRMGMCQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVCDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
g098	QIRMSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 349>:

```
a098.seq
1  ATGACCGCCG ATGGTCTCTT CGTCGCTTTC AACCTCAATG CGTTTGCCGT
51  TGTGCGAATA TTGATACCAG TACAAGAGGA TGCTGCCAG GCTGGCGATC
```



304

```

101 AGTTTGTCCG CGATGTCGCG CGCTTCACTT TCCGGATGGC TTTCACGTC
151 AGGATGAACG CAGCCCAGCA TGGATACGCC GGTACGCATT ACGTCCATCG
201 GATGGGTATG TGCAGGCAGG CTTTCCAAAA CTTTAATCAC ACGGATAGGC
251 AGGCCGCGCA TGGATTTGAG CTTGGTTTTA TAAGCGGCCA GCTCGAATTT
301 GTTGGGCAGA TGGCCGTGAA TCAGCAGGTG GCGGACTTCT TCAAACCTCG
351 ATTTTGTGC CAAATCAGAA TGTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 350; ORF 098.a>:

a098.pep

```

1 MTADGLFVAF NLNAFAVVRI LIPVQEDAAE AGDQFVGDDVA RFTFRMAFTF
51 RMNAAQHGYA GTHYVHRMGM CROAFQNFNH TDRQAAHGFE LGFISGQLEF
101 VGQMAVNQQV GDFFKLAFLC QIRMS*

```

m098/a098 100.0% identity in 125 aa overlap

	10	20	30	40	50	60
m098.pep	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
a098	MTADGLFVAFNLNAFAVVRI LIPVQEDAAEAGDQFVGDDVARFTFRMAFTFRMNAAQHGYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m098.pep	GTHYVHRMGMCRQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
a098	GTHYVHRMGMCRQAFQNFNHTDRQAAHGFELGFISGQLEFVGQMAVNQQVGDFFKLAFLC					
	70	80	90	100	110	120
m098.pep	QIRMSX					
a098	QIRMSX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 351>:

g099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTGGA
51 GCTGACGGGC AAACGGCAGG CGGGCATTAC TGCCACAGAC ATCGTGTGTTG
101 CACTGACCGA ATTCTTGCGT AAAGAGCGCG TGGTCGGGGC GTTTGTGCGAA
151 TTTTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCCATG TTCGCCATCG
251 ACGCGCAAAC TATTGATTAT TTGAAACTGA CCGGACGTGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTAT GGGCAGGTGG
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGCCACC
451 GCCGATTGCG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCGTGTA
551 CCAATACTTC CAACCCGCGC AACGTGTGCG CCGCCGCACT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GAAACGCAAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAAGTAG CCGGAATCTA TTTGAAAGAA GCAGGCTTGT
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTCGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAgcgG CGCGCTGgaC CCGAAAATCC AACAGAAAT
801 CATCGACCGC GAtttgtacg cCACCGCCGT ATTGTCAGGC AACCGCAACT
851 TCGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTTCT CGCTTCGCCT
901 CCTTTGGTCG TTGCCTACGC ATTGGCAGGT AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGCCCG CGAAATCCGC CTGAAAGATA
1001 TCTGGCCGAC AGACGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAACAAT TCCGCGACAT TTATATCCCG ATGTCCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGACCGATG TCCACCTACA
1151 TCCGCCGTCC GCCCTATTGG GAAGGCCGAC TGGCAGGGGA ACGTACATTA
1201 AGAGGTATGC GTCCGCCGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CATCTCgcca tCCAATGCGA TTTTGCCCGG cagTGcGca ggtgaATATT

```

```

1301 TGGCGAAAAT GGGTTTGCCT GAAGAagaCT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTtcgt
1451 tggcacgcgT tgaacCAGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTT ATCATCATTG CCGGTGCGGA
1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC GGCGAAGGGC GTGCGGCTGG
1601 CGGGTGTGGA AGCCATCGCC GCCGAAGGTT TCGAGCGCAT CCACCGCACC
1651 AACCTCATCG GCATGGGCGT CTTGCCGCTG CAATTCAAAC CCGGCACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGGC CTGACCCTCG TGATTACCG TAAAAACGGA
1801 GAAACCGTCG AAGTTCCGGT TACCTGCCGC CCCGATACCG CAGAAGAAGC
1851 ATTGGTATAT GAAGCCGGCG GCGTATTGCA ACGGTTTGCA CAGGACTTTT
1901 TGAAGGGGAA CGCGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 352; ORF 099.ng>:

g099.pep

```

1 MLGRASMMRL PDIVGVELTG KRQAGITATD IVLALTEFLR KERVVGAFVE
51 FFGEGARSLS IGDRTISNM TPEFGATAAM FAIDAQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWAGGLKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEPPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAAALLAR
201 NANRLGLKRR PWVKSSFAPG SKVAGIYLKE AGLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQEIIIDR DLYATAVLGS NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGREIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDIYIP MSDTGTAKA PSPLYDWRPM STYIRRPPYW EGALAGERTL
401 RGMRPAILP DNITTDHISP SNAILAGSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE GQTMRMWEAI
501 ETYMRKQPL IIIAGADYGQ GSSRDWAAKG VRLAGVEAIA AEGFERIHRT
551 NLIGMGVLP LQFKPGTNRHT LQLDGTETYD VVGERTPRCG LTLVIHRKNG
601 ETVEVPVTCR PDTAEEALVY EAGGVLQRF A QDFLEGNA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 353>:

m099.seq

```

1 ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51 GCTGAACGGC AAACGCGAGG CGGGCATTAC GCGCAGCGAT ATTGTGTTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCCGTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAACCTA CGCCAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAACC GCCGTTTATC CTCGCGTTT GAAATTTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCAAGTAACC CGCATGCCCG TTTTGCAGAC
451 GCCGATTGG CGGCGAAAGG GCTGGCGAAG CCTTACGAAG AGCCTTCGGA
501 CGGCCAAATG CCCGACGGCT CGGTCAATCAT CGCCGCGATT ACCAGTTGCA
551 CCAACACTTC CAACCCGCGC AACGTTGTTG CCGCCGCGCT CTTGGCACGC
601 AATGCCAACC GTCTCGGCTT GAAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTGAAAGAA GCGGGCCTGT
701 TGCCCCGAAT GGA AAAACTC GGCTTCGGTA TCGTCGCCTT CGCCTGCACC
751 ACCTGCAACG GCATGAGTGG CGCGCTGGAT CCGAAAATCC AGAAAGAAAT
801 CATCGACCGC GATTGTACG CCACGCGCGT ATTATCAGGC AACC GCAACT
851 TCGACGGCCG TATCCACCGG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGTATCCGTT TCGATATTGA
951 AAACGACGTA CTCGCGGTTG CAGACGCAA GGAAATCCGC CTGAAAGACA
1001 TTTGGCCTGC CGATGAAGAA ATCGATGCCG TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAGT TCCGCGATGT GTATGTACCG ATGTTGACA CCGGCACAGC
1101 GCAAAAAGCA CCCAGTCCGC TGTACGATTG GCGTCCGATG TCCACCTACA
1151 TCCGCGTCC GCCTTACTGG GAAGGCGCGC TGGCAGGGGA ACGCACATTA
1201 AGAGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA
1251 CCTCTCGCCG TCCAATGCGA TTTTGGCCGT CAGTGCCGCA GGCGAGTATT
1301 TGGCGAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGCGGCGACC ACTTGACCGC CCAACGCGCT ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAAAA ACGAAGACGG CAGCGTGC GC CAAGGCTCGT
1451 TCGCCCGCGT CGAACCCGAA GCGGAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGTGCGGA

```

```

1551 CTATGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTAGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACCTTATCG GCATGGGCGT GTTGCCGCTG CAGTTCAAAC CCGACACCAA
1701 CCGCCATACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTGGTCGGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTCG TGATTACCG TAAAAACGGC
1801 GAAACCGTGT AAGTTCCTGT TACCTGCTGC CTCGATACTG CAGAAGAAGT
1851 ATTGGTATAT GAAGCCGGCG GCGTGTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGAA CGCGGCTTAG

```

This corresponds to the amino acid sequence <SEQ ID 354; ORF 099>:

```

m099.pep
1  MLGRASMMRL PDIVGVELNG KRQAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VLKVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAAKGLAK PYEEPSDQOM PDGSVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLKRK PWVKSSFAPG SKVAEIYLKE AGLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVL SG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPADEE IDAVVAEYVK
351 PQQFRDVYVP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 RGMRLAILP DNITDHLSP SNAILAVSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVKNEDGSVR QGSFARVEPE GETMRMWEAI
501 ETYMRKQPL IIIAGADYGO GSSRDWAAKG VRLAGVEAIV AEGFERIHR
551 NLIGMGVLPL QFKPDTNRHT LQLDGTETD VVGERTPRCD LTLVIHRKNG
601 ETVEVPVTC LDTAEEVLVY EAGGVLQRF A QDFLEGNA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 099 shows 96.2% identity over a 639 aa overlap with a predicted ORF (ORF 099.ng) from *N. gonorrhoeae*:

m099/g099

	10	20	30	40	50	60
m099.pep	MLGRASMMRLPDIVGVELNGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	:					
g099	MLGRASMMRLPDIVGVELTGKRQAGITATDIVLALTEFLRKERVVGAFVEFFGEGARSLS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m099.pep	IGDRATISNMTPEFGATAAMFAIDEQTIDYLKLTGRDDAQVKLVETYAKTAGLWADALKT					
	:					
g099	IGDRATISNMTPEFGATAAMFAIDAQTIDYLKLTGRDDAQVKLVETYAKTAGLWAGGLKT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m099.pep	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEEPSDQOMPDGSVIIAAI					
	:					
g099	AVYPRVLKFDLSSVTRNMAGPSNPHARFATADLAAKGLAKPYEEPSDQOMPDGAVIIAAI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m099.pep	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAEIYLKEAGLLPEMEKL					
g099	TSCTNTSNPRNVVAAALLARNANRLGLKRKPWKSSFAPGSKVAGIYLKEAGLLPEMEKL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m099.pep	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFILASP					
	:					
g099	GFGIVAFACCTCNGMSGALDPKIQKEIIDRDLYATAVLSGNRNFDGRIHPYAKQAFILASP					
	250	260	270	280	290	300
	310	320	330	340	350	360

307

m099 . pep	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPADEEIDAVVAEYVKPQQFRDVYVP
g099	PLVVAYALAGSIRFDIENDVLGVADGREIRLKDIWPTDEEIDAIVA EYVKPQQFRDIYIP
	310 320 330 340 350 360
m099 . pep	MFDTGTAQKAPSPLYDWRPMSTYIRRPYWEALAGERTLRGMRPLAILPDNITTDHLS
g099	MSDTGTAQKAPSPLYDWRPMSTYIRRPYWEALAGERTLRGMRPPAILPDNITTDHISP
	370 380 390 400 410 420
m099 . pep	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR
g099	SNAILAGSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR
	430 440 450 460 470 480
m099 . pep	QGSFARVEPEGETMRMWEAIEYTMNRKQPLIIAGADYQGSSRDWAAGVRLAGVEAIV
g099	QGSLARVEPEGQTMRMWEAIEYTMNRKQPLIIAGADYQGSSRDWAAGVRLAGVEAIA
	490 500 510 520 530 540
m099 . pep	AEGFERIHRTNLIGMVLPLQFKPDTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG
g099	AEGFERIHRTNLIGMVLPLQFKPGTNRHTLQLDGTETYDVVGERTPRCGLTLVIHRKNG
	550 560 570 580 590 600
m099 . pep	ETVEVPVTCCLDTAEVLVYEAGGVLRFAQDFLEGNAAX
g099	ETVEVPVTCRPDTAEALVYEAGGVLRFAQDFLEGNAAX
	610 620 630 640

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 355>:

a099 . seq

```

1  ATGCTGGGAC GCGCGTCCAT GATGCGCCTG CCCGATATTG TCGGCGTTGA
51  GCTGAACGGC AAACGGAAGG CGGGCATTAC GCGCAGCGAT ATTGTGTGG
101 CACTGACCGA GTTCTGCGC AAAGAACGCG TGGTCGGGGC GTTGTGCGAA
151 TTCTTCGGCG AGGGCGCGAG AAGCCTGTCT ATCGGCGACC GCGCGACCAT
201 TTCCAACATG ACGCCGGAGT TCGGCGCGAC TGCCGCGATG TTCGCTATTG
251 ATGAGCAAAC CATTGATTAT TTGAAACTGA CCGGACGCGA CGACGCGCAG
301 GTGAAATTGG TGGAAACCTA CGCCAAAACC GCAGGCTTGT GGGCAGATGC
351 CTTGAAAACC GCCGTTTATC CGCGCGTTTT GAAATTGAT TTGAGCAGCG
401 TAACGCGCAA TATGGCAGGC CCGAGCAACC CGCACGCGCG TTTTGGCACC
451 GCCGATTGGC CCGGCAAAGG CTTGGCTAAA CCTTACGAAG AGCCTTCAGA
501 CGGCCAAATG CCTGACGGTG CAGTGATTAT TGCCGCGATT ACTTCCTGTA
551 CCAATACTTC CAATCCGCGC AACGTTGTCG CCGCCGCGCT GTTGGCACGC
601 AATGCCAACC GCCTCGGCTT GCAACGCAA CCTTGGGTGA AATCTTCGTT
651 TGCCCCGGGT TCAAAAGTAG CCGAAATCTA TTTGAAAGAA GCAGATCTGC
701 TGCCCCGAAAT GGAAAACTC GGCTTCGGTA TCGTTGCCTT CGCATGTACC
751 ACCTGTAACG GCATGAGCGG CGCGCTGGAT CCGAAATCC AGAAAGAAAT
801 CATCGACCGC GATTTGTACG CCACCGCCGT ATTGTCAGGC AACC GCAACT
851 TTGACGGCCG TATCCATCCG TATGCGAAAC AGGCTTTCCT CGCTTCGCTT
901 CCGTTGGTCG TTGCCTACGC GCTGGCAGGC AGCATCCGTT TCGATATTGA
951 AAACGACGTA CTCGGCGTTG CAGACGGCAA AGAAATCCGC CTGAAAGACA
1001 TTTGGCTTAC CGATGAAGAA ATCGATGCCA TCGTTGCCGA ATATGTGAAA
1051 CCGCAGCAAT TTCGCGACGT TTATATCCCG ATGTTTCGACA CCGGCACAGC
1101 GCAAAAAGCA CCAAGCCCGC TGTACGACTG GCGTCCAATG TCTACCTATA
1151 TCCGCCGCCC ACCTTACTGG GAAGGCGCAC TGGCAGGGGA ACGCACATTA
1201 AGCGGTATGC GTCCGCTGGC GATTTTGCCC GACAACATCA CCACCGACCA

```

```
1251 TCTCTCGCCA TCCAATGCGA TTTTGGCAAG CAGTGCCGCA GGCGAATATT
1301 TGGCAAAAAT GGGTTTGCCT GAAGAAGACT TCAACTCTTA CGCAACCCAC
1351 CGTGGCGACC ACTTGACCGC CCAACGCGCA ACCTTCGCCA ATCCGAAACT
1401 GTTTAACGAA ATGGTGAGAA ACGAAGACGG CAGCGTACGC CAAGGTTTCGC
1451 TGGCACGCGT TGAACCCGAA GGCCAAACCA TGCGCATGTG GGAAGCCATC
1501 GAAACCTATA TGAACCGCAA ACAGCCGCTC ATCATCATTG CCGGCGCGGA
1551 CTACGGTCAA GGCTCAAGCC GCGACTGGGC TGCAAAAGGC GTACGCCTCG
1601 CCGGCGTGGA AGCGATTGTT GCCGAAGGCT TCGAGCGTAT CCACCGCACC
1651 AACTTGATCG GTATGGGCGT GTTGCCGCTG CAGTTCAAAC CGGGTACCAA
1701 CCGCCACACC CTGCAACTGG ACGGTACGGA AACCTACGAC GTTGTGCGCG
1751 AACGCACACC GCGCTGCGAC CTGACCCTTG TGATTACCCG TAAAAACGGC
1801 GAGACCGTCG AAGTCCCAT TACCTGCCGC CTCGATACCG CAGAAGAAGT
1851 GTTGGTATAT GAAGCCGGTG GCGTATTGCA ACGGTTTGCA CAGGATTTTT
1901 TGAAGGGGAA CGCGGCTTAG
```

This corresponds to the amino acid sequence <SEQ ID 356; ORF 099.a>:

a099.pep

```
1  MLGRASMMRL PDIVGVELNG KRKAGITATD IVLALTEFLR KERVVGAFVE
51  FFGEGARSLS IGDRATISNM TPEFGATAAM FAIDEQTIDY LKLTGRDDAQ
101 VKLVETYAKT AGLWADALKT AVYPRVLKFD LSSVTRNMAG PSNPHARFAT
151 ADLAGKGLAK PYEEPSDGQM PDGAVIIAAI TSCTNTSNPR NVVAAALLAR
201 NANRLGLQRK PWVKSSFAPG SKVAEIYLKE ADLLPEMEKL GFGIVAFAC
251 TCNGMSGALD PKIQKEIIDR DLYATAVLSG NRNFDGRIHP YAKQAFILASP
301 PLVVAYALAG SIRFDIENDV LGVADGKEIR LKDIWPTDEE IDAIVAEYVK
351 PQQFRDVYIP MFDTGTAQKA PSPLYDWRPM STYIRPPYW EGALAGERTL
401 SGMRLAILP DNITDHLSP SNAILASSAA GEYLAKMGLP EEDFNSYATH
451 RGDHLTAQRA TFANPKLFNE MVRNEDGSVR QGSLARVEPE QOTMRMWEAI
501 ETYMNKQPL IIAAGADYGQ GSSRDWAAGK VRLAGVEAIV AEGFERIHR
551 NLIGMGVLP QFKPGTNRHT LQLDGTETYD VVGERTPRCD LTLVIHRKNG
601 ETVEVPITCR LDTAEVLVY EAGGVLRFA QDFLEGNA*
```

m099/a099 97.5% identity in 639 aa overlap

m099.pep	10	20	30	40	50	60
a099	10	20	30	40	50	60
m099.pep	70	80	90	100	110	120
a099	70	80	90	100	110	120
m099.pep	130	140	150	160	170	180
a099	130	140	150	160	170	180
m099.pep	190	200	210	220	230	240
a099	190	200	210	220	230	240
m099.pep	250	260	270	280	290	300
a099	250	260	270	280	290	300
m099.pep	310	320	330	340	350	360
a099	310	320	330	340	350	360

a099						
	310	320	330	340	350	360
	PLVVAYALAGSIRFDIENDVLGVADGKEIRLKDIWPTDEEIDAIVAEYVKPQQFRDVYIP					
m099.pep	370	380	390	400	410	420
	MFDTGTAQKAPSPLYDWRPMSYIRRPYWEALAGERTLRGMRPLAILPDNITTDHLSP					
a099	370	380	390	400	410	420
	MFDTGTAQKAPSPLYDWRPMSYIRRPYWEALAGERTLSGMRPLAILPDNITTDHLSP					
m099.pep	430	440	450	460	470	480
	SNAILAVSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVKNEDGSVR					
a099	430	440	450	460	470	480
	SNAILASSAAGEYLAKMGLPEEDFNSYATHRGDHLTAQRATFANPKLFNEMVRNEDGSVR					
m099.pep	490	500	510	520	530	540
	QGSFARVEPEGETMRMWEAIEYTMNRKQPLIIAGADYGQSSRDWAAGVRLAGVEAIV					
a099	490	500	510	520	530	540
	QGSLARVEPEGQTMRMWEAIEYTMNRKQPLIIAGADYGQSSRDWAAGVRLAGVEAIV					
m099.pep	550	560	570	580	590	600
	AEGFERIHRTNLIGMGVLPLOFKPDNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG					
a099	550	560	570	580	590	600
	AEGFERIHRTNLIGMGVLPLOFKPGTNRHTLQLDGTETYDVVGERTPRCDLTLVIHRKNG					
m099.pep	610	620	630	640		
	ETVEVPVTCCLDTAEVLVYEAGGVLRFAQDFLEGNAAX					
a099	610	620	630	640		
	ETVEVPITCRLDTAEVLVYEAGGVLRFAQDFLEGNAAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 357>:

g102.seq

```

1  AtgtCCGCCA AAactccgtc gctcttcggc ggcgcgatga Ttattcgccg
51  gaagggtatc ggcgcAGgta tgttccccaa cccacccgcc aacttggggg
101 acgggttaat aggtcgtctg attgtgctgc tgtacacctg gtttccattc
151 tcctccggcg ccctcatgat ttggaagtc aacaccata acCCccgagg
201 ggcaAGtttt gacaccATGg tcAAagacct gctcgGACGc ggctggaaca
251 tcatcaacgg catcgccgtc gctttggtCc tatacggctc gacctacgcg
301 tacatthttag tcggcggtga cctGACCGCC AAAGGCatcg GCAGCGCAGT
351 AGGCGGCAAA ATTCgctca CCGTCGGACA actcgtcttc tTCGGCATCC
401 TCGCCTTTTG CGTATGGGCA TCCGCACGCT TGGTCGACCG CTTTACCGGC
451 GTCCTCATCG GCGGCATGGT ATTAACCTTT ATTTGGGCAA CCGGCGGCCT
501 GGTGCGCGAT GCCAAACCGT CCGTCCTCTT CGACACCCAA GCGCCGCTCG
551 GCACCGGCTA CTGGATTAC GCCGCCACCG CCCTGCCCGT CTGCCTCGCT
601 TCCTTCGGCT TCCACGGCAA CGTTTCCAGC CTGCTCAAAT ACTTTAAAGG
651 CGACGgcgcC aaagtGgCGA aATCcatctg gGcaggtaga ttggtTGCCt
701 tggtaattta cgtccTCTg caaaccgcca tCcaaagcaa ccTGcgcgcg
751 aacgagttcg cCCcgtgat tgccgccgag aggcaactCT CCGTCCTgaa
801 tgaaccctTG tccaaattcg cccaaaccgg cgatatggat aAaatattgt
851 ccctatttcc ctacatggca atcgccacct cctttttagg cgTAACctta
901 ggctgtttg acaacatcgc cgacatcttc aaatggaacg acagtatgtc
951 cgggcggggc accaaaaccg tcgcgctgaa cttcctgccg CCCctgattt
1001 cctggctgct cctccccacc ggcttcttta ccgccattgg tgcgtccggc
1051 ctggcggcaa ccgtctggga ccaagGcatc atccccgcca tgctgtctta
1101 cgtttcccc caaaaaattG gcGcaggcaa gacttataAa gtttaCGGCG
1151 gcttgtgct gatgttagtc ttccttttcg gcacgcgcaa catcgccgca
1201 CAGGTATTGA GccaAatgGa ACTcgtCccc GTATTAAAG GATAA

```

This corresponds to the amino acid sequence <SEQ ID 358; ORF 102.ng>:

g102.pep

```

1  MSAKTPSLFG  GAMIIAGKVI  GAGMFPNPTA  NLGDGLIGSL  IVLLYTWFPF
51  SSGALMILEV  NTHNPRGASF  DTMVKDLLGR  GWNIINGIAV  ALVLYGSTYA
101 YILVGGDLTA  KGIGSAVGGK  ISLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLIGGMVLTF  IWATGGLVAD  AKPSVLFDTO  APVGTGYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWAGT  LVALVIYVLW  QTAIQSNLPR
251 NEFAPVIAAE  RQLSVLNETL  SKFAQTGDMD  KILSLFPYMA  IATSFGLVTL
301 GLFDNIADIF  KWNDMSGRG  TKTVALNFLP  PLISWLLLP  GFFTAIGASG
351 LAATVWDQGI  IPAMLLYVSP  QKIGAGKTYK  VYGLWMLLV  FLFGIANIAA
401 QVLSQMELVP  VFKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 359>:

```

m102.seq
1  ATGCCCAACA  AAACCCCTTC  ACTGTTCCGC  GCGCGATGA  TTATCGCCGG
51  CACGGTCATC  GCGCGAGGCA  TGCTCGCCAA  CCCGACCGCC  ACATCCGGCG
101 TATGTTTAC  CGGCTCGCTG  GCCGTGTTGC  TGTACACCTG  GTTTTCTATG
151 CTTTCCAGCG  GCCTGATGAT  TTTGGAAGTC  AACACCCATT  ATCCGCACGG
201 CGCAAGTTTC  GACACGATGG  TCAAAGACCT  GCTCGGACGC  GGCTGGAACA
251 TCATCAACGG  CATCGCCGTC  GCCTTCGTTT  TATACCTGCT  TACTTACGCT
301 TATATCTTCG  TCGGCGGCGA  CCTGACCGCC  AAAGGCTTAG  GCAGCGCGGC
351 AGGCGGCGAC  GTTCACTCA  CCGTCGGACA  ACTCGCTTTC  TTCGGCATCC
401 TCGCCTTTTG  CGTATGGGCA  TCCGCACGCT  TGGTCGACCG  CTTACCCGGC
451 GTCCTTATCG  CGGCGATGGT  ATTGACCTTT  ATTGGGCGG  CCGGCGGGCT
501 GATTGCCGAT  GCCAAGCCGT  CCGTCCTCTT  CGATACCCAA  GCCCCGCCG
551 GCACAACTA  CTGGATTAC  GCCGCCACCG  CCCTGCCCGT  CTGCCTCGCT
601 TCCTTCGGCT  TCCACGGCAA  CGTCTCCAGC  CTGCTCAAAT  ACTTTAAAGG
651 CGACGCGCCC  AAAGTGGCTA  AATCCATCTG  GACGGGCACA  CTGATTGCGC
701 TGGTAATTTA  CGTCTCTGG  CAAACCGCCA  TCCAAGGCAA  CCTGCCCGGC
751 AACGAGTTCG  CCCCCGTCAT  CGCCGCCGAA  GGGCAAGTCT  CCGTCCTCAT
801 CGAAACCCCTG  TCCAAATTCG  CCCAAACCGG  CAATATGGAC  AAAATATTGT
851 CCCTGTTTTT  CTATATGGCG  ATCGCCACCT  CGTTTTTAGG  CGTAACGCTC
901 GGACTCTTCG  ACTACATCGC  CGACATCTTC  AAATGGAACG  ACAGCATCTC
951 CGGCCGACCC  AAAACCGCCG  CGCTGACCTT  CCTGCCGCC  CTGATTTCCT
1001 GCCTGCTCTT  CCCACCGGC  TTCGTTACCG  CCATCGGCTA  CGTCGGCCTG
1051 GCGGCAACCG  TCTGGACAGG  CATCATCCCC  GCCATGTGTC  TCTACCGTTC
1101 GCGCAAAAAA  TTCGGCGCAG  GCAAAACCTA  TAAAGTTTAC  GGCGGCTTGT
1151 GGCTGATGGT  TTGGGTCTTC  CTTTTCGGCA  TCGTCAACAT  CGCCGCACAG
1201 GTATTGAGCC  AATGGAAC  CGTCCCCGTA  TTAAAGGAT  AA

```

This corresponds to the amino acid sequence <SEQ ID 360; ORF 102>:

```

m102.pep..
1  MPNKTPSLFG  GAMIIAGTVI  GAGMLANPTA  TSGVWFTGSL  AVLLYTWFSM
51  LSSGLMILEV  NTHYPHGASF  DTMVKDLLGR  GWNIINGIAV  AFVLYLLTYA
101 YIFVGGDLTA  KGLGSAAGGD  VSLTVGQLVF  FGILAFVCWA  SARLVDRFTG
151 VLIGGMVLTF  IWAAGGLIAD  AKPSVLFDTO  APAGTNYWIY  AATALPVCLA
201 SFGFHGNVSS  LLKYFKGDAP  KVAKSIWGT  LIALVIYVLW  QTAIQNLPR
251 NEFAPVIAAE  QQSVLIETL  SKFAQTGNMD  KILSLFSYMA  IATSFGLVTL
301 GLFDYIADIF  KWNDISISRT  KTAALTFLEP  LISCLLFTG  FVTAIGYVGL
351 AATVWTGIIP  AMLLYRSRKK  FGAGKTYKVY  GGLWLMVWVF  LFGIVNIAAQ
401 VLSQMELVPV  FKG*

```

m102/g102 86.0% identity in 415 aa overlap

	10	20	30	40	50	60
m102.pep	MPNKTPSLFGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
g102	MSAKTPSLFGGAMIIAGKVIAGMFPNPTANLGDGLIGSLIVLLYTWFPFSSGALMILEV					
	10	20	30	40	50	60
m102.pep	NTHYPHGASFDTMVKDLLGRGWNIINGIAVAFVLYLLTYAIFVGGDLTAKGLGSAAGGD					
g102	NTHNPRGASFDTMVKDLLGRGWNIINGIAVALVLYGSTYAYILVGGDLTAKGIGSAVGGK					
	70	80	90	100	110	120
m102.pep	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTO					
g102	ISLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTO					
	130	140	150	160	170	180
m102.pep	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					
g102	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWGTIALLVIYVLW					
	190	200	210	220	230	240
m102.pep						
g102						

a102.seq

1	ATGCCACCA	AAACCCCTTC	ACTGTTCCGC	GCGCGATGA	TTATCGCCGG
51	CACGNTCATC	GGCGCAGGTA	TGCTCGCCAA	CCCAGCCGCC	ACATCCGGCG
101	TATGGTTTAC	CGGCTCGCTG	GCCGTGTTGC	TGTACACCTG	GTTTTCCATG
151	CTCTCCAGCG	GCCTGATGAT	TTTGGAAGTC	AACACCACT	ACCCCCACGG
201	CGCGANCTTC	GACACCATGG	TAAAGACCT	CTCGGACGG	AGCTGGAACA
251	TCATCAACGG	CATCGCCGTC	GCCTTCTGTT	TATACCTGCT	TACTTACGCT
301	TATATCTTCG	TCGGCGGCGA	CCTGACCGCC	AAAGGCTTAG	GCAGCGCGGC
351	AGGCGGCAAT	GTTTCACTCA	CCGTCCGACA	ACTCGTCTTC	TTCGGCATTTC
401	TCGCTTTTTC	CGTATGGGCA	TCCGACCGCT	TGGTCGACCG	ATTACCACAG
451	GTCTCTCATG	GCGGCATGGT	ATTAACCTTT	ATTGCGCAA	CGCCGGCCCT
501	GATTGCCGAT	GCCAAACTGC	CCGTCCTCTT	CGACACCCAA	GCCCCATTCCG
551	GCACCAACTA	CTGGATTTAT	GTGCGCACCG	CCCTGCCCGT	CTGCCTTGCG
601	TCATTTCGTT	TCCACGGCAA	CGTCTCCAGC	CTGCTCAAAT	ACTTTTAAAGG
651	CGACGCGCCC	AAAGTGGCTA	AATCCATCTG	GACGGGCACA	CTGATTGCGC
701	TGGTAATTTA	CGTCTCTTGG	CAAAACCGCA	TCCAAGCAA	CTGTCCGCGC
751	AACGAGTTTC	CCCCCGTGAT	TGCGCGCGAA	GCGCAAGTCT	CCGTCTNTGAT
801	TGAAACCCCTG	TCCAAATTCTG	CCCAAACCGG	CAATATGGAC	AAAATATTGT
851	CCCTGTTTTTC	CTATATGGCG	ATCGCCACCT	CGTTTTTATG	CGTAACGCTC
901	GGACTCTTTC	ACTACATCGC	CGACATCTTC	AAATGGAACG	ACAGCTGTGC
951	CGGCCCGACC	AAAACCGCCG	CGTGACCTT	CTGCGCCGCT	NTAATTTCTT
1001	GCGTGCTCTT	CCCCACCGGC	TTGTTTACCG	CCATCGGNTA	CGTCGGCCGTG
1051	GCGGCAACCG	TCTGGACAGG	CATCATCCCC	GCCATGCTGC	TNTACCGTTC
1101	GCGCAAAAAA	TTCGGCGCAG	GCAAAACCTA	TAAAGTTTAC	GGCGGCTTGT
1151	GGCTGATGGT	TTGGGTCTTC	CTTTTCGSCA	TCNTCAACAT	CGCCGCACAN
1201	GTATTGAGCC	AAATGGAAC	CGTCCCCGTA	TTTAAAGGAT	AA
1202					

This corresponds to the amino acid sequence <SEQ ID 362; ORF 102.a>:

**a102.pep**

1	MPTKTPSLEF	GAMI IAGTXI	GAGMLANPTA	TSGVWFTGSL	AVLLYTWFMS
51	LSSGLMILEV	NTHYPHGAXF	DTMVKDLLGR	SWNIINGIAV	AFVLYLLTYA
101	YIFVGGDLTA	KGLGSAAGGN	VSLTVLQDTV	FGILAFCVWA	SARLVDRFSS
151	VLIGGMWLTIF	IWATGGILAD	AKLPVFGDLQ	APTGTNYWIY	VATALPVCLA
201	SLFGHGNVSS	LLKYFKGDAP	KVAKSIWTGT	LIALVIYVLW	QTAIQXNLPR
251	NEFAPVIAAE	GQVSVXIETL	SKFAQTGNMD	KILSLFSYMA	IATSFLGVTL
301	GLFDYIADIF	KWNDSVSGRT	KTAALTFLPP	XISCLLFPTG	FVTAIGYVGL
351	AATSVWGTGII	AMLLYRSRKK	FGAGKTYKVY	GGLWLMVWVF	LFGIXNIAAX
401	VLVSOMELPVF	FKG*			

m102 / a102 95.9% identity in 413 aa overlap



312

m102.pep	10	20	30	40	50	60
	MPNKTPSLFEGGAMIIAGTVIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
a102	MPTKTPSLFEGGAMIIAGTXIGAGMLANPTATSGVWFTGSLAVLLYTWFSMLSSGLMILEV					
	10	20	30	40	50	60
m102.pep	70	80	90	100	110	120
	NTHYPHGASFDTMVKDLLGRGWNIIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGD					
a102	NTHYPHGAXFDTMVKDLLGRSWNIINGIAVAFVLYLLTYAYIFVGGDLTAKGLGSAAGGN					
	70	80	90	100	110	120
m102.pep	130	140	150	160	170	180
	VSLTVGQLVFFGILAFVCWASARLVDRFTGVLIGGMVLTFIWAAGGLIADAKPSVLFDTQ					
a102	VSLTVGQLVFFGILAFVCWASARLVDRFTSVLIGGMVLTFIWATGGLIADAKLPVLFDTQ					
	130	140	150	160	170	180
m102.pep	190	200	210	220	230	240
	APAGTNYWIYAATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
a102	APTGTNYWIYVATALPVCLASFGFHGNVSSLLKYFKGDAPKVAKSIWTGTLIALVIYVLW					
	190	200	210	220	230	240
m102.pep	250	260	270	280	290	300
	QTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
a102	QTAIQXNLPNEFAPVIAAEGQVSVXLIETLSKFAQTGNMDKILSLFSYMAIATSFLGVTL					
	250	260	270	280	290	300
m102.pep	310	320	330	340	350	360
	GLFDYIADIFKWNDSISGRKTAAALTFPLPLISCLLFPTGFVTAIGYVGLAATVWTGIIP					
a102	GLFDYIADIFKWNDSVSGRKTAAALTFLPPXISCLLFPTGFVTAIGYVGLAATVWTGIIP					
	310	320	330	340	350	360
m102.pep	370	380	390	400	410	
	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIVNIAAQVLSQMEI LVPVFKGX					
a102	AMLLYRSRKKFGAGKTYKVYGGGLWLMVWVFLFGIXNIAAXVLSQMEI LVPVFKGX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 363>:

g105.seq

```

1  Atgtccgcag aaaCATACac acAAAtcggc tGGgtaggct taggGcaaat
51  gGgtctgcct atgGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCgCg CAAAGGAGCA
151 AAAGTTTACG GCagcACCGC CGAACTCGTC CGCGCCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCCGTTTCCG GATCGGTCGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTTCGGCG ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGAAT CGCCTATGTT
651 TCAAACAAAA AAATCACTAT GGGCAAACCG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAACA CGCTTCCAAA GAcctTAACC TCGccgtcAA AGAGCTTGAA
751 CAGGCAGGCA ACACCCTGCC CGCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 364; ORF 105.ng>:

```
g105.pep
  1  MSAETYTQIG WVGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
 51  KVGYSTAELV RACPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101  TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLILFGG SEAVLNPLQK
151  IFSLVGKKTf HFGDVGKSGG AKLVNLNLLG IFGEAYSEAM LMARQFGIDT
201  DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251  QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 365>:

```
m105.seq
  1  ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGaTAGGCT TAGGGCAAAT
 51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGa CGGCGGCATC GAAGTCGGCG
101  TATACAACCG CTCGCCCACG AAAACTGCCG CCATCTCCGC CAAAGGCGCA
151  AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201  CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACCGAGTCC
251  GCGACGGATT GGCCGGCAAm ATCATCGTCA ACATGAGCAC CATCTCCCCG
301  ACCGAAAaGC TCGCCGTCAA AGCACTTGTC GAAGCGCAGm GaCAGTTTGC
351  CGAAGCACCC GTTTCGGGAT CGGTCCGGCC CGCCACCAAC GGCACGCTGC
401  TGATTCTGTT CGGCGGCAGC GAaCCGtTTT AAACCCGCTG CAAAAATAT
451  TTTCCCTCGT CGGCAAAAAA ACCTTCCATT TCGGCGATGT CGGCAAGGT
501  TCGGGCGCGA AACTCGTCTT GAACTCGCTC TTGGGCATTT TCGGCGAaCG
551  TACAGCGAAs GmTgCTGATG GCGCGGCAGT TCGGCATCGA TACCGACACC
601  ATCGTCGAAG CCATCGGsGA CTCGGCAATG GACTCGCCCA TGTTCCAAAC
651  CAAAAATCC CTGTGGGCAA ACCGCGAATT CCCGmCCGmC TTCGCCCTCA
701  AACACGCCTC CAAAGACCTC AACCTCGCCG TCAAAGAGCT TGAACAGGCA
751  GGCAACACCC TGCCCCCGGT CGAAACCGTT GCTGCCAGCT ACCGCAAAGC
801  AGTCGAAGCC GGCTACGGGA CACAGGACGT TTCCGGCGTT TACCTGAAAC
851  TGGCAGAAAC CTGA
```

This corresponds to the amino acid sequence <SEQ ID 366; ORF 105>:

```
m105.pep
  1  MSANEYAQIG WIGLGQMGLP MVTRLLDGGI EVGVYNRSPD KTAPISAKGA
 51  KVGNTAELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGX IIVNMSTISP
101  TEKLAVKALV EAQRQFAEAP VSGSVGPATN GTLLILFGGS EPFXTRCKKY
151  FPSSAKKPSI SAMSAKVRAR NSSXTRSWAF SANVQRXXLM ARQFGIDTDT
201  IVEAIGDSAM DSPMFQTKS LWANREFPXX FALKHASKDL NLAVKELEQA
251  GNTLPAVETV AASYRKAVEA GYGTQDVSGV YLKLAEH
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 105 shows 79.9% identity over a 289 aa overlap with a predicted ORF (ORF 105.ng) from *N. gonorrhoeae*:

```
m105/g105

      10      20      30      40      50      60
g105.pep  MSAETYTQIGWVGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGSTAEVLV
          |||: ||: ||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m105      MSANEYAQIGWIGLGQMGLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAEVLV
          10      20      30      40      50      60

      70      80      90     100     110     120
g105.pep  RACPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
          | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m105      RDYPVIFLMVSDYAAVCDILNGVRDGLAGXIIIVNMSTISPTEKLAVKALVEAQR-QFAEA
          70      80      90     100     110

      130     140     150     160     170     180
g105.pep  PVSGSVGPATNGTLILFGGSEAVLNPLQKIFSLVGKKTfHFGDVGKSGGAKLVNLSLLG
          ||||| ||||| ||||| ||||| : ||| : || : : : || : :
m105      PVSGSVGPATNGTLILFGGSEFPFXTRCKKYFPSSAKKP-SISAMSAKVRARNSSXTRSW
          120     130     140     150     160     170
```

314

	190	200	210	220	230	240
g105.pep	IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	:	::				
m105	AFSANVQRXXLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPXXFALKHASK					
	180	190	200	210	220	230
	250	260	270	280	289	
g105.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEH					
m105	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGTQDVSGVYLKLAEH					
	240	250	260	270	280	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 367>:

a105.seq

```

1  ATGTCCGCAA  ACGAATACAC  ACAAATCGGC  TGGATAGGCT  TAGGGCAAAT
51  GGGTCTGCCT  ATGGTAACGC  GGCTCTTGGA  CGGCGGCATC  GAAGTCGGCG
101 TATACAACCG  CTCGCCGAC  AAAACTGCCC  CCATCTCCGC  CAAAGGCGCA
151 AAAGTTTACG  GCAACACCG  CGAACTCGTC  CGCGACTATC  CCGTCATTTT
201 CCTGATGGTT  TCCGACTATG  CCGCCGTGTG  CGACATCCTG  AACGGAGTCC
251 GCGACGGATT  GGCCGGCAAA  ATCATCGTCA  ACATGAGCAC  CATCTCCCCG
301 ACCGAAACC  TCGCCGTCAA  AGCACTTGTC  GAAGCCGCAG  GCGGACAGTT
351 TGCCGAAGCA  CCCGTTCCG  GATCGGTCGG  GCCCGCCACC  AACGGCACGC
401 TGCTGATTCT  GTTCGGCGG  AGCGAAGCCG  TTTTAAACCC  GCTGCAAAAA
451 ATATTTTCCC  TCGTCGGCAA  AAAACCTTC  CATTTCGGCG  ATGTCGGCAA
501 AGGTTTCGGG  GCGAACTCG  TCTTGAAC  GCTCTGGGC  ATTTTCGGCG
551 AAGCGTACAG  CGAAGCGATG  CTGATGGCG  GGCAGTTCGG  CATCGATACC
601 GACACCATCG  TCGAAGCCAT  CGGCGGCTCG  GCAATGGACT  CGCCCATGTT
651 CCAAACCAA  AAATCCCTGT  GGGCAAACCG  CGAATTCCCA  CCCGCCTTCG
701 CCCTCAAACA  CGCCTCCAAA  GACCTCAACC  TCGCCGTCAA  AGAGCTTGAA
751 CAGGCAGGCA  ACACCTGCC  CGCCGTCGAA  ACCGTTGCTG  CCAGCTACCG
801 CAAAGCAGTC  GAAGCCGGCT  ACGGCGAACA  GGACGTTTCC  GCGGTTTACC
851 TGAAATTGGC  AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 368; ORF 105.a>:

a105.pep

```

1  MSANEYTQIG  WIGLGQMLP  MVTRLLDGGI  EVGVYNRSPD  KTAPISAKGA
51  KVGNTAELV  RDYPVIFLMV  SDYAAVCDIL  NGVRDGLAGK  IIVNMSTISP
101 TENLAVKALV  EAAGGQFAEA  PVSGSVGPAT  NGTLLILFGG  SEAVLNPLQK
151 IFSLVGKKT  FFGDVGKSG  AKLVNLSLLG  IFGEAYSEAM  LMARQFGIDT
201 DTIVEAIGGS  AMDSPMFQTK  KSLWANREFP  PAFALKHASK  DLNLAVKELE
251 QAGNTLPAVE  TVAASYRKAV  EAGYGEQDVS  GYVLKLAEH*

```

m105/a105 96.5% identity in 289 aa overlap

	10	20	30	40	50	60
m105.pep	MSANEYAQIGWIGLGQMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
a105	MSANEYTQIGWIGLGQMLPMVTRLLDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m105.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAG-QFAEA					
a105	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	120	130	140	150	160	170
m105.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG					
a105	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVNLSLLG					
	130	140	150	160	170	180
	180	190	200	210	220	230

```

m105.pep    IFGDV-QRXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPFAFALKHASK
             |||:: :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        IFGEAYSEAMLMARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPFAFALKHASK
             190      200      210      220      230      240

m105.pep    240      250      260      270      280
             DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
             ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a105        DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVSGVYLKLAEHX
             250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 369>:

g105-1.seq

```

1   ATGTCCGCAG AACATACAC ACAAATCGGC TGGGTAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGAGCA
151 AAAGTTTACG GCAGCACCGC CGAACTCGTC CGCGCTGCC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCGTTTCCG GATCGGTGGG ACCCGCCACC AACGGCACAC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TTGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGCTCGGGC GCGAAACTCG TCTTGAATC GCTCTTAGGC ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCTATGTT
651 TCAAAACAAA AAATCACTAT GGGCAAAACG TGAGTTCCCC CCTGCCTTTG
701 CACTCAAAAC CGTTTCCAA GACCTTAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTT GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAATTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 370; ORF 105-1.ng>:

g105-1.pep

```

1   MSAETTYQIG WVGLQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGSTAELV RACPVIPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP
101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK
151 IFSLVGKKEF HFGDVGKGSF AKLVNLSLFG IFGEAYSEAM LMARQFGIDT
201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE
251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 371>:

m105-1.seq

```

1   ATGTCCGCAA ACGAATACGC ACAAATCGGC TGGATAGGCT TAGGGCAAAT
51  GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGGCGGCATC GAAGTCGGCG
101 TATACAACCG CTCGCCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA
151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT
201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC
251 GCGACGGATT GGCCGGCAAA ATCATCGTCA ACATGAGCAC CATCTCCCCG
301 ACCGAAAACC TCGCCGTCAA AGCACTTGTC GAAGCCGCAG GCGGACAGTT
351 TGCCGAAGCA CCGTTTCCG GATCGGTGGG GCCCGCCACC AACGGCACGC
401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA
451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGGC ATGTCGGCAA
501 AGGTTTCGGG GCGAAACTCG TCTTGAATC GCTCTTGGG ATTTTCGGCG
551 AAGCGTACAG CGAAGCGATG CTGATGGCGC GGCAGTTCGG CATCGATACC
601 GACACCATCG TCGAAGCCAT CGGSGACTCG GCAATGGACT CGCCCATGTT
651 CCAAAACAAA AAATCCCTGT GGGCAAAACG CGAATTCGG CCGCGCTTCG
701 CCCTCAACA CGCTCCAAA GACCTCAACC TCGCCGTCAA AGAGCTTGAA
751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG
801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GCGGTTTACC
851 TGAAACTGGC AGAACACTGA

```

This corresponds to the amino acid sequence <SEQ ID 372; ORF 105-1>:

m105-1.pep

```

1   MSANEYAQIG WIGLQMGLP MVTRLDDGGI EVGVYNRSPD KTAPISAKGA
51  KVYGNTEALV RDYPIVPLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP

```

316

101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK  
 151 IFSLVGKTF HFGDVGKSG AKLVNLSLLG IFGEAYSEXM LMARQFGIDT  
 201 DTIVEAIGDS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE  
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS GVYLKLAEH\*

m105-1/g105-1 96.9% identity in 289 aa overlap

	10	20	30	40	50	60
m105-1.pep	MSANEYAQIGWIGLGQMG LPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGNTAELV					
g105-1	MSAETYTQIGWVGLGQMG LPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGSTAELV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m105-1.pep	RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA					
g105-1	RACPVIIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m105-1.pep	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKTFHFGDVGKSGAKLVNLSLLG					
g105-1	PVSGSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKTFHFGDVGKSGAKLVNLSLLG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m105-1.pep	IFGEAYSEXMLMARQFGIDTDTIVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK					
g105-1	IFGEAYSEAMLARQFGIDTDTIVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK					
	190	200	210	220	230	240
	250	260	270	280	290	
m105-1.pep	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVS G VYLKLAEHX					
g105-1	DLNLAVKELEQAGNTLPAVETVAASYRKAVEAGYGEQDVS G VYLKLAEHX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 373>:

a105-1.seq

1 ATGTCCGCAA AC GAATACAC ACAAATCGGC TGGATAGGCT TAGGGCAAAT  
 51 GGGTCTGCCT ATGGTAACGC GGCTCTTGGA CGCGCGCATC GAAGTCGGCG  
 101 TATACAACCG CTCGCCGAC AAAACTGCCC CCATCTCCGC CAAAGGCGCA  
 151 AAAGTTTACG GCAACACCGC CGAACTCGTC CGCGACTATC CCGTCATTTT  
 201 CCTGATGGTT TCCGACTATG CCGCCGTGTG CGACATCCTG AACGGAGTCC  
 251 GCGACGGATT GGCCGGCAA ATCATCGTCA ACATGAGCAC CATCTCCCGG  
 301 ACCGAAAACC TCGCCGTC AAAGCACTTGT GAAGCCGCG GCGGACAGTT  
 351 TGCCGAAGCA CCGGTTTCCG GATCGGTCCG GCCCGCCACC AACGGCACGC  
 401 TGCTGATTCT GTTCGGCGGC AGCGAAGCCG TTTTAAACCC GCTGCAAAAA  
 451 ATATTTTCCC TCGTCGGCAA AAAAACCTTC CATTTCCGCG ATGTCGGCAA  
 501 AGGTTCGGGC GCGAACTCG TCTTGAATC GCTCTTGGGC ATTTTCGGCG  
 551 AAGCGTACAG CGAAGCGATG CTGATGGCG GGCAGTTCGG CATCGATACC  
 601 GACACCATCG TCGAAGCCAT CGGCGGCTCG GCAATGGACT CGCCCATGTT  
 651 CCAAAACAAA AAATCCCTGT GGGCAAACCG CGAATTCCTA CCCGCTTCCG  
 701 CCCTCAACA CGCTCCAAA GACCTCAACC TCGCCGTC AAAGAGCTTGAA  
 751 CAGGCAGGCA ACACCTGCC CGCCGTCGAA ACCGTTGCTG CCAGCTACCG  
 801 CAAAGCAGTC GAAGCCGGCT ACGGCGAACA GGACGTTTCC GGCCTTTACC  
 851 TGAATTGGC AGAACACTGA

This corresponds to the amino acid sequence <SEQ ID 374; ORF 105-1.a>:

a105-1.pep

1 MSANEYTQIG WIGLGQMG LPMVTRLLDGGI EVGVYNRSPD KTAPISAKGA  
 51 KVGYNTELV RDYPVIFLMV SDYAAVCDIL NGVRDGLAGK IIVNMSTISP  
 101 TENLAVKALV EAAGGQFAEA PVSGSVGPAT NGTLLILFGG SEAVLNPLQK  
 151 IFSLVGKTF HFGDVGKSG AKLVNLSLLG IFGEAYSEAM LMARQFGIDT  
 201 DTIVEAIGGS AMDSPMFQTK KSLWANREFP PAFALKHASK DLNLAVKELE  
 251 QAGNTLPAVE TVAASYRKAV EAGYGEQDVS G VYLKLAEH\*

a105-1/m105-1 99.0% identity in 289 aa overlap

	10	20	30	40	50	60
a105-1.pep	MSANEYTQIGWIGLGQMG LPMVTRLLDGGIEVG VYNRSPDKTAPISAKGAKVYGNTAELV					

```

m105-1      MSANEYAQIGWIGLGQMGLPMVTRLDDGGIEVGVYNRSPDKTAPISAKGAKVYGNTAELV
              10      20      30      40      50      60
a105-1.pep  RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120
m105-1      RDYPVIFLMVSDYAAVCDILNGVRDGLAGKIIVNMSTISPTENLAVKALVEAAGGQFAEA
              70      80      90      100     110     120
a105-1.pep  PVSQSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
              130     140     150     160     170     180
m105-1      PVSQSVGPATNGTLLILFGGSEAVLNPLQKIFSLVGKKTFFHFGDVGKSGAKLVLSLLG
              130     140     150     160     170     180
a105-1.pep  IFGEAYSEAMLMARQFGIDTDITVEAIGGSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240
m105-1      IFGEAYSEXMLMARQFGIDTDITVEAIGDSAMDSPMFQTKKSLWANREFPPAFALKHASK
              190     200     210     220     230     240
a105-1.pep  DLNLAVKELEQAGNTLPAVETVAASYRKA VEAGYGEQDVSGVYLKLAHX
              250     260     270     280     290
m105-1      DLNLAVKELEQAGNTLPAVETVAASYRKA VEAGYGEQDVSGVYLKLAHX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 375>:

```

g107.seq
1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGGTTG CCGATGCCAA
51  ACCGTCCGTC CTCTTCGACA CCAAGCCCC CGTCGGCACC GGCTACTGGA
101 TTTACGCCGC CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG cgcCcaaagt
201 GgCGAaATCc atctggGcag gtacattggT TGCcttggtta atttacgtcc
251 TCTggcaaac cgccatCcaa agcaaccTGC cgcgcaacga gttcgcCCCC
301 gtgattgccg ccgagaggca actCTCCGTC CTgaatgaaa cctTgtccaa
351 attcgcccaa accggcgata tggataAaat attgtcccta tttccctaca
401 tggcaatcgc cacctccttt ttaggcgTAA Ccttaggcct gtttgacaac
451 atcgccggac atcttcaaat ggaacgacag tatgtccggg cggcaccaaa
501 accgtcgcgc tga

```

This corresponds to the amino acid sequence <SEQ ID 376; ORF 107.ng>:

```

g107.pep
1  MVLTFIWATG GLVADAKPSV LFDTPAPVGT GYWIYAATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWAGTLVALV IYVLWQTAIQ SNLPRNEFAP
101 VIAAERQLSV LNETLSKFAQ TGDMDKILSL FPYMAIATSF LGVTLGLFDN
151 IAGHLQMERQ YVRAAPKPSR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 377>:

```

m107.seq
1  ATGGTATTGA CCTTTATTTG GGCGGCCGCG GGGCTGATTG CCGATGCCAA
51  GCCGTCCGTC CTCTTCGATA CCAAGCCCC CGCCGGCACA AACTACTGGA
101 TTTACGCCGg CACCGCCCTG CCCGTCTGCC TCGCTTCCTT CGGCTTCCAC
151 GGCAACGTTT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTCATCGCCG CCGAAGGGCA AGTCTCCGTC CTCATCGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGCGGTAA CGCTCGGACT CTTCGACTAC
451 ATCGCCCATC TTCAAATGGA ACGACAGCAT CTCCGGgCCG CACCAAACC
501 GCCGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 378; ORF 107>:

```

m107.pep..
1  MVLTFIWAAG GLIADAKPSV LFDTPAPAGT NYWIYAXTAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTAIQ GNLPRNEFAP

```

101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTGLGLFDY  
 151 IAHLMQERQH LRAAPKPPR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 107 shows 89.4% identity over a 170 aa overlap with a predicted ORF (ORF 107.ng)  
 from *N. gonorrhoeae*:

m107/g107

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	:     :     :     :     :					
g107	MVLTFIWAATGGLVADAKPSVLFDTQAPVGTGYWIYAATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTALIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	:     :     :     :     :					
g107	KGDAPKVAKSIWAGTLVALVIYVLWQTALIQGNLPRNEFAPVIAAERQLSVLNETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFGLVTLGLFDYIA-HLMQERQHLRAAPKPPR					
	:     :     :     :     :					
g107	TGDMDKILSLFFPYMAIATSFGLVTLGLFDNIAGHLMQERQYVRAAPKPSR					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 379>:

a107.seq

```

1  ATGGTATTAA CCTTTATTTG GGCAACCGGC GGCCTGATTG CCGATGCCAA
51  ACTGCCCGTC CTCTTCGACA CCCAAGCCCC TACCGGCACC AACTACTGGA
101 TTTATGTGCG CACCGCCCTG CCCGTCTGCC TTGCGTCATT CGGTTTCCAC
151 GGCAACGTCT CCAGCCTGCT CAAATACTTT AAAGGCGACG CGCCCAAAGT
201 GGCTAAATCC ATCTGGACGG GCACACTGAT TGCCTGGTA ATTTACGTCC
251 TCTGGCAAAC CGCCATCCAA GGCAACCTGC CGCGCAACGA GTTCGCCCCC
301 GTGATTGCCG CCGAAGGGCA AGTCTCCGTC CTGATTGAAA CCCTGTCCAA
351 ATTCGCCCAA ACCGGCAATA TGGACAAAAT ATTGTCCCTG TTTTCCTATA
401 TGGCGATCGC CACCTCGTTT TTAGGCGTAA CGCTCGGACT CTTCCGACTAC
451 ATCGCCGACA TCTTCAAATG GAACGACAGC GTGTCCGGCC GCACCAAAC
501 CGCGCGCTG ACCTTCCTGC CGCCTCTAAT TTCCTGCCTG CTCTTCCCCA
551 CCGGCTTTGT TACCGCCATC GGCTACGTCG GCCTGGCGGC AACCGTCTGG
601 ACAGGCATCA TCCCCGCCAT GCTGCTCTAC CGTTCGCGCA AAAAATTCGG
651 CGCAGGCAAA ACCTATAAAG TTACGGCGG CTTGTGGCTG ATGGTTTGGG
701 TCTTCCTTTT CGGCATCGTC AACATCGCCG CACAGGTATT GAGCCAAATG
751 GAACTCGTCC CCGTATTTAA AGGATAA

```

This corresponds to the amino acid sequence <SEQ ID 380; ORF 107.a>:

a107.pep

```

1  MVLTFIWAATG GLIADAKLPV LFDQAPTGT NYWIYVATAL PVCLASFGFH
51  GNVSSLLKYF KGDAPKVAKS IWTGTLIALV IYVLWQTALQ GNLPRNEFAP
101 VIAAEGQVSV LIETLSKFAQ TGNMDKILSL FSYMAIATSF LGVTGLGLFDY
151 IADIFKWNDS VSGRTKTAAL TFLPPLISCL LFPTGFVTAI GYVGLAATVW
201 TGIIPAMLLY RSRKKFGACK TYKVYGLWL MVWVFLFGIV NIAAQVLSQM
251 ELVPVFKG*

```

m107/a107 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m107.pep	MVLTFIWAAGGLIADAKPSVLFDTQAPAGTNYWIYAXTALPVCLASFGFHGNVSSLLKYF					
	:     :     :     :     :					
a107	MVLTFIWAATGGLIADAKLPVLFDTQAPTGTNYWIYVATALPVCLASFGFHGNVSSLLKYF					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m107.pep	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
a107	KGDAPKVAKSIWTGTLIALVIYVLWQTAIQGNLPRNEFAPVIAAEGQVSVLIETLSKFAQ					
	70	80	90	100	110	120
	130	140	150	160	170	
m107.pep	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIAHLQMERQHLRAAPKPPRX					
a107	TGNMDKILSLFSYMAIATSFLGVTGLGLFDYIADIFKWNDSVSGRTKTAALTFLPPLISCL					
	130	140	150	160	170	180
a107	LFPTGFVTAIGYVGLAATVWTGIIPAMLLYRSRKKFGAGKTYKVYGGWLWMVWVFLFGIV					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 381>:

g108.seq

```

1  ATGttgccgg gCTTCAACCG GATATTCAaa cggTTTGCTC CAACACTCGG
51  AACggCGCAT AAAACGCCGc cTTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATCCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGCG GCAATCTTAC TCGCGGGGTG
201 CGCCGCCGGC GGCAACACAT TCGGCAGCTT AGACGGCGGC ACGGGTATGG
251 GTGGCAGCAT CGTCAAAATG ACGGTAGAAA gccAATGCCG TCGGAATTG
301 GACAGCGGCA GCGAATGGCG TTTGACCGCG CTGGCGATGA GTGCCGAAAA
351 ACAGGCGGAA TGGGAAAACA AGATTTCGG CTGCGCTACC GAAGAAGCAC
401 CTAACAGCT GACCGCAAC GATGTGATGC AGATGCTGaa ccagtcacg
451 CGCaatcagg cacTtgccgc CCTgaccgTC AAAacgggTT CcgctgctT
501 CAaacgctg tACCGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 382; ORF 108.ng>:

g108.pep

```

1  MLPGFNRIK RFAPTLGTAH KTPPFALSRT GRLIRSYRHK RRGFNRKGIE
51  MNKTLILPA AILLGGCAAG GNTFGSLDGG TGMGGSIVKM TVESQCRAEL
101 DRRSEWRLTA LAMSAEKQAE WENKICGCAT EEAPNQLTGN DVMQMLNQST
151 RNQALAAALTV KTVSACFKRL YR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 383>:

m108.seq

```

1  ATGTTGCCGG GCTTCAACCG GATATTCAAA CGGTTTGTTT CAACACTCGG
51  AACGGCGCAT AAAACGCCGC CCTTCGCGTT ATCCCGAACG GGGCGGCTAA
101 TCAGATTCTA TCGCCATAAA AGGCGGGGTT TCAACCGAAA AGGAATTGAG
151 ATGAATAAAA CCTTGTCTAT TTTGCCGGTG GCAATCTTAC TCGCGGGCTG
201 CGCCGCCGGA GGCGGTAACA CATTCGGCAG CTTAGACGGT GGCACAGGCA
251 TGGGCGGCAG CATCGTCAA ATGGCGGTTG GGAGCCAATG CCGTGCGGAA
301 TTGGACAAAC GCAGCGAATG GCGTTTGACC GCGCTGGCGA TGAGTGCCGA
351 AAAACAGGCG GAGTGGGAAA ACAAGATTG CCGTTGCGTC GCCCAAGAAG
401 CACCCGAACG GATGACCGGC AACGATGTGA TGCAGATGCT GGCTCCGTCC
451 ACGCGCAATC AGGCACTTGC CGCCCTGACC GCCAAAACGG TTTCGCCTG
501 CTTCAAACAC CTGTACCGCT AA

```

This corresponds to the amino acid sequence <SEQ ID 384; ORF 108>:

m108.pep

```

1  MLPGFNRIK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRKGIE
51  MNKTLILPV AILLGGCAAG GGNTFGSLDG GTGMGGSIVK MAVGSQCRAE
101 LDKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPERMTG NDVMQMLAPS
151 TRNQALAAAL AKTVSACFKH LYR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 108 shows 89.6% identity over a 173 aa overlap with a predicted ORF (ORF 108.ng) from *N. gonorrhoeae*:

m108/g108



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 385>:

1	ATGTTGCCGG	GCTTCAACCG	GATATTCAA	CGGTTTGTC	CAACACTCGG
51	AACGGCGCAT	AAAACGCCGC	CCTTCGCGTT	ATCCCGAACG	GGGCGGCTAA
101	TCAGATTCTA	TCGCCATAAA	AGGCGGGGTT	TCAACCGAAA	AGGAATTGAG
151	ATGAATAAAA	CCTTGTCTAT	TTTGCCGGTG	GCAATCTTAC	TCGGCGGTG
201	CGCCGCGCGG	GCGCGTAACA	CATTCCGCAG	CTTAGACGGC	GGCAACAGGT
251	TGGCGCGCAG	CATCGTCAAA	ATGGCGGTAG	AAAGCCAATG	CCGTGCGGAA
301	TTGAACAAAC	GCAGCGAATG	GCGTTTGACC	GCGCTGGCGA	TGAGTGCCGA
351	AAAACAGGCG	GAATGGGAAA	ACAAGATTG	CGCTTGCGTC	GCCCAAGAA
401	CACCCAACCA	GCTGACCGGC	AACGATGTGA	TGCAGATGCT	GGATCCGCTC
451	ACGCGCAATC	AGGCATTTGC	CGCCTTGACC	GCCAAAACGG	TTTCCGCTCG
501	CTTCAAAAC	CTGTACCGCT	AA		

This corresponds to the amino acid sequence <SEQ ID 386; ORF 108.a>:

1 MLPGFNRIFK RFVPTLGTAH KTPPFALSRT GRLIRFYRHK RRGFNRRKQIE  
51 MNKTLSILPV AAILGGCAAG GGNTFGSLDG GTGMGGSIVK MAVESQCRAE  
101 LNKRSEWRLT ALAMSAEKQA EWENKICACV AQEAPNQLTG NDVMQMLDPS  
151 TRNQALAAIT AKTVSACFKH LYR\*

**m108/a108** 96.5% identity in 173 aa overlap

```

10      20      30      40      50      60
m108.pep  MLPGFNRIKRFVPTLGTAHKTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKTL SILPV
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a108      MLPGFNRIKRFVPTLGTAHKTPPFALSRTGRLIRFYRHKRRGFNRKGIEMNKTL SILPV
          10      20      30      40      50      60

70      80      90      100     110     120
m108.pep  AILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVGSQCRAELDKRSEWRLTALAMSAEKQA
          |||||||||||||||||||||||||||||||||||:|||||||||||||
a108      AILLGGCAAGGGNTFGSLDGGTGMGGSIVKMAVESQCRAELNKRSEWRLTALAMSAEKQA
          70      80      90      100     110     120

130     140     150     160     170
m108.pep  EWENKICACVAQEAPERMTGNDVQMQLAPSTRNQALAALTAKTVSACFKHLYRX
          |||||||||||:|||||||||
a108      EWENKICACVAQEAPNQLTGNDVQMQLDPSTRNQALAALTAKTVSACFKHLYRX
          130     140     150     160     170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 387>:

This corresponds to the amino acid sequence <SEQ ID 388; ORF 109.ng>:

g109.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 389>:

m109.seq

This corresponds to the amino acid sequence <SEQ ID 4; ORF 109>:

m109.pcp

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 109 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 109.ng) from *N. gonorrhoeae*:

m109/g109

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 391>:

a109.seq

1 ATGTATTATC GCCGGGTGT GGGGCTATCC GATGGACTTG GCGATTTGGC  
51 AGCCGGTATT GAGCGTAGCC TTGGTCGTAG GCGTATACTT ACCGCTTTTG  
101 GAAGCGGGCA TGGAAATGAC GCGCAAAGGC AAAACCAACC AATCCGCCGC  
151 CACCGTGGTG TTCTCTCCG CTTGGTCAAT CCGGTTTTCG GCTGGGCGTT

**a109.pep**

1 MYRRRVVGLS DGLGDLAAGI ERSLGRRRIL TAFSGHGND AQRQNHPIRR  
51 HRGVLFRLVN PVFGWALTML LDNLGLIGCK ERSAQLGFTG RVLIPVVGFL  
101 ILCVAMGAVG MLPGIPFFLE HFKSLG\*

m109/a109 97.6% identity in 126 aa overlap

m109.pep	10	20	30	40	50	60
	MYYRRVMGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND	AQRQNHPIRRHRGVLFRLVN				
a109	:					
	MYYRRVVGLSDGLGDLAAGIERSLGRRRILTAFGSGHGND	AQRQNHPIRRHRGVLFRLVN				
	10	20	30	40	50	60
m109.pep	70	80	90	100	110	120
	PVFGWALTMLLDNLGLIGCKERSAQLGFAGRVLI	PAVGFLILCVAMGAVGMLPGIPPFLE				
a109						
	PVFGWALTMLLDNLGLIGCKERSAQLGFTGRVLI	PVVGFLILCVAMGAVGMLPGIPPFLE				
	70	80	90	100	110	120
m109.pep	HFKSLGX					
a109						
	HFKSLGX					

g111.seq

seq					
1	ATGCCGTCGTG	AAACACGCCT	GCCGAACCTT	ATCCGCGCCT	TGATATTTGC
51	CTGGGGTTC	ATCTTCTGA	ACGCTGTTC	GGAacaaac	GCGCAaaccg
101	TTACCCTGCA	AGGCGAAACG	ATGGGTACGA	CCTATACCGT	CAAATACCTT
151	TCAAATAATC	GGACAAACT	CCCCCCCCCT	GCCAAAATAC	AAAAGCGCAT
201	TGATGATGCG	CTTAAAGAAG	TCAACCGGCA	GATGtccaCC	TACCAGACCG
251	ATTCCGAAAT	CAGCCGGTtT	atacagacan	atgctggaga	gctcttcgcg
301	tntcatgcag	nttctataac	tgattccgcc	gaagactgtc	tgccctaatac
351	qcttatctca	tcggcgctct	ga		

g111.pap

```

1  MPSETRLPNL IRALIFALGF IFLNACSEQT AQTVTLQGET MGTTYTVKYK
51 SNNRDKLPSP AKIQKRIDDA LKEVNRQMST YQTDSEISRF IQTAGELFAH
101 ASITDSAEDC LPNTPISSAL *

```

m111.seq

seq					
1	ATGCCGCTCTG	AAACACGCCT	GCCGAACTTT	ATCCGCGTCT	TGATATTTGC
51	CCTGGGTTTC	ATCTTCTCTGA	ACGCCTGTTC	GGAACAAACC	GCGCAAACCG
101	TTACCCTGCA	AGGCGAAACG	ATGGGCACGA	CCTATATyCGT	CAAATTACCTT
151	TCAAATAATC	GGGACAAACT	CCCCTACCTT	GCCGAAATAC	AWAAACGCAT
201	CGATGACGCG	CTTAAAGAAK	TCAACCGGyA	GATGTCCACC	TATCAGCCCG
251	ACTCCGAAT	CAGCCGGTTC	AACCAACACA	CAGCGCGCAA	GCCCCTCCGC
301	ATTTCAGCG	ACTTCGCATA	CGTTACTGCC	GAAGCCGTCC	GCCTGAACCG
351	CCTGACACAC	GGCGCGCTGG	ACGTAACCGT	CGGCCCTTGG	GTCAACCTTT
401	GGGATTTCGG	CCCCGACAAA	TCCGTTACC	GTGAACCGTC	GCCGGAAACA
451	ATCAAAACAG	CGGCATCTTA	TACGGGCATA	GACAAATATCA	TTTTGAACA
501	AGGCAAGAT	TACGTTCTCT	TGAGCAAAAC	CCACCCCAAG	GCCTATTTTGG
551	ATTTATCTTC	GATTGCCAAA	GGCTTCGGCG	TTGATAAAGT	TGCGGGCGGAA

```

601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCGTGGCGC ATCGGTATCG
701 AGCAGCCCAA TATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAACGGC AAACGCCTCT CCCATATCAT CAACCCGAAC AACAAACGCA
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCGATG
901 ACGGCGGACG GCTTGTCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTTAAAGCTG GCAGAGCGCG AAAAAGCTCG TGTTCCTCTG ATTGTCAGGG
1001 ATAAAGCGG CTACCGCACC GCCATGTCTT CCGAATTGTA AAAAGTGC TC
1051 CGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 396; ORF 111>:

```

m111.pep
  1 MPSETRLPNF IRVLIFALGF IFLNACSEQT AQTVTLOGET MGTTYXVKYL
 51 SNNRDKLPSP AEIXKRIDDA LKEXNRXMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVRLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ
151 IKQAASYTGI DKIIILKQGD YASLSKTHPK AYLDLSSIAK GFGVDKVGAE
201 LEKYGIQNYL VEIGGELHKG KKNARGEPWR IGIEQPNIVQ CGNTQIIVPL
251 NNRLATSGD YRIFHVDKNG KRLSHIINPN NKRPIHNLA SISVVDASAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

ORF 111 shows 88.7% identity over a 97 aa overlap with a predicted ORF (ORF 111.ng) from *N. gonorrhoeae*:

m111.pep/g111.pep

	10	20	30	40	50	60
m111.pep	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLOGETMGTTYXVKYLSNNRDKLPSP					
	: :     :     :     :     :     :     :     :     :					
g111	MPSETRLPNLIRALIFALGFIFLNACSEQTAQTVTLOGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m111.pep	AEIXKRIDDA LKEXNRXMSY YQPDSEISRF NQHTAGKPLR ISSDFAHVTA EAVRLNRLTH					
	:                         : :					
g111	AKIQKRIDDA LKEVNROMST YQTDSEISRF IQTXAGELFAXHXSITDSAEDCLPNTPI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m111.pep	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIIILKQGDYASLSKTHPK					
g111	SALX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 397>:

```

a111.seq
  1 ATGCCGCTCG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTGC
 51 CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG
101 TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151 TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201 CGATGACGCG CTTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251 ACTCCGAAT CAGCCGGTTC AACCACACA CAGCCGGCAA GCCCTCCCG
301 ATTTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG
351 CCTGACACAC GCGCGCTGG ACGTAACCGT CGGCCCTTG GTCAACCTTT
401 GGGGATTCCG CCCCACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAACAAG CAGCATCTTA TACGGGCATA GACAAAATCA TTTTGAAACA
501 AGGCAAGAT TACGCTTCCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGA AAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGCAAAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GGCGGCAATA CGCAGATTAT CGTCCCCTG
751 AACAAACGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA

```

801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC  
 851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGCAGA CAGTGCATG  
 901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC  
 951 CTTAAAGCTG GCAGAGCGCG AAAAATCGC TGTTCCTG ATTGTCAGGG  
 1001 ATAAAGGCGG CTACCGCACC GCCATGTCTT CCGAATTGA AAAACTGCTC  
 1051 CGCTAA

This corresponds to the amino acid sequence <SEQ ID 398; ORF 111.a>:

a111.pep

1 MPSETRLPNF IRTLIFALS IFLNACSEQT AQTVTLOGET MGTITYTVKYL  
 51 SNNRDKLPSP AEIQKRIDDA LKEVNRQMS YQPDSEISRF NQHTAGKPLR  
 101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFDPK SVTREPSPEQ  
 151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE  
 201 LEKYGIQNYL VEIGGELHGK GKNARGEPR IGIEQPNIVQ GGNTQIIVPL  
 251 NNRLATSGD YRIFHVDKSG KRLSHIINPN NKRPIHNLASISVVADSAM  
 301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL  
 351 R\*

m111/a111 97.7% identity in 351 aa overlap

m111.pep	10	20	30	40	50	60
	MPSETRLPNFIRVLIFALGFIFLNACSEQTAQTVTLQGETMGTTYXVKYLSNNRDKLPSP					
a111	MPSETRLPNFIRTLIFALSIFLNACSEQTAQTVTLQGETMGTTYTVKYLSNNRDKLPSP					
	10	20	30	40	50	60
m111.pep	70	80	90	100	110	120
	AEIXKRIDDALKEXNRXMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
a111	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVHLNRLTH					
	70	80	90	100	110	120
m111.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIILKQKGDYASLSKTHPK					
a111	GALDVTVGPLVNLWGFDPKSVTREPSPEQIKQAASYTGIDKIILKQKGDYASLSKTHPK					
	130	140	150	160	170	180
m111.pep	190	200	210	220	230	240
	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRIGIEQPNIVQ					
a111	AYLDLSSIAKGFGVDKVAGELEKYGIQNYLVEIGGELHGKGKNARGEPRIGIEQPNIVQ					
	190	200	210	220	230	240
m111.pep	250	260	270	280	290	300
	GGNTQIIVPLNNRLATSGDYRIFHVDKNGKRLSHIINPNKRPIHNLASISVVADSAM					
a111	GGNTQIIVPLNNRLATSGDYRIFHVDKSGKRLSHIINPNKRPIHNLASISVVADSAM					
	250	260	270	280	290	300
m111.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
a111	TADGLSTGLFVLGETEALKLAEREKLAVFLIVRDKGGYRTAMSSEFEKLLRX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 399>:

g111-1.seq

1 ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCGCCT TGATATTTGC  
 51 CCTGGGTTTC ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAAACCG  
 101 TTACCCTGCA AGGCGAAACG ATGGGTACGA CCTATACCGT CAAATACCTT  
 151 TCAAATAATC GGGACAAACT CCCCTCCCTT GCCAAAATAC AAAAGCGCAT  
 201 TGATGATGCG CTTAAAGAAG TCAACCGCA GATGTCCACC TACCAGACCG

**g111-1.pap**

1	MPSETRLPNL	IRALIFALGF	IFLNACSEQT	AQTVTLQGET	MGTTYTVKYL
51	SNNRDKLPSP	AKTQKRIDDA	LKEVNRQMSF	YQTDSEISRF	NQHTAGKFLR
101	ISSDFAHVTA	EAVRNLRLTH	GALDVTVGPL	VNLWGFSGDP	SVTREPSPEQ
151	IKQAASYTGI	DKIILLQQGD	YASLSKTHPK	AYLDLSSIAK	GFGRDQKVAE
201	LEKYGIQNYL	VEIGGELHGK	GKNAHGEPWR	IGIEQPNIIQ	GGNTQIIIVL
251	NNRSLATSGD	YRIFHVDKNG	KRLSHIINPN	NKRPISHNLA	SISVVSDSAM
301	TADGLSTGLF	VLGETEALRL	AEQEKLAVFL	IVRDKDGYRT	AMSSEFAKLL
351	R*				

m111-1.seq

1	ATGCCGCTCTG	AAACACGCCT	GCCGAAC TTT	ATCCGCGTCT	TGATATTTGC
51	CCTGGGTTTC	ATCTTCCTGA	ACGCCTGTTT	GGAACAAACC	GCGCAAAACCG
101	TTACCTGTCA	AGGCGAAACG	ATGGGCACGA	CCTATACCGT	CAAAATACCTT
151	TCAAATAATC	GGGACAAACT	CCCCTACCT	GCGGAATAAC	AAAAACGCGAT
201	CGATGACGCG	CTTAAAGAGG	TCAACCCGGCA	GATGTCCACC	TATCAGCCCG
251	ACTCCGAAAT	CAGCCGGTTC	AACCAACACA	CAGCCCGGCA	GCCCTCCCGC
301	ATTTCAAGCG	ACTTCGCACA	CGTTACTGCC	GAAGCGCTCC	CGCTGAACCG
351	CCTGACACAC	GGCGCGCTGG	ACGTAACCGT	CGGCCCTTGG	GTCAACCTTT
401	GGGGATTTCG	CCCCAGACAA	TCCGTTACCC	GTGAACCCGT	GCCGGAAACAA
451	ATCAAAACAG	GGCATCTTTA	TACGGGCATA	GACAAATCA	TTTTGAARCA
501	AGGCAAGAT	TACGCTTCGT	TGAGCAAAAC	CACCCCCAAG	GCCTTTTGGG
551	ATTTATCTTC	GATTGCCAAA	GGCTTCGGCG	TTGATAAAGT	TGCGGGCGGAA
601	CTGGAAAAAT	ACGGCATTTCA	AAATTATCTG	GTGCAAAATCG	GCGCGAGGTT
651	GCACGGCAAA	GGCAAAAACG	CGCGCGGCGA	ACCGTGGCGC	ATCGGTATCG
701	AGACGCCCAA	TATCGTCCAA	CGGCGCAATA	CGAGATTAT	CGTCCCGCTG
751	AACAACCGTT	CGCTTGCCAC	TTCCGCGCAT	TACCGTATTT	TCCACGTCGA
801	TAAAAACGGC	AAACGCCTCT	CCCATATCAT	TACCCCGAAC	AACAACACGAC
851	CCATAGCCCA	CAACCTGC6C	TCCATCAGCG	TGGTCGCAGA	CAGTGCAGAT
901	ACGGCGGACG	GCTTGTCCAC	AGGATTATTC	GTATTGGGCG	AAACCGAAGC
951	CTTAAAGCTG	GCAGAGCGCG	AAAAACTCGC	TGTTTTCTTG	ATTGTCAGGG
1001	ATAAGGCGGG	CTACCGCACC	GCCATGTCTT	CCGAATTTGA	AAAACTGCTC
1051	CTGATAA				

m111-1.pgp

1	MPSETRLPNF	IRVLIFALGF	IFLNACSEQT	AQTVTLQGET	MGTTYTVKYL
51	SNNRDKLPSP	AEIQKRIDDA	LKEVNRQMSL	YQPDSEISRF	NQHTAGKPLR
101	ISSDAFHVTA	EAVRLNRLTH	GLADSVTVGPI	VNLWGFPGPD	SVTREPSPEQ
151	KQAASTYGTI	DKIILKQKGD	YASLSTKTHPK	AYLDLSSIAK	GFGVDKVAEG
201	LEKYGIQNYL	VEIGGELHGK	GKNARGEPPWR	IGIEQPNIVQ	GGNTQIIVPL
251	NNRSLATSGD	YRIFHVDKNG	KRLSHIINPN	NKRPISHNLA	SISVVADSAM
301	TADGLSTGLF	VLGETEALKL	AEREKLAVLF	IVRDKGGYRT	AMSSEFEKLL
351	R*				

m111-1/g111-1 96.6% identity in 351 aa overlap

**mll1-1.pep**

10          20          30          40          50          60	
	MPSETRLPNIRVLIFALGFIFLNACSEQTAQTVTLQETMGTTYTVKYLSNNRDKLPSP        :::  :

**qlll-1**

	MPSETRLPNILRALIFALGFIFLNACSEQTAQTVTLQETMGTTYTVKYLSNNRDKLPSP
--	---

326

	10	20	30	40	50	60
m111-1.pep	70	80	90	100	110	120
	AEIQKRIDDALKEVNRQMSYQPDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
g111-1	70	80	90	100	110	120
	AKIQKRIDDALKEVNRQMSYQTDSEISRFNQHTAGKPLRISSDFAHVTA EAVRLNRLTH					
m111-1.pep	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSP EIQQAASYTGIDKIILKQKDYASLSKTHPK					
g111-1	130	140	150	160	170	180
	GALDVTVGPLVNLWGFGPKSVTREPSP EIQQAASYTGIDKIILQKQKDYASLSKTHPK					
m111-1.pep	190	200	210	220	230	240
	AYLDLSSIAKGFVGVKVAELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQ					
g111-1	190	200	210	220	230	240
	AYLDLSSIAKGFVGVKVAELEKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIIQ					
m111-1.pep	250	260	270	280	290	300
	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPI SHNLASISVVADSAM					
g111-1	250	260	270	280	290	300
	GGNTQIIIVPLNNRSLATSGDYRIFHVDKNGKRLSHIINPNKRPI SHNLASISVVSAMSAM					
m111-1.pep	310	320	330	340	350	
	TADGLSTGLFVLGETEALKLAEREKLAFLIVRDKGGYRTAMSSEFEKLLRX					
g111-1	310	320	330	340	350	
	TADGLSTGLFVLGETEALRLAEQEKLAFLIVRDKGGYRTAMSSEFAKLLRX					

g111-1/p44550

sp|P44550|YOJL\_HAEIN HYPOTHETICAL LIPOPROTEIN HI0172 PRECURSOR >gi|1074292|pir||C64144  
 hypothetical protein HI0172 - Haemophilus influenzae (strain Rd KW20) >gi|1573128 (U32702)  
 lipoprotein, putative [Haemophilus influenzae Rd] Length = 346  
 Score = 349 bits (885), Expect = 2e-95  
 Identities = 177/328 (53%), Positives = 240/328 (72%), Gaps = 4/328 (1%)

Query: 23 LNACSEQTAQTVTLQGETMTGTTYXVKYLSNNRDKLPSPAEIXKRIDDALKEVNRXMSYQ 82  
 L AC ++T + ++L G+TMGTTY VKYL + S + + I+ LK+ N MSTY+  
 Sbjct: 17 LAACQKET-KVISLSGKTMGTTYHVKYLDGSGITATS-EKTHEEIEAILKDVNAKMSTYK 74

Query: 83 PDSEISRFNQHT-AGKPLRISSDFAHVTA EAVRLNRLTHGALDVTVGPLVNLWGFGPKS 141  
 DSE+SRFNQ+T P+ IS+DFA V AEA+RLN++T GALDVTVG+VNLWGFGP+K  
 Sbjct: 75 KDSLSRFNQHTQVNTPIEISADFAKVLAEAIRLNKVTGALDVTVGPPVNLWGFGPEKR 134

Query: 142 VTREPSP EIQQAASYTGIDKIILKQKDYASLSKTHPKAYLDLSSIAKGFVGVKVAEL 201  
 ++P+PEQ+ + ++ GIDKI L K+ A+LSK P+ Y+DLSSIAKGFVD+VA +L  
 Sbjct: 135 PEKQPTPEQLAERQAWVGIDKITLDTNKEKATLSKALPQVYVDLSSIAKGFVDQVAEKL 194

Query: 202 EKYGIQNYLVEIGGELHGKGNARGEPWRIGIEQPNIVQGGNTQIIIVPLNNRSLATSGDY 261  
 E+ QNY+VEIGGE+ KGKN G+PW+I IE+P + ++ LNN +A+SGDY  
 Sbjct: 195 EQLNAQNYMVEIGGEIRAKGNIEGKPWQIAIEKPTTGERAVEAVIGLNNMGMASSGDY 254

Query: 262 RIFHVDKNGKRLSHIINPNKRPI SHNLASISVVADSAMTADGLSTGLFVLGETEALKLA 321  
 RI+ ++NGKR +H I+P PI H+LASI+V+A ++MTADGLSTGLFVLGE +AL++A  
 Sbjct: 255 RIY-FEENGKRF AHEIDPKTGYPHQHLLASITVLAPTSMTADGLSTGLFVLGEDKALEVA 313

Query: 322 EREKLAFLIVRDKGGYRTAMSSEFEKL 349  
 E+ LAV+LI+R G+ T SS F+KL  
 Sbjct: 314 EKNNLAVYLIIRTDNGFVTKSSSAFKKL 341

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 403>:

a111-1.seq

```

1  ATGCCGCTCTG AAACACGCCT GCCGAACCTT ATCCGCACCT TGATATTTC
51  CCTGAGTTTT ATCTTCCTGA ACGCCTGTTC GGAACAAACC GCGCAACCG
101  TTACCCTGCA AGGTGAAACG ATGGGCACGA CCTATACCGT CAAATACCTT
151  TCAAATAATC GGGACAAACT CCCCTCACCT GCCGAAATAC AAAAGCGCAT
201  CGATGACGCG CTAAAGAAG TCAACCGGCA GATGTCCACC TATCAGCCCG
251  ACTCCGAAT CAGCCGGTTC AACCAACACA CAGCCGGCAA GCCCTCCGC
301  ATTCAAGCG ACTTCGCACA CGTTACTGCC GAAGCCGTCC ACCTGAACCG

```

```

351 CCTGACACAC GGC GCGCTGG ACGTAACCGT CGGCCCTTG GTC AACCTTT
401 GGGGATTTCG CCCGACAAA TCCGTTACCC GTGAACCGTC GCCGGAACAA
451 ATCAAAACAAG CAGCATCTTA TACGGGCATA GACAAATCA TTTTGAAACA
501 AGGCAAAAGAT TACGTTCTCT TGAGCAAAAC CCACCCCAAG GCCTATTTGG
551 ATTATCTTC GATTGCCAAA GGCTTCGGCG TTGATAAAGT TCGGGCGGAA
601 CTGGAAAAAT ACGGCATTCA AAATTATCTG GTCGAAATCG GCGGCGAGTT
651 GCACGGCAAA GGC AAAACG CGCGCGGCGA ACCTTGGCGC ATCGGCATCG
701 AACAGCCCAA CATCGTCCAA GCGGCAATA CGCAGATTAT CGTCCCGCTG
751 AACACCGTT CGCTTGCCAC TTCCGGCGAT TACCGTATTT TCCACGTCGA
801 TAAAAGCGGC AAACGCCTCT CCCATATCAT TAATCCGAAC AACAAACGAC
851 CCATCAGCCA CAACCTCGCC TCCATCAGCG TGGTCGAGA CAGTCCGATG
901 ACGGCGGACG GCTTGTCCAC AGGATTATTC GTATTGGGCG AAACCGAAGC
951 CTAAAGCTG GCAGAGCGCG AAAAATCGC TGTTCCTG ATTGTCAGGG
1001 ATAAAGCGG CTACCGCACG GCCATGTCTT CCGAATTGA AAACTGCTC
1051 CGTAA

```

This corresponds to the amino acid sequence <SEQ ID 404; ORF 111-1.a>:

a111-1.pep

```

1  MPSETRLPNF IRTLIFALSF IFLNACSEQT AQTVTLQGET MGTITYVKYL
51  SNNRDKLPSP AEIQKRIDDA LKEVNRQMSY YQPDSEISRF NQHTAGKPLR
101 ISSDFAHVTA EAVHLNRLTH GALDVTVGPL VNLWGFGPK SVTREPSPEQ
151 IKQAASYTGI DKILKQKGD YASLSKTHPK AYLDLSSIAK GFGVDKVAGE
201 LEKYGIQNYL VEIGGELHGK GKNARGEPWR IGIEQPNIVQ GGNTQIIVPL
251 NNRSLATSGD YRIFHVDKSG KRLSHIINPN NKRPISHNLA SISVVADSAM
301 TADGLSTGLF VLGETEALKL AEREKLAVFL IVRDKGGYRT AMSSEFEKLL
351 R*

```

a111-1/m111-1 98.9% identity in 351 aa overlap

a111-1.pep	10	20	30	40	50	60
	MPSETRLPNF	IRTLIFALSF	IFLNACSEQT	AQTVTLQGET	MGTITYVKYL	SNNRDKLPSP
m111-1	MPSETRLPNF	IRTLIFALSF	IFLNACSEQT	AQTVTLQGET	MGTITYVKYL	SNNRDKLPSP
	10	20	30	40	50	60
a111-1.pep	70	80	90	100	110	120
	AEIQKRIDDA	LKEVNRQMSY	YQPDSEISRF	NQHTAGKPLR	ISSDFAHVTA	EAVHLNRLTH
m111-1	AEIQKRIDDA	LKEVNRQMSY	YQPDSEISRF	NQHTAGKPLR	ISSDFAHVTA	EAVHLNRLTH
	70	80	90	100	110	120
a111-1.pep	130	140	150	160	170	180
	GALDVTVGPL	VNLWGFGPK	SVTREPSPEQ	IKQAASYTGI	DKILKQKGD	YASLSKTHPK
m111-1	GALDVTVGPL	VNLWGFGPK	SVTREPSPEQ	IKQAASYTGI	DKILKQKGD	YASLSKTHPK
	130	140	150	160	170	180
a111-1.pep	190	200	210	220	230	240
	AYLDLSSIAK	GFGVDKVAGE	LEKYGIQNYL	VEIGGELHGK	GKNARGEPWR	IGIEQPNIVQ
m111-1	AYLDLSSIAK	GFGVDKVAGE	LEKYGIQNYL	VEIGGELHGK	GKNARGEPWR	IGIEQPNIVQ
	190	200	210	220	230	240
a111-1.pep	250	260	270	280	290	300
	GGNTQIIVPL	NNRSLATSGD	YRIFHVDKSG	KRLSHIINPN	NKRPISHNLA	SISVVADSAM
m111-1	GGNTQIIVPL	NNRSLATSGD	YRIFHVDKSG	KRLSHIINPN	NKRPISHNLA	SISVVADSAM
	250	260	270	280	290	300
a111-1.pep	310	320	330	340	350	
	TADGLSTGLF	VLGETEALKL	AEREKLAVFL	IVRDKGGYRT	AMSSEFEKLL	RX
m111-1	TADGLSTGLF	VLGETEALKL	AEREKLAVFL	IVRDKGGYRT	AMSSEFEKLL	RX
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 405>:

g114.seq

```

1  ATGGCTTCCA TCACTTCGCC GCTGCACGGG GCGCAGCAGG AATGCAGCAA
51  GACTTTTTTA TGTCCGCCGG GCGGGACGAG TATGGGGCGG TCAATGTCGG

```



g114.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 407>:

m114.seq

**This corresponds to the amino acid sequence <SEQ ID 408; ORF 114>:**

m114.pcp

m114/g114 90.0% identity over a 140 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 409>:

a114.seq

1	ATGCCGGAGG	CAAGCATCGC	CTCCATCACT	TCGCCGCTGC	ACGGGGCGCA
51	ACAGGAATGC	AGCAAGACTT	TTTTATGTCC	GCCGGGCGGG	ACGAGTATGG
101	GGCGGTCAT	CTCGGTAACG	GTAGGTTTGT	TTTGTGTTTC	CATTAACTTA
151	ACGATATCTG	TGCAATACGG	TTGAAGCGCG	TATTTATCA	GAGCCGCCCT
201	ATGTAATAACA	GGGTGTCAGG	GCATCAGCCC	GAGTCCCTG	AACGAACGGA
251	CGGTTTGCGC	CGTTACGATA	AAATGGTCGA	GCAGCGACAC	ATCGACCAGC
301	GACATTGCCT	GTGCCAGCCG	CCTTGTGAAC	ATGATGCTCT	CCTGCGAAGG
351	TTCGGGCGAG	CCGCCCGGAT	GGTTGTGCGC	GATAATCAGG	CTGTCCGCAT
401	ATTTCGTCAA	TGCCAGTTTG	ACAATTTAC	GGATGTAA	

This corresponds to the amino acid sequence <SEQ ID 410; ORF 114.a>:

a114.pep

```

1 MPEASIASIT SPLHGAQQEC SKTFLCPPGG TSMGRSMSVT VGLFCVSINL
51 TISVEYG*SG YFIRAAACKT GCQGISPCL NERTVCAVTI KWSSSDTSTS
101 DIACASRLVN MMSSCEGSGE PPGWLCAIIR LSAYSSNASL TISM*
```

m114/a114 92.9% identity in 140 aa overlap

```

          10      20      30      40      50
m114.pep      MASITSPLHGAHRECSKTFLCPPGGTSMGRSMSVTVGLFCVSINLTISVEYGXSG
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           MPEASIASITSPLHGAQQECSKTFLCPPGGTSMGRSMSVTVGLFCVSINLTISVEYGXSG
          10      20      30      40      50      60

          60      70      80      90      100     110
m114.pep      YFIRAAACKTECQGINPSCLEQTLXVTIKWSSSDTSTSDIACASRLVNMMSSCEXSSE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           YFIRAAACKTGCGGISPCLNERTVCAVTIKWSSSDTSTSDIACASRLVNMMSSCEGSSE
          70      80      90      100     110     120

          120     130     140
m114.pep      PPGWLCAIIRLSAYSSNASLTISM*
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a114           PPGWLCAIIRLSAYSSNASLTISM*
          130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 411>:

g117.seq

```

1 atggtcgacg aactcgacCT GCTGCCCGAT GCCGTCGCCG CCACCCTGCT
51 TGCCGACATC GGACGCTACG TCCCGGATG GAACCTATTG GTTTCGAGC
101 GCTGCAACAG CACCGTCGCC GAGCTGGTCA AAGGTgtgga CGAAGTGCAG
151 AAACCTACCC ACTTCGCCCC GGTGGACAGC CTCGCCACGC CGGAAGAACG
201 CGCACAGCAA GCGGAAACCA TCGGAAAT GCTGCTGGCg atggttaccg
251 Acatccgct cgtATTAAAT AAAGTGGCGA TCGTAcgcy caccCTGcta
301 ttTTtaagCA ACGCCCCGA CAGCCCTGAA AAAGcgccg TCgccaAga
351 aacctTCGAC ATCTTCGCCC CGCTCGCCAA CCGCTTGGGC GTGTGGCAGC
401 TCAAATGGCA GCTCGAAGAT TTGGGCTTCC GCCATCAAGA ACCCGAAAAA
451 TACCGCGAAA TCGCCCTGCT TTTGGACGAA AAACGCACCG AACGCCTCGA
501 ATACATCGAA AACTTCCTCG ATATCTGCG TACGGAACCT AAAAAATACA
551 ATATCCACTT TGAAGTCGCC GGCCGTCCGA AACACATCTA CTCCATTTAC
601 AAAAAAATGG TGAAGAAAAA ACTCAGCTTC GACGgctGT TCGACATCCG
651 CGCCGTGCGG ATTCTGGTCG ATACCGTCCC CGaGTGTAC ACCACGCTGG
701 gcaTCGTCCA CAGCCTCTGG CAGCCCATTC CCGCGagtt CGAcgactAC
751 ATCGCCAACC CCAAAGgcaA CGgttATAAA AGtTTGCACA CCGTCATCGT
801 cggcccGGAA gacaaagggtg tggaaGtgCA AATCCGCACC TTCGAtatGC
851 accAATTCAa CgaatTcggT gtcgcccGCC ACTGGCGtta caaagaaggc
901 ggcaaaggcg attccGCCTa cgaacaaAAA ATcgccTggt TGCgccaACT
951 CTTGGAAGTG CGCGAAAATA TGGCGGAAAG CGGCAAGGAA GACCTCGCCG
1001 CCGCCTTCAA AACCAGAGCTT TTCAACGACA CGATTATGT TTTGACCCCG
1051 CACGGCAAAG TCCTCTCTCT GCCAACGGGC GCAACCCCA TCGACTTCGC
1101 CTACGCCCTG CACAGCAGCA TcggCGACCG CTGCCGGGGC GCGAAAGTCG
1151 AaggGCAGAT TGTGCGCTG TCCACCCGC TCGAAAACGG ACAGCGCGTC
1201 GAAATcatta cCGCcaaAGA AGGGCATCCT TCCGTCAACT GGCTTTACGA
1251 AGGctgGGtc aaATCCGGCA AGGCCATCGG caaAATCCGC GCCTAcacCC
1301 GCCAGcaaAa cgCgaCACC GTGCGGAAG AAGGCCGTGT CCAACTCGAC
1351 AAGCAGCTTG CCAAACTCAC GCCCAAACCC AACCTGCAAG AGCTTgcca
1401 aaATCTCGGC tacaaAAAGC cagaagacct ctacacCGCc gtcggacaag
1451 gcgaaatttc caaccgcgcc atCaaaaag cctgcggcac GCTgaacgaa
1501 ccgccccCG TGCCCGTCAG CGCAACCACC ATCGTCAAA AGTCCAAAAT
```

```

1551 CAAAAAAGGT GGCAAAACCG GCGTGCTCAT CGACGGCGAA GACGGCTTGA
1601 TGACCACGCT TGCCAAATGC TGCAAACCCG CGCCGCCCGA CGATATTGCC
1651 GGCTTCGTTA CCCGCGAGCG CGGCATTTCG GTCCACCGCA AAACCTGCCC
1701 CTCTTTCCGA CACCTTGCCG AACACGCGCC CGAAAAAGTA CTGGACGCAA
1751 GTTGGGCGGC GTTGCAGGAA GGGCAAGTGT TCGCCGTCTGA TATCGAAATC
1801 CGCGCCCAAG ACCGCTCCGG GCTTTTGCGC GACGTATCCG ACGCGCTCGC
1851 CCGCCACAAA CTCAACGTTA CCGCCGTGCA AACCCAGTCC CGCGACTTGG
1901 AAGCCAGCAT GAGGTTACAG CTCGAAGTCA AACAAGtCAA CGacCTCCCC
1951 CGCGTCCTCG CCGGCCTCGG CGATGTCAAA GCGGTATTGA GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 412; ORF 117.ng>:

g117.pep

```

1 MVDEL DLLPD AVAATLLADI GRYVPDWNLL VSERCNSTVA ELVKGVDEVQ
51 KLTHFARVDS LATPEERAQQ AETMRKMLLA MVTDIRVLI KLAMRTRTLL
101 FLSNAPDSPE KRAVAKETLD IFAPLANRLG VWQLKWQLED LGFRHQEPEK
151 YREIALLLDE KRTERLEYIE NFLDI LRTEL KKYNIHFEVA GRPKHIYSIY
201 KKMVKKKLSF DGLFDIRAVR ILVDTVPECY TTLGIVHSLW QPIPGFDDY
251 IANPKGNGYK SLHTVIVGPE DKGVEVQIRT FDMHQFNEFG VAAHWRYKEG
301 KGKDSAYEQK IAWLRQLLDW RENMAESGKE DLAAAFKTEL FNDTIYVLT
351 HGKVLSLPTG ATPIDFAYAL HSSIGDRCRG AKVEGQIVPL STPLENGQVR
401 EIITAKEGHP SVNWLYEGWV KSGKAIGKIR AYIRQONADT VREEGRVQLD
451 KQLAKLT PKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE
501 PPPVPVSATT IVKQSKI KKG GKTGVLIDG DGLMTTLAKC CKPAPPDDIA
551 GFVTRERGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GQVFAVDIEI
601 RAQDRSGLLR DVSDALARHK LNVTA VQTQS RDLEASMRFT LEVKQVNDLP
651 RVLAGLG DVK GVLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 413>:

m117.seq (partial)

```

1 ..GTGAACTCA AGAAATACAA TGTCCATTTC GAAGTCGCCG GCCCGCCGAA
51 ACACATCTAC TCCATTTACA AAAAAATGGT GAAGAAAAAA CTCAGCTTCG
101 ACGGCCTCTT TGACATCCGC GCCGTGCGAA TTCTGGTTGA TACCGTCCCC
151 GAGTGTACCA CCACGCTGGG TATCGTCCAC AGCCTCTGGC AGCCATTTC
201 CGGCGAGTTC GACGACTACA TCGCCAATCC CAAAGGCAAC GGCTATAAAA
251 GTTTGCACAC CGTCATCGTC GGCCCGGAAG ACAAGGCGT GGAAGTACAA
301 ATCCGCACCT TCGATATGCA CCAATCAAC GAATTCGGTG TCGCCGCCCA
351 CTG9CGTTAC AAAGAGGGCG GCAAGGGCGA TTCCGCCTAC GAACAGAAAA
401 TCGCCTGGTT GCGCCAATC TTGGACTGGC GCGAAAACAT GCGCGAAAGC
451 GGCAAGGAAG ACCTCGCCGC CGCCTTCAAA ACCGAGCTTT TCAACGACAC
501 GATTTATGTT TTGACCCCGC ACGGCAAGT CCTCTCCCTG CCCACGGGCG
551 CGACCCCATC CGACTTCGCC TACGCCCTGC ACAGCAGCAT CGGCGACCGT
601 TGCCGCGGTG CGAAAGTCGA AGGGCAGATT GTGCCGCTGT CCACCCGCT
651 CGAAAACGGA CAGCGCGTCG AAATCATTAC CGCCAAAGAA GGGCATCCTT
701 CCGTCAACTG GCTTTACGAA GGCTGGGTCA AATCCAACAA GGCAATCGGC
751 AAAATCCGCG CCTACATCCG CCAGCAAAAC GCCGACACCG TGCGCGAAGA
801 AGGCCGCGTC CAACTCGACA AACAGCTTGC CAAACTCACG CCCAAACCCA
851 ACCTGCAAGA GCTTGCCGAA AATCTCGGCT ACAAAAAGCC AGAAGACCTC
901 TACACCGCCG TCGGACAAGG CGAAATTTCC AACCGCGCCA TCCAAAAAGC
951 CTGCGGCACg CTGAACGAAC CGCCGCCCGT ACCCGTCAGC GAAACCACCA
1001 TCGTCAAAAC GTCCAAAATC AAAAAAGGCG GCAAAAACGG CGTGCTCATC
1051 GACGGCGAAG ACGGTCTGAT GACCACGCTT GCCAAATGCT GCAAACCCGC
1101 GCCGCCCAGC GATATTATCG GCTTCGTTAC CCGCGAGCGC G9CATTTCAG
1151 TGACCCGCAA AwyyTkCyCG TCTTTCCAAC ACCTCGCCGA ACACGCGCCC
1201 GAWAAAGTGC TGGACGCAAG CTGGGCGGCA TTGCAGGAAG GACAAGTATT
1251 CGCCGTCGAT ATCGAAATCC GCGCCCAAGA CCGCTCCGGG CTTTTCGCG
1301 ACGTATCCGA CGCGCTCGCC CGCCACAAAC TCAACGTTAC CGCCGTGCAA
1351 ACCCAGTCCC GCGACTTGA AGCCAGCATG AGGTTACAGC TCGAAGTCAA
1401 ACAAGTCAAC GACCTCCCGC GCGTCCTCGC CAGCCTCGGC GACGTCAAAG
1451 GCGTATTGAG CGTTACCCGG CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 414; ORF 117>:

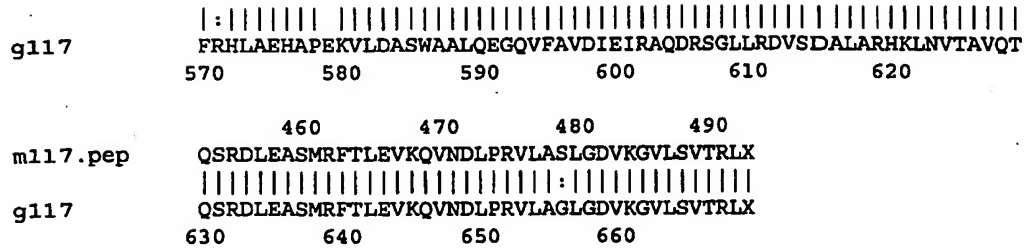
m117.pep (partial)

**Homology with a predicted ORF from *N. gonorrhoeae***

m117/g117

[illegible]

332



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 415>:

a117.seq

```

1  ATGGTTCATG  AACTCGACCT  GCTCCCCGAT  GCCGTCGCCG  CCACCCTGCT
51  TGCCGACATC  GGACGCTACG  TCCCCGACTG  GAACCTATTG  GTTTCGGAAC
101 GCTGCAACAG  TACCGTCGCC  GAGCTGGTCA  AAGGTGTGGA  CGAAGTGCAG
151 AAACCTACCC  ACTTCGCCCG  GGTGGACAGC  CTCGCCACGC  CGGAAGAACG
201 CGCCGAGCAG  GCAGAACTA  TGCGGAAAT  GCTGCTGGCG  ATGGTTACCG
251 ACATCCGCGT  CGTGTTAATC  AAATGGCGA  TGCGTACGCG  CACCCTGCAA
301 TTTTAAAGCA  ACGCCCCGA  CAGCCCCGAA  AAACGCGCGG  TCGCCAAAGA
351 AACCTCGAC  ATCTTCGCC  CGCTCGCCAA  CCGTTTGGGC  GTGTGGCAGC
401 TCAAATGGCA  GCTCGAAGAT  TTGGGCTTCC  GCCATCAAGA  ACCCGAAAAA
451 TACCGCGAAA  TCGCCCTGCT  TTTGGACGAA  AAACGCACCG  AACGCCTCGA
501 ATACATCGAA  AACTTCCTTA  ATATCCTGCG  TACGGAACCT  AAAAAATACA
551 ATATCCAATT  TGAAGTCGCC  GGCCGTCCGA  AACACATCTA  CTCCATTTAC
601 AAAAAAATGG  TGAAGAAAAA  ACTCAGCTTC  GACGGTTGT  TCGACATCCG
651 CGCCGTGCGG  ATTCTGGTTG  ATACCGTCCC  CGAGTGTAC  ACCACACTGG
701 GCATTGTCCA  CAGCCTCTGG  CAGCCATTC  CCGGCGAGTT  CGACGACTAC
751 ATCGCAAC  CGAAAGGCAA  CGGCTATAAA  AGTTTGACACA  CCGTCATCGT
801 CGGCCCGGAA  GACAAAGGCG  TGAAGTGCA  AATCCGCACC  TTCGATATGC
851 ACCAATTCAA  CGAATTCCGT  GTCGCCGCGC  ACTGGCGTTA  CAAAGAGGGC
901 GGCAAAGGCG  ATTCCGCCTA  CGAACAAAAA  ATCGCCTGGT  TACGCCAACT
951 TTTGGACTGG  CGCGAAAACA  TGGCGGAAAG  CGGCAAGGAA  GACCTCGCCG
1001 CCGCCTTCAA  AACCAGAGCT  TTCAACGACA  CGATTATGT  TTTGACCCCG
1051 CACGGCAAAG  TCCTCTCCCT  GCCACAGGC  GCGACCCCA  TCGACTTCGC
1101 CTACGCCCTG  CACAGCAGCA  TCGGCGACCG  TTGCCGCGGT  GCGAAAGTCG
1151 AAGGGCAGAT  TGTGCCGCTG  TCCACCCCGC  TCGAAACGG  ACAGCGTGTG
1201 GAAATCATT  CCGCCAAAGA  AGGGCATCCT  TCCGTCAACT  GGCTTTACGA
1251 AGGCTGGGTC  AAATCCAACA  AGGCAATCGG  CAAATCCGC  GCCTACATCC
1301 GCCAGCAAAA  CGCCGACACC  GTGCGCGAAG  AAGCCGCGT  CCAACTCGAC
1351 AAACAGCTTG  CCAAACTCAC  GCCCAAACCC  AACCTGCAAG  AGCTTGCCGA
1401 AAATCTCGGC  TACAAAAGC  CAGAAGACCT  CTACACCGCC  GTCGGACAAG
1451 GCGAAATTT  CAACCGCGCC  ATCCAAAAG  CCTGCGGCAC  GCTGAACGAA
1501 CCGCCGCCCG  TACCCGTCAG  CGAAACCACC  ATCGTCAAC  AGTCCAAAT
1551 CAAAAAAGGC  GGCAAAAACG  GCGTGCTCAT  CGACGGCGAA  GACGGTCTGA
1601 TGACCACGCT  TGCCAAATGC  TGCAAACCCG  CGCCGCCCGA  CGACATTGTC
1651 GGCTTCGTTA  CCCGCGATCG  CGGCATTTG  GTACACCGCA  AAACCTGCCC
1701 CTCTTTCCGA  CACCTCGCCG  AACACGCGCC  CGAAAAGTA  CTGGACGCAA
1751 GTTGGGCGGC  GTTGCAGGAA  GGACAAGTGT  TCGCCGTCGA  TATCGAAATC
1801 CGCGCCCAAG  ACCGCTCCGG  GCTTTTGCGC  GACGTATCCG  ACGCGCTCGC
1851 CCGCCACAAA  CTCAACGTTA  CCGCCGTGCA  AACCAGTCC  CGCGACTTGG
1901 AAGCCAGCAT  GAGGTTACG  CTCGAAGTCA  AACAAGTTAC  CGACCTCCCA
1951 CGCGTCCTCG  CCAGCCTCGG  CGACGTCAA  GGCGTATTGA  GCGTTACCCG
2001 GCTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 416; ORF 117.a>:

a117.pep

```

1  MVHELDLLPD  AVAATLLADI  GRYVPDWNLL  VSERCNSTVA  ELVKGVDEVO
51  KLTHFARVDS  LATPEERAQQ  AETMRKMLLA  MVTDIRVLI  KLAMRTRTLQ
101 FLSNAPDSPE  KRAVAKETLD  IFAPLANRLG  VWQLKWQLED  LGFRHQEPEK
151 YREIALLLDE  KRTERLEYIE  NFLNILRTEL  KKYNIHFEVA  GRPKHIYSIY
201 KKMVKKKLSF  DGLFDIRAVR  ILVDTVPECY  TTLGIVHSLW  QPIPGFDDY
251 IANPKNGYK  SLHTVIVGPE  DKGVEVQIRT  FDMHQFNEFG  VAAHWRYKEG
301 KGKDSAYEQK  IAWLRQLLDW  RENMAESGKE  DLAAAFKTEL  FNDTIYVLTP
351 HGKVLSLPTG  ATPIDFAYAL  HSSIGDRCRG  AKVEGQIVPL  STPLENGQRV

```

333

401 EIITAKEGHP SVNWLYEGWV KSNKAIGKIR AYIRQONADT VREEGRVQLD  
 451 KQLAKLTPKP NLQELAENLG YKKPEDLYTA VGQGEISNRA IQKACGTLNE  
 501 PPPVPVSETT IVKQSKIKKG GKNGLVIDGE DGLMTTLAKC CKPAPPDDIV  
 551 GFVTRDRGIS VHRKTCPSFR HLAEHAPEKV LDASWAALQE GOVFAVDIEI  
 601 RAQDRSGLLR DVSDALARHK LNVAVQTQS RDLEASMRFT LEVKQVTDLP  
 651 RVLASLGDKV GVLVTRL\*

m117/a117 98.0% identity in 490 aa overlap

m117.pep				10	20	30
				VKLKKYNVHFEVAGRPKHIYSIYKKMVKKKL		
a117	EKYREIALLLDEKRTERLEYIENFLNILRTELKKYNHFEVAGRPKHIYSIYKKMVKKKL					
	150	160	170	180	190	200
m117.pep		40	50	60	70	80
		SFDGLFDIRAVRILVDTVPECYTTGLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVG				
a117	SFDGLFDIRAVRILVDTVPECYTTGLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVG					
	210	220	230	240	250	260
m117.pep		100	110	120	130	140
		PEDKGVQVQIRTFDMHQFNEFGVAHWRYKEGKGDSAYEQKIAWLQQLDWRENMAESG				
a117	PEDKGVQVQIRTFDMHQFNEFGVAHWRYKEGKGDSAYEQKIAWLQQLDWRENMAESG					
	270	280	290	300	310	320
m117.pep		160	170	180	190	200
		KEDLAAAFKTELFNDTIYVLTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV				
a117	KEDLAAAFKTELFNDTIYVLTPHGKVLSPGTGATPIDFAYALHSSIGDRCRGAKVEGQIV					
	330	340	350	360	370	380
m117.pep		220	230	240	250	260
		PLSTPLENGQORVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQONADTVREEGRVQ				
a117	PLSTPLENGQORVEIITAKEGHPSVNWLYEGWVKSNAIGKIRAYIRQONADTVREEGRVQ					
	390	400	410	420	430	440
m117.pep		280	290	300	310	320
		LDKQLAKLTPKPNLQELAENLGKYPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSE				
a117	LDKQLAKLTPKPNLQELAENLGKYPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSE					
	450	460	470	480	490	500
m117.pep		340	350	360	370	380
		TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKXXXS				
a117	TTIVKQSKIKKGGKNGVLIDGEDGLMTTLAKCCKPAPPDDIVGFVTRDRGISVHRKTCPS					
	510	520	530	540	550	560
m117.pep		400	410	420	430	440
		FQHLAEHAPXKVLDAASWAALQEQGVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT				
a117	FRHLAEHAPEKVLDAASWAALQEQGVFAVDIEIRAQDRSGLLRDVSDALARHKLNVTAVQT					
	570	580	590	600	610	620
m117.pep		460	470	480	490	
		QSRDLEASMRFTLEVQVNDLPRVLASLGDKVGVLSVTRLX				
a117	QSRDLEASMRFTLEVQVTDLPRVLASLGDKVGVLSVTRLX					
	630	640	650	660		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 417>:

g117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CCCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTCGCTGG CGCAGGAACA TTATCTGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GGCAGAAATG GTCGACGAAC TCGACCTGCT GCCCGATGCC GTCGCCGCCA
251 CCCTGCTTGC CGACATCGGA CGTACGTCC CCGATTGGAA CCTATTGGTT
301 TCCGAGCGCT GCAACAGCAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAGAAA CTTACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAAGCGCG ACAGCAAGCG GAAACCATGC GGAAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT ATTAATCAAA CTGGCGATGC GTACGCCGAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCTGAAAAA CGCGCCGTCG
551 CCAAAGAAAC CCTCGACATC TTCGCCCCGC TCGCCAACCG CTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAACC
651 CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAAC TTCTCGATA TCCTGCGTAC GGAACTCAAA
751 AAATACAATA TCCACTTTGA AGTCGCGCGC CGTCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTGTTTC
851 ACATCCGCGC CGTGGCGGAT CTGGTCGATA CCGTCCCCGA GTGTTACACC
901 ACGCTGGGCA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGagttCGA
951 cgactACATC GCCAACCCCA AAGgcaACGg ttATAAAAGt TTGCACACCG
1001 TCATCGTcgg cccGGAagaa aaaggtgtgg aagtgcAAAT CCGCACCTTC
1051 GATATGCacc AATTcAaCga ATTCCGGTGC GCCGCCCACT GGCgTTACAA
1101 AGAAGGCGGC AAAGGCGGAT CCGCTACGA ACAAAAAATC GCCTGGTTGC
1151 GCCAACTCTT GGAATGGCGC GAAATATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCGCGC CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCGCGAC GGCAAAGTCC TCTCTCTGCC AACGGGCGCA ACCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGCTG CCGGGGCGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCCGCTCG AAAACGGACA
1401 CGCGCTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAAA TCCGGCAAGG CCATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGTGTCCA
1551 ACTCGACAAG CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAAGCCT GCGGCACGCT
1701 GAACGAACCG CCGCCCGTGC CCGTCAGCGC AACCACCATC GTCAAAACAGT
1751 CCAAAATCAA AAAAGGTGGC AAAACCGGCG TGCTCATCGA CGCGGAAGAC
1801 GGCTTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTGCGCGC TTCGTTACCC GCGAGCGCGG CATTTCCGTC CACCGCAAAA
1901 CCTGCCCTCT TTTCCGACAC CTTGCCGAAC ACGCGCCCGA AAAAGTACTG
1951 GADGCAAGTT GGGCGGCGTT GCAGGAAGGG CAAGTGTTCC CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAAC CCAGTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCTCGCGG GCCTCGGCGA TGTCAAAGGC GTATTAGCGG
2201 TTACCCGGCT TTA

```

This corresponds to the amino acid sequence <SEQ ID 418; ORF 117-1.ng>:

g117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCAALP DNDKNLIGTA WSLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VDELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLDILRTELK
251 KYNIHFEVAG RPKHIYSYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNKYKS LHTVIVGPPE KGEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGRED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVRE IITAKEGHPS VNWLYEGWVK SGRKIGKIRA
501 YIRQQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSATTI VKQSKIKKGG KTGVLIDGED
601 GLMTTLAKCC KPAPPDDIAG FVTRERGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLAGLGDVKG VLSVTRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 419>:

m117-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA

```

```

51  ATTGCGCGAA TGGTTCGACA GCTACTGCGC CGCTCTGCCG GACAACGATA
101 AAAACCTCAT CGGTACCGCA TGGTTGCTGG CGCAGGAACA TTACCCCGCC
151 GATGCCGCCA CGCCGTATGG CGAGCCGCTG CCCGACCACT TCCTCGGCGC
201 GCGCGAAATG GTTCATGAAC TCGACCTGCT CCCCGATGCC GTCGCGGCCA
251 CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301 TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351 AGTGCAAGAA CTCACCCACT TCGCCCGGGT GGACAGCCTC GCCACGCCGG
401 AAGAACCGCG CCAGCAGGCA GAAACTATGC GGAAATGCT GCTGGCGATG
451 GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501 CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCGAAAAA CGCGCCGTCG
551 CCAAAGAAAC CCTCGACATC TTCGCCCGCG TCGCCAAACG TTTGGGCGTG
601 TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCGCC ATCAAAAGCC
651 CGAAAAATAC CGCGAAATCG CGCTGCTTTT GGACGAAAAA CGCACCGAAC
701 GCCTCGAATA CATCGAAAC TTCTCAACA TCCTGCGCGG TGAACCTAAG
751 AAATACAAAT TCCATTTTCA AGTCGCCGGC CGCCGAAAC ACATCTACTC
801 CATTTACAAA AAAATGGTGA AGAAAAAACT CAGCTTCGAC GGCCTCTTTG
851 ACATCCCGCG CGTGCGAATT CTGGTTGATA CCGTCCCGCA GTGTTACACC
901 ACGCTGGGTA TCGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCGA
951 CGACTACATC GCCAATCCCA AAGGCAACGG CTATAAAAGT TTGCACACCG
1001 TCATCGTCTG CCGCGAAGAC AAAGGCGTGG AAGTACAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTCCGGTGT CCGCGCCACT GGCCTTACAA
1101 AGAGGGCGCG AAGGGCGATT CCGCCTACGA ACAGAAAAAT GCCTGGTTGC
1151 GCCAACTCTT GGAATGGCGC GAAAACATGG CGGAAAGCGG CAAGGAAGAC
1201 CTCGCCCGCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAAGTCC TCTCCCTGCC CACGGGCGCG ACCCCCATCG
1301 ACTTCGCCTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCCGCTGTCC ACCCGGCTCG AAAACGGACA
1401 GCGCGTCGAA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CGCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCACGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGTC
1651 GGACAAGGCG AAATTTCCAA CCGCGCCATC CAAAAGCCTC GCGGCACGCT
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAACACGT
1751 CCAAATCAA AAAAGGCGGC AAAAACGGCG TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 TATTATCGGC TTCGTTACCC GCGAGCGCGG CATTTCAGTG CACCGCAAAA
1901 CCTGCCCGTC TTTCCAACAC CTCGCCGAAC ACGCGCCCGA AAAAGTGCTG
1951 GACGCAAGCT GGGCGGCATT GCAGGAAGGA CAAGTATTCT CCGTCGATAT
2001 CGAAATCCGC GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAAACTC AACGTTACCG CCGTGCAAAC CCAGTCCCGC
2101 GACTTGGAG CCAGCATGAG GTTCACGCTC GAAGTCAAAC AAGTCAACGA
2151 CCTCCGCGC GTCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTA

```

This corresponds to the amino acid sequence <SEQ ID 420; ORF 117-1>:

m117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFD SYCAALP DNDKNLIGTA WLLAQEHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVOK LTHFARVDSL ATPEERAQQA ETMRKMILLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WOLKWQLEDL GFRHQKPEKY REIALLLDEK RTERLEYIEN FLNILRGELK
251 KYNVHFEVAG RPKHIYSYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKGNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELF NDTIYVLTPH GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGORVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIRQONADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIIG FVTRERGISV HRKTCPSFQH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVNDLPR VLASLGDVKG VLSVTRL*

```

m117-1/g117-1 98.2% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
g117-1	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWSLAQEHYPADAATPYGEPL					
	10	20	30	40	50	60
	70	80	90	100	110	120



m117-1.pep PDHFLGAAQMVHEDLLPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDVQK  
|||||  
g117-1 PDHFLGAAQMVDELDPDAVAATLLADIGRYVPDWNLLVSERCNSTVAELVKGVDVQK  
70 80 90 100 110 120

m117-1.pep 130 140 150 160 170 180  
LTHFARVDSLATPEERAQQAETMRKMMLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK  
|||||  
g117-1 LTHFARVDSLATPEERAQQAETMRKMMLAMVTDIRVVLIKAMRTRTLQFLSNAPDSPEK  
130 140 150 160 170 180

m117-1.pep 190 200 210 220 230 240  
RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQQPEKYREIALLLDEKRTERLEYIEN  
|||||  
g117-1 RAVAKETLDIFAPLANRLGVWQLKWQLEDLGFHQQPEKYREIALLLDEKRTERLEYIEN  
190 200 210 220 230 240

m117-1.pep 250 260 270 280 290 300  
FLNILRGELKKYNVHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT  
|||:|||||  
g117-1 FLDILRTELKKYNIHFEVAGRPKHIYSIYKKMVKKLSFDGLFDIRAVRILVDTVPECYT  
250 260 270 280 290 300

m117-1.pep 310 320 330 340 350 360  
TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV  
|||||  
g117-1 TLGIVHSLWQPIPGFDDYIANPKNGYKSLHTVIVGPEEKGVEVQIRTFDMHQFNEFGV  
310 320 330 340 350 360

m117-1.pep 370 380 390 400 410 420  
AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH  
|||||  
g117-1 AAHWRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH  
370 380 390 400 410 420

m117-1.pep 430 440 450 460 470 480  
GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS  
|||||  
g117-1 GKVLSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS  
430 440 450 460 470 480

m117-1.pep 490 500 510 520 530 540  
VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQDKQLAKLTPKPNLQELAENLGY  
|||:|||||  
g117-1 VNWLYEGWVKSNAIGKIRAYIROQNADTVREEGRVQDKQLAKLTPKPNLQELAENLGY  
490 500 510 520 530 540

m117-1.pep 550 560 570 580 590 600  
KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKIKKGGKNGVLIDGED  
|||||  
g117-1 KKPEDLYTAVGQGEISNRAIQKACGTLNEPPVPVSATTIVKQSKIKKGGKGTGVLIDGED  
550 560 570 580 590 600

m117-1.pep 610 620 630 640 650 660  
GLMTTLAKCCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAWALQEG  
|||||  
g117-1 GLMTTLAKCCKPAPPDDIAGFVTRERGISVHRKTCPSFRHLAEHAPEKVLDAWALQEG  
610 620 630 640 650 660

m117-1.pep 670 680 690 700 710 720  
QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR  
|||||  
g117-1 QVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTAQTQSRDLEASMRFTLEVQVNDLPR  
670 680 690 700 710 720

m117-1.pep 730  
VLASLGDKGVLSVTRLX  
|||:|||||  
g117-1 VLAGLGDKGVLSVTRLX  
730

m117-1/RelA

sp|P55133|RELA\_VIBSS GTP PYROPHOSPHOKINASE (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) >gi|537617 (U13769) ppGpp synthetase I [Vibrio sp.] Length = 744  
Score = 536 bits (1366), Expect = e-151  
Identities = 288/685 (42%), Positives = 432/685 (63%), Gaps = 31/685 (4%)

Query: 74 LDLLPDAVAATILLADI---GRYVPDWNLLVSERCNSTVAELVKGVDDEVQKLTHFARVDSL 130  
L + D + A LL + G Y D + E + T+ LV+GV+++ ++ ++ S  
Sbjct: 68 LSMDADTLIAALLYPLVEGGCYSTD---ALKEEYSGTILHLVQGVQMCAS---QLKST 121

Query: 131 ATPEERAQQAETMRKMLLAMVTDIRVVLIKAMRTRLQFLSNAPDSPEKRAVAKETLDI 190  
A +A Q + +R+MLL+MV D R V+IKLA R L+ + + PD +RA A+E +I  
Sbjct: 122 AEETAQAQVDNIRRMLLSMVDDFRVCVVKLAERICNLREVKDQDEV-RRAAAQECANI 180

Query: 191 FAPLANRLGVWQLKWQLEDLGFRRHQKPEKYREIALLLDEKRTERLEYIENFLNIRGELK 250  
+APLANRLG+ QLKW++ED FR+Q P+ Y++IA L E+R +R +YI +F++ L +K  
Sbjct: 181 YAPLANRLGIGQLKWEIEDYAFRYQHPDTYKQIAKQLSERRIDREDYITHFVDDLS DAMK 240

Query: 251 KYNVHFEVAGRPKHIYSIYKMKVKKLSFDGLFDIRAVRILVDTVPECYTTLGIVHSLWQ 310  
N+ EV GRPKHIYSI++KM KK L FD LFD+RAVRI+ + + +CY LG+VH+ ++  
Sbjct: 241 ASNIRAEVQGRPKHIYSIWRKMQKKSLEFDELFDVRAVRIVAEELQDCYAALGVVHTKYR 300

Query: 311 PIPGEFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFVAAHWRYKEG- 369  
+P EFDDY+ANPK NGY+S+HTV++GPE K +E+QIRT MH+ +E GVAHW+YKEG  
Sbjct: 301 HLPKEFDDYVANPKPNGYQSIHTVVLGPEGKTIETIQTQKMHSEELGVAAHWRYKEGT 360

Query: 370 --GKGDSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPHGKVLSP 427  
G SAY++KI WLR+LL W+E M++SG ++ +++++F+D +Y TP G V+ LP  
Sbjct: 361 ASGGAQSAYDEKINWLRKLLAWQEEMSDSG--EMLDELRSQVDDRVAFTPKGDVVDLP 418

Query: 428 TGATPIDFAYALHSSIGDRRCGAKVEGQIVPLSTPLENGQRVEIITAKEGHPSVNWLYE- 486  
+ ATP+DFAY +HS +G RC GAKVEG+IVP + L+ G +VEIIT KE +PS +WL  
Sbjct: 419 SNATPLDFAYHIHSEVGHRCIGAKVEGRIVPFTYHLQMGDQVEIITQKEPNPSRDWLNPN 478

Query: 487 -GWVKSNAIGKIRAYIRQQNADTVREEGRVQLDKQLAKL--TPKPNLQELAENLGYKKP 543  
G+V S++A K+ A+ R+Q+ D G+ L+ +L K+ T K A+ K P  
Sbjct: 479 LGFVTSSRARAKVHAWFRKQDRDKNIIAGKEILEAEVKIATLKDAQYAAKRFNVKSP 538

Query: 544 EDLYTAVGQGEIS-NRAIQKACGTLEPPPPVSETTIVKQSKI-----KRGKNGV 594  
E+LY +G G++ N+ I +N+P + + K S+ KK ++ V  
Sbjct: 539 EELYAGIGSGDLRINQVINHINALVNKPTAEEDQQLLEKLSEASNKQATSHKKPQDAV 598

Query: 595 LIDGEDGLMTTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAW 654  
+++G D LMT LA+CC+P P DDI GFVT+ RGISVHR C + L HAPE+++D W  
Sbjct: 599 VVEGVNDLMTHLARCCQPIPGDDIQGFVTQGRGISVHRMDCEQLEELRHAPERIIDTVW 658

Query: 655 AALQEQGVFAVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQ--SRDLEASMRFTLEV 712  
G + + + + A +R+GLL++++ L K+ V +++++ + + M F LE+  
Sbjct: 659 GGGFVGN-YTITVRVTASERNGLLKELTNTLMNEKVKVAGMKSRVDYKKQMSINDFELEL 717

Query: 713 KQVNDLPRVLASLGDVKGVLVSVTRL 737  
+ L RVL + VK V RL  
Sbjct: 718 TDLEVLGRVLKRIEQVKDVAEAKRL 742

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 421>:

all17-1.seq

```

1  ATGACCGCCA TCAGCCCGAT TCAAGACACG CAAAGCGCGA CTCTGCAAGA
51  ATTGCGCGAA TGGTTCGACA GCTACTGCAC CGCGCTGCCG AACAAACGATA
101  AAAAATTGT CTTAGCCGCC CGTTCGCTGG CGGAAGCACA TTACCCCGCC
151  GATGCCGCCA CGCCGTATGG CGAACCGCTG CCCGACCACT TCCTCGGCGC
201  GGCGCAAATG GTTCATGAAC TCGACCTGCT CCCCAGTGCC GTCGCGCCA
251  CCCTGCTTGC CGACATCGGA CGCTACGTCC CCGACTGGAA CCTATTGGTT
301  TCCGAACGCT GCAACAGTAC CGTCGCCGAG CTGGTCAAAG GTGTGGACGA
351  AGTGCAGAAA CTCACCACT TCGCCCGGT GGACAGCCTC GCCACGCCGG
401  AAGAACGCGC CCAGCAGGCA GAACTATGC GGAAATGCT GCTGGCGATG
451  GTTACCGACA TCCGCGTCGT GTTAATCAAA CTGGCGATGC GTACGCGCAC
501  CCTGCAATTT TTAAGCAACG CCCCAGACAG CCCCAGAAAA CGCGCCGTCG
551  CCAAGAGAAC CCTCGACATC TTCGCCCGC TCGCCAACCG TTTGGCGGTG
601  TGGCAGCTCA AATGGCAGCT CGAAGATTG GGCTTCCGCC ATCAAGAACC
651  CGAAAAATAC CGCGAAATCG CCCTGCTTTT GGACGAAAAA CGCACCAGAAC
701  GCCTCGAATA CATCGAAAC TTCCTTAATA TCCTGCGTAC GGAACATAA
751  AAATACAATA TCCACTTTGA AGTCGCCGGC CGTCCGAAAC ACATCTACTC
801  CATTACAAA AAAATGGTGA AGAAAAAAT CAGCTTCGAC GGGTTGTTGC

```

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851 ACATCCGCGC CGTGCGGATT CTGGTTGATA CCGTCCCCGA GTGTTACACC
901 ACACTGGGCA TTGTCCACAG CCTCTGGCAG CCCATTCCCG GCGAGTTCCA
951 CGACTACATC GCCAACCCGA AAGGCAACGG CTATAAAGT TTGCACACCG
1001 TCATCGTCGG CCCGGAAGAC AAAGGCGTGG AAGTGCAAAT CCGCACCTTC
1051 GATATGCACC AATTCAACGA ATTGGGTGTC GCCGCGCACT GGCGTTACAA
1101 AGAGGGCGGC AAAGGCGATT CCGCCTACGA ACAAAAAATC GCCTGGTTAC
1151 GCCAACTTTT GGACTGGCGC GAAAACATGG CCGAAAGCGG CAAGGAAGAC
1201 CTCGCCCGCG CCTTCAAAAC CGAGCTTTTC AACGACACGA TTTATGTTTT
1251 GACCCCGCAC GGCAAGTCC TCTCCCTGCC CACAGGCGCG ACCCCCATCG
1301 ACTTCGCTTA CGCCCTGCAC AGCAGCATCG GCGACCGTTG CCGCGGTGCG
1351 AAAGTCGAAG GGCAGATTGT GCGCTGTCC ACCCGCTCG AAAACGGACA
1401 GCGTGTCCGA ATCATTACCG CCAAAGAAGG GCATCCTTCC GTCAACTGGC
1451 TTTACGAAGG CTGGGTCAA TCCAACAAGG CAATCGGCAA AATCCGCGCC
1501 TACATCCGCC AGCAAAACGC CGACACCGTG CCGAAGAAG GCCGCGTCCA
1551 ACTCGACAAA CAGCTTGCCA AACTCAGGCC CAAACCCAAC CTGCAAGAGC
1601 TTGCCGAAAA TCTCGGCTAC AAAAAGCCAG AAGACCTCTA CACCGCCGCT
1651 GGACAAGCGC AAATTTCCTA CCGCGCCATC CAAAAGCCT GCGGCGTCCA
1701 GAACGAACCG CCGCCCGTAC CCGTCAGCGA AACCACCATC GTCAAACAGT
1751 CCAAAATCAA AAAAGCGCGC AAAAACGCGC TGCTCATCGA CGCGGAAGAC
1801 GGTCTGATGA CCACGCTTGC CAAATGCTGC AAACCCGCGC CGCCCGACGA
1851 CATGTGCGGC TTCGTTACCC GCGATCGCGG CATTTGCGTA CACCGCAAAA
1901 CCTGCCCTTC TTCCGACAC CTCGCCGAC ACGCGCCGA AAAAGTACTG
1951 GACGCAAGTT GGGCGGCGTT GCAGGAAGGA CAAGTGTTCG CCGTCGATAT
2001 CGAAATCCCG GCCCAAGACC GCTCCGGGCT TTTGCGCGAC GTATCCGACG
2051 CGCTCGCCCG CCACAACTC AACGTTACCG CCGTGCAAA CCACTCCCGC
2101 GACTTGGAAG CCAGCATGAG GTTACGCTC GAAGTCAAC AAGTTACCGA
2151 CCTCCACGCG GTCTCGCCA GCCTCGGCGA CGTCAAAGGC GTATTGAGCG
2201 TTACCCGGCT TTA

```

This corresponds to the amino acid sequence <SEQ ID 422; ORF 117-1.a>:

#### a117-1.pep

```

1  MTAISPIQDT QSATLQELRE WFDSYCTALP NNDKKLVLA RSLAEAHYPA
51  DAATPYGEPL PDHFLGAAQM VHELDLLPDA VAATLLADIG RYVPDWNLLV
101 SERCNSTVAE LVKGVDEVQK LTHFARVDSL ATPEERAQQA ETMRKMLLAM
151 VTDIRVVLIK LAMRTRTLQF LSNAPDSPEK RAVAKETLDI FAPLANRLGV
201 WQLKWQLEDL GFRHQEPEKY REIALLLDEK RTERLEYIEN FLNLRTELK
251 KYNIHFEVAG RPKHIYSIYK KMKKKLSFD GLFDIRAVRI LVDTVPECYT
301 TLGIVHSLWQ PIPGEFDDYI ANPKNGYKS LHTVIVGPED KGVEVQIRTF
351 DMHQFNEFGV AAHWRYKEGG KGDSAYEQKI AWLRQLLDWR ENMAESGKED
401 LAAAFKTELE NDTIYVLTPL GKVLSLPTGA TPIDFAYALH SSIGDRCRGA
451 KVEGQIVPLS TPLENGQVE IITAKEGHPS VNWLYEGWVK SNKAIGKIRA
501 YIROQNADTV REEGRVQLDK QLAKLTPKPN LQELAENLGY KKPEDLYTAV
551 GQGEISNRAI QKACGTLNEP PPVPVSETTI VKQSKIKGG KNGVLIDGED
601 GLMTTLAKCC KPAPPDDIVG FVTRDRGISV HRKTCPSFRH LAEHAPEKVL
651 DASWAALQEG QVFAVDIEIR AQDRSGLLRD VSDALARHKL NVTAVQTQSR
701 DLEASMRFTL EVKQVTDLPR VLASLGDVKG VLSVTRL*

```

a117-1/m117-1 97.7% identity in 737 aa overlap

	10	20	30	40	50	60
m117-1.pep	MTAISPIQDTQSATLQELREWFD SYCAALPDNDKNLIGTAWLLAQEHYPADAATPYGEPL					
a117-1	MTAISPIQDTQSATLQELREWFD SYCTALPNNDKKLVLAARSLAEAHYPADAATPYGEPL					
	10	20	30	40	50	60
m117-1.pep	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
a117-1	PDHFLGAAQMVHELDLLPDAVAATLLADIGRYVPDWNLLV SERCNSTVAELVKGVDEVQK					
	70	80	90	100	110	120
m117-1.pep	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIK LAMRTRTLQFLSNAPDSPEK					
a117-1	LTHFARVDSLATPEERAQQAETMRKMLLAMVTDIRVVLIK LAMRTRTLQFLSNAPDSPEK					
	130	140	150	160	170	180
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDL GFRHQEPEKYREIALLLDEK RTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDL GFRHQEPEKYREIALLLDEK RTERLEYIEN					
	190	200	210	220	230	240
m117-1.pep	RAVAKETLDIFAPLANRLGVWQLKWQLEDL GFRHQEPEKYREIALLLDEK RTERLEYIEN					
a117-1	RAVAKETLDIFAPLANRLGVWQLKWQLEDL GFRHQEPEKYREIALLLDEK RTERLEYIEN					

m117-1.pep	250	260	270	280	290	300
	FLN	ILRGELKKYNVHFEVAGRPKHIYSIYKMKVKKLSFDGLFDIRAVRILVDTVPECYT				
a117-1	250	260	270	280	290	300
	FLN	ILRTELKKYNHFEVAGRPKHIYSIYKMKVKKLSFDGLFDIRAVRILVDTVPECYT				
m117-1.pep	310	320	330	340	350	360
	TLG	IVHSLWQPIPGEFFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV				
a117-1	310	320	330	340	350	360
	TLG	IVHSLWQPIPGEFFDDYIANPKGNGYKSLHTVIVGPEDKGVEVQIRTFDMHQFNEFGV				
m117-1.pep	370	380	390	400	410	420
	AAH	WRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH				
a117-1	370	380	390	400	410	420
	AAH	WRYKEGGKGSAYEQKIAWLRQLLDWRENMAESGKEDLAAAFKTELFNDTIYVLTTPH				
m117-1.pep	430	440	450	460	470	480
	GKV	LSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS				
a117-1	430	440	450	460	470	480
	GKV	LSLPTGATPIDFAYALHSSIGDRCRGAKVEGQIVPLSTPLENGQORVEIITAKEGHPS				
m117-1.pep	490	500	510	520	530	540
	VNW	LYEGWVKSNAIGKIRAYIRQONADTVREEGRVOLDKOLAKLTPKPNLQELAENLGY				
a117-1	490	500	510	520	530	540
	VNW	LYEGWVKSNAIGKIRAYIRQONADTVREEGRVOLDKOLAKLTPKPNLQELAENLGY				
m117-1.pep	550	560	570	580	590	600
	KKP	EDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KKGKNGVLIDGED				
a117-1	550	560	570	580	590	600
	KKP	EDLYTAVGQGEISNRAIQKACGTLNEPPVPVSETTIVKQSKI KKGKNGVLIDGED				
m117-1.pep	610	620	630	640	650	660
	GLM	TTLAKCKPAPPDDIIGFVTRERGISVHRKTCPSFQHLAEHAPEKVLDAASWAALQEG				
a117-1	610	620	630	640	650	660
	GLM	TTLAKCKPAPPDDIIGFVTRDRGISVHRKTCPSFRLAEHAPEKVLDAASWAALQEG				
m117-1.pep	670	680	690	700	710	720
	QVF	AVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR				
a117-1	670	680	690	700	710	720
	QVF	AVDIEIRAQDRSGLLRDVS DALARHKLNVTA VQTQSRDLEASMRFTLEVQVNDLPR				
m117-1.pep	730					
	VLAS	LGDVKGVL SVTRLX				
a117-1	730					
	VLAS	LGDVKGVL SVTRLX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 423>:

```

g118.seq
1  ATGTGCGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAGCTG GAGAATGATT TAATcgaGGT TAGGAGAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTT GAAATTAAG
251 CTTCCCTTG GTTGCCTGAT AGCGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAaCA AAAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 424; ORF 118.ng>:

```

g118.pep
1  MCEFKDFRRN IPCFEEYDEN SFIGKWYDDG VWDDEEYWKL ENDLIEVRRK
51  YPYPM DIPRD IVIGIGTIID FLMV PNWELF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVRED YYNKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 425>:

```
m118.seq
1  ATGTGTGAGT TCAAGGATAT TATAAGAAAC GTTCCTTATT TTGAGGGGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAATTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGACAT ACCAAGATAT GTTGTGATTG GAATCGGTAC
201 CATTATTGAT TTCTTAATGG TTCCAAATTG GAAACTTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 426; ORF 118>:

```
m118.pep
1  MCEFKDIIRN VPFEGYDEN SFIGKYYDDG VWDDEEYWLK ENDLIEVRKK
51  YPYPM DIPRY VVIGIGTIID FLMVPNWKLF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVREF YNNKK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 118 shows 92.8% identity over a 125 aa overlap with a predicted ORF (ORF 118.ng) from *N. gonorrhoeae*:

```
m118/g118

          10          20          30          40          50          60
m118.pep  MCEFKDIIRNVVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118       MCEFKDFRRNIPCFEEDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10          20          30          40          50          60

          70          80          90          100         110         120
m118.pep  VVIGIGTIIDFLMVPNWKLF EIKAS PWLPD SVGIHERYERFTT MLRYIFTEK DIVNVREF
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g118       IVIGIGTIIDFLMVPNWELFEIKAS PWLPD SVGIHERYERFTT MLRYIFTEK DIVNVREF
          70          80          90          100         110         120

m118.pep  YNNKKX
          |||||
g118       YNNKKX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 427>:

```
a118.seq
1  ATGTGTGAGT TCAAGGATTT TAGAAGAAAC ATCCCTTGTT TTGAAGAGTA
51  TGACGAAAAT TCATTATTG GCAAATGGTA TGATGACGGG GTGTGGGATG
101 ATGAAGAATA TTGGAAATTG GAGAATGATT TAATCGAGGT TAGAAAAAAA
151 TATCCTTATC CGATGGATAT ACCAAGGGAT ATTGTGATTG GAATCGGTAC
201 CATTATTGAT TTTTAAATGG TTCCAAATTG GGAGCTTTTT GAAATTAAAG
251 CTTCCCCTTG GTTGCCCTGAT AGTGTGGGAA TTCATGAACG TTATGAAAGA
301 TTCACAACGA TGCTCCGTTA TATTTTACC GAGAAAGACA TAGTCAACGT
351 GCGATTGAT TATTACAACA AAAAATAG
```

This corresponds to the amino acid sequence <SEQ ID 428; ORF 118.a>:

```
a118.pep
1  MCEFKDFRRN IPCFEEYDEN SFIGKYYDDG VWDDEEYWLK ENDLIEVRKK
51  YPYPM DIPRD IVIGIGTIID FLMVPNWELF EIKAS PWLPD SVGIHERYER
101 FTTMLRYIFT EKDIVNVREF YNNKK*
```

m118/a118 93.6% identity in 125 aa overlap

```
m118.pep  MCEFKDIIRNVVPYFEGYDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRY
          |||||: ||:| || |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a118       MCEFKDFRRNIPCFEEDENSFIGKYYDDGVWDDEEYWKLENDLIEVRKKYPYPM DIPRD
          10          20          30          40          50          60
```

341

	70	80	90	100	110	120
m118.pep	VVIGIGTIIDFLMVPNWKLFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD					
a118	IVIGIGTIIDFLMVPNWELFEIKASPWLPDSVGIHERYERFTTMLRYIFTEKDIVNVRFD					
	70	80	90	100	110	120
m118.pep	YYNKXX					
a118	YYNKXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 429>:

g120.seq

```

1   ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAAGGCTACC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAATCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTGCCTACT
251 ATAAAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CCTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGTCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGCC TGAATAAGGC GGTACGGGA AAATACAGCA Tagggggcgt
501 gGAAACCGAA GTCGTCAAAT ATCGGGTGC GCGCGCGAC GATACGGTAA
551 CGTATTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGAcgaCG GCAAACCTA TACGCTGAAG CTCAAATCGG TGCAGATCAA
651 CGGACAGGCC GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 430; ORF 120.ng>:

g120.pep

```

1   MMKTFKNIFS AAILSAAALPC AYAARLPQSA VLHYSYSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PAYYKDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DTVTYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 431>:

m120.seq

```

1   ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGmACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTGCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CTTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGC GCGCGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCG

```

This corresponds to the amino acid sequence <SEQ ID 432; ORF 120>:

m120.pep

```

1   MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLXYSYSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLTH PTYYRDIRRG KLYAEAKFAD
101 GSVTYGKAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 120 shows 97.3% identity over a 223 aa overlap with a predicted ORF (ORF 120.ng) from *N. gonorrhoeae*:

m120/g120

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAAALPC	AYAAGLPQSA	VLHYSGSYGI	PATMTFERSG	NAYKIVSTIK
g120	MMKTFKNIFS	AAILSAAALPC	AYAARLPQSA	VLHYSGSYGI	PATMTFERSG	NAYKIVSTIK
	70	80	90	100	110	120
m120.pep	VPLYNIRFES	GGTVVGNLH	PTYRDIRRG	KLYAEAKFAD	GSVTYKGAGE	SKTEQSPKAM
g120	VPLYNIRFES	GGTVVGNLH	PAYYKDIRR	GKLYAEAKFAD	GSVTYKGAGE	SKTEQSPKAM
	70	80	90	100	110	120
	130	140	150	160	170	180
m120.pep	DLFTLAWQLA	ANDAKLPPGL	KITNGKKLYS	VGGLNKAGTG	KYSIGGVETE	VVKYRVRRGD
g120	DLFTLAWQLA	ANDAKLPPGL	KITNGKKLYS	VGGLNKAGTG	KYSIGGVETE	VVKYRVRRGD
	130	140	150	160	170	180
	190	200	210	220		
m120.pep	DAVMYFFAPS	LNNIPAQIGY	TDDGKTYTL	KLKSVQINGQA	AKP	
g120	DTVYFFAPS	LNNIPAQIGY	TDDGKTYTL	KLKSVQINGQA	AKPX	
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 433>:

a120.seq

```

1  ATGATGAAGA CTTTAAAAA TATATTTTCC GCCGCCATT TGTCCGCCGC
51  CCTGCCGTGC GCGTATGCGG CAGGGCTGCC CCAATCCGCC GTGCTGCACT
101 ATTCCGGCAG CTACGGCATT CCCGCCACGA TGACATTGTA ACGCAGCGGC
151 AATGCTTACA AAATCGTTTC GACGATTAAA GTCCCGCTAT ACAATATCCG
201 TTTCGAGTCC GCGCGTACGG TTGTCGGCAA TACCCTGCAC CCTACCTACT
251 ATAGAGACAT ACGCAGGGGC AAATGTATG CGGAAGCCAA ATTCGCCGAC
301 GGCAGCGTAA CTACGGCAA AGCGGGCGAG AGCAAACCG AGCAAAGCCC
351 CAAGGCTATG GATTGTGTTCA CGCTTGCTG GCAGTTGGCG GCAAATGACG
401 CGAAACTCCC CCCGGGGCTG AAAATCACCA ACGGCAAAA ACTTTATTCC
451 GTCGGCGGTT TGAATAAGGC GGGTACAGGA AAATACAGCA TAGGCGGCGT
501 GGAAACCGAA GTCGTCAAAT ATCGGGTGCG GCGCGGCGAC GATGCGGTAA
551 TGTATTTCTT CGCACCGTCC CTGAACAATA TTCCGGCACA AATCGGCTAT
601 ACCGACGACG GCAAACCTA TACGCTGAAA CTCAAATCGG TGCAGATCAA
651 CGGCCAGGCA GCCAAACCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 434; ORF 120.a>:

a120.pep

```

1  MMKTFKNIFS AAILSAAALPC AYAAGLPQSA VLHYSGSYGI PATMTFERSG
51  NAYKIVSTIK VPLYNIRFES GGTVVGNLH PTYRDIRRG KLYAEAKFAD
101 GSVTYKGAGE SKTEQSPKAM DLFTLAWQLA ANDAKLPPGL KITNGKKLYS
151 VGGLNKAGTG KYSIGGVETE VVKYRVRRGD DAVMYFFAPS LNNIPAQIGY
201 TDDGKTYTLK LKSVQINGQA AKP*

```

m120/a120 99.6% identity in 223 aa overlap

	10	20	30	40	50	60
m120.pep	MMKTFKNIFS	AAILSAAALPC	AYAAGLPQSA	VLHYSGSYGI	PATMTFERSG	NAYKIVSTIK
a120	MMKTFKNIFS	AAILSAAALPC	AYAAGLPQSA	VLHYSGSYGI	PATMTFERSG	NAYKIVSTIK

343

	10	20	30	40	50	60
m120.pep	70	80	90	100	110	120
	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
a120	VPLYNIRFESGGTVVGNTLHPTYYRDIRRGKLYAEAKFADGSVTYKGAGESKTEQSPKAM					
	70	80	90	100	110	120
m120.pep	130	140	150	160	170	180
	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEVEVVKYRVRGD					
a120	DLFTLAWQLAANDAKLPPGLKITNGKKLYSVGGLNKAGTGKYSIGGVETEVEVVKYRVRGD					
	130	140	150	160	170	180
m120.pep	190	200	210	220		
	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
a120	DAVMYFFAPSLNNIPAQIGYTDDGKTYTLKLKSVQINGQAAKPX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 435>:

g121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATTATG TCGGGAACCA GTATGGACGG
51  GCGCGATGCC GTGCTGGTAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCTGACC GGTTGCGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCAC AGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCTCCGTGC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTtac AGCATACAGC TTGCCGATTT
351 GCGCTGCTG GCGGAACTGa cgcggatttT TACCGTCggc gacttcCGCA
401 GCCGCGACCT TGCTGCCGGC GgacaAGGTG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCGCGA TGACAGGGAA ACACGCGTGG TACTGAACAT
501 CGGCGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCGGGC AATATGCTGA TGGAcgcgtg gacgcaggca
601 cacTGGcagc TGCCTTACGA CAAAaaccgt gcAAAGgcgg cacAAGGCAA
651 catatTGCcg cAACTGCTCG gcaggctGCT CGCCcaccCG TATTCTCAC
701 AACCCcacc aaAAAGCACG GGgcGCGaac TgtttgcccT AAattggtc
751 gaaacctAcc ttgacggcgg cgaaaaccga tacgacgtat tgcggacgt
801 tccccgattc accgcgcaaA ccgTttggga cgccgtctca CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGCGG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCTCAATG GGTGGAGGCG gccgCATTtg
1001 cgtggttggc GCGGTGTTGG ATTAACCGCA TTCCCGGTAG TCCGCACAAA
1051 GCGACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 436; ORF 121.ng>:

g121.pep

```

1  METQLYIGIM SGTSMGDADA VLVRMDGGKW LGAEGHAFTP YPDRLRRKLL
51  DLQDTGTDEL HRSRMLSQEL SRLYAQTAAE LLCSQNLAPC DITALGCHGQ
101 TVRHAPENGY SIQLADLPLL AELTRIFTVG DFRSRDLAAG GQGAPLVPFAF
151 HEALFRDDRE TRVVLNIGGI ANISVLPPGA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLGRLLAHP YFSQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLRF TAQTVWDVAV HAAADARQMY ICGGGINRVF
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWLAACW INRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 437>:

m121.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGCGATGCC GTACTGATAC GGATGGACGG CGGCAAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCC TACCCCGGCA GGTTACGCG CCAATTGCTG

```



```

151 GATTTCAGG ACACAGGCGC AGACGAACTG CACCGCAGCA GGATTTTGTC
201 GCAAGAACTC AGCCGCCCTAT ATGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCCTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCCGAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
401 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
451 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
501 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
551 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
601 xxxxxxXcAGC TTCCTTACGA CAAAACGGT GCAAAGTCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACGCCACCC TAAAAGCAGC GGGCGCGAAC TGTTTGCCAT AAATTGGCTC
751 GAAACCTACC TTGACGGCGG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCCGCGCAA CCGTTGCGA CGCCGCTCA CACGCAGCGG
851 CAGATGCCCG TCAATGTAC ATTTGCGACG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCTGCGACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGnATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACGGCGC CATCCAAACC GTGTATTCTG AnCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 438; ORF 121>:

m121.pep

```

1 METQLYIGIM SGTSMGDGADA VLIRMDGGKW LGAEGHAFTF YPGRLLRRQLL
51 DLQDTGADEL HRSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL Axxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
151 xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx xxxxxxxxxxx
201 xxQLPYDKNG AKSAQGNILP QLLDRLLAHP YFAQRHPKST GRELFAINWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDAYS HAAADARQMY ICDGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 121 shows 73.5% identity over a 366 aa overlap with a predicted ORF (ORF121.ng) from *N. gonorrhoeae*:

m121/g121

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTFPYPGRLLRRQLLDLQDTGADEL					
g121	METQLYIGIMSGTSMGDGADAVLVRMDGGKWLGAEGHAFTFPYDRLRRKLLDLQDTGTDEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSONLAPSDITALGCHGQTVRHAPEHGYSIQLADLPLL					
g121	HRSRMLSQELSRLYAQTAAELLCSONLAPCDITALGCHGQTVRHAPEHGYSIQLADLPLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m121.pep	AXXX					
g121	AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
g121	PAFGFDTGPGNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST					
	190	200	210	220	230	240
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDAVSHAAADARQMYICDGGIRNPV					
g121	GRELFALNWLETYLDGGENRYDVLRTLSRFTAQTVWDAVSHAAADARQMYICGGGIRNPV					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
g121	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL					
	310	320	330	340	350	360
m121.pep	XAGYYYYX					
g121	GAGYYYYX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 439>:

```

a121.seq
1  ATGGAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGCACGC CTTTACCCCG TACCCCGGCA GGTACGCCG CAAATTGCTG
151 GATTTCAGG ACACAGGCGC GGACGAACTG CACCGCAGCA GGATGTTGTC
201 GCAAGAACTC AGCCGCCTGT ACGCGCAAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCGCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCAGAC ACGCGCGGGA ACACAGTTAC AGCGTACAGC TTGCCGATT
351 GCCGCTGCTG GCGGAACGGA CTCAGATTTT TACCGTCGGC GACTTCCGCA
401 GCCGCGACCT TGCGGCGGCG GGACAAGGCG CGCCGCTCGT CCCCGCCTTT
451 CACGAAGCCC TGTTCCGCGA CGACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGGGGATT GCCAACATCA GCGTACTCCC CCCCAGCGCA CCGGCCTTCG
551 GCTTCGACAC AGGACCGGGC AATATGCTGA TGGACGCGTG GATGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCCACCCG TATTTCCGAC
701 AACCCACCC TAAAGCACG GGGCGCGAAC TGTTTGCCCT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGATTC ACCGCGCAAA CCGTTTTCGA CGCCGTCTCA CACGCAGCGG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAA CTGAACCTCG ATCCGCAATG GGTAGAAGCC GCCGCGTTCG
1001 CATGGATGGC GCGGTGTTGG GTCAACGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGGCG CATCCAAACC GTGTATTCTG GCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 440; ORF 121.a>:

```

a121.pep
1  METQLYIGIM SGTSMGDADA VLIRMDGGKW LGAEGHAFTP YPGRLLRRKLL
51  DLQDTGADEL HRSRMLSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPESY SVQLADLPLL AERTQIFTVG DFRSRDLAAG GQGAPLVPF
151 HEALFRDDRE TRAVLNIGGI ANISVLPPDA PAFGFDTPG NMLMDAWMQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK
351 ATGASKPCIL GAGYYY*

```

m121/a121 74.0% identity in 366 aa overlap

	10	20	30	40	50	60
m121.pep	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
a121	METQLYIGIMSGTSMGDADAVLIRMDGGKWLGAEGHAFTPYPGRLLRRQLDLQDTGADEL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m121.pep	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
a121	HRSRILSQELSRLYAQTAAELLCSQNLAPSDITALGCHGQTVRHAPHEHGYISQLADLPLL					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m121.pep	XX					
a121	: : : : :					
	130	140	150	160	170	180
	AERTQIFTVGDFRSRDLAAGGQGAPLVPAFHEALFRDDRETRAVLNIGGIANISVLPDA					
	190	200	210	220	230	240
m121.pep	XXXXXXXXXXXXXXXXXXXXXXXXXQLPYDKNGAKSAQGNILPQLLDRLLAHPYFAQRHPKST					
a121	:      :     :     :     :					
	190	200	210	220	230	240
	PAFGFDTGPGNMLMDAWMQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST					
	250	260	270	280	290	300
m121.pep	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVCDVASHAAADARQMYICDGGIRNPV					
a121	:     :     :     :     :					
	250	260	270	280	290	300
	GRELFAINWLETYLDGGENRYDVLRTLSRFTAQTVFCDVASHAAADARQMYICGGGIRNPV					
	310	320	330	340	350	360
m121.pep	LMADLAECFGTRVSLHSTADLNLDPOWVEAAXFAWLAACWINRIPGSPHKATGASKPCIL					
a121	:     :     :     :     :					
	310	320	330	340	350	360
	LMADLAECFGTRVSLHSTAE LNLDPOWVEAAAFWMAACWVNRI PGSPHKATGASKPCIL					
m121.pep	XAGYYYY					
a121						
	GAGYYYY					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 441>:

m121-1.seq

```

1  ATGGAAACAC AGCTTTACAT CGGCATCATG TCGGGAACCA GCATGGACGG
51  GGCGGATGCC GTACTGATAC GGATGGACGG CGGCAATGG CTGGGCGCGG
101 AAGGGGACCG CTTTACCCCC TACCCCGGCA GGTACGCCG CCAATTGCTG
151 GATTTGCAGG ACACAGGCGC AGACGAATG CACCGCAGCA GGATTTGTG
201 GCAAGAACTC AGCCGCTTAT ATGCGCAAC CGCCGCCGAA CTGCTGTGCA
251 GTCAAAACCT CGCACCGTCC GACATTACCG CCCTCGGCTG CCACGGGCAA
301 ACCGTCGCAC ACGCGCCGGA ACACGGTTAC AGCATACAGC TTGCCGATTT
351 GCCGCTGCTG GCGGAACGGA CGCGGATTTT TACCGTCGGC GACTTCCGCA
401 GCCCGGACCT TCGGCGCGGC GGACAAGGCG CGCCACTCGT CCGCGCCTTT
451 CACGAAGCCC TGTTCGCGCA CAACAGGGAA ACACGCGCGG TACTGAACAT
501 CGCGCGGATT GCCAACATCA GCGTACTCCC CCGCGACGCA CCGCCTTCG
551 GCTTCGACAC AGGGCCCGGC AATATGCTGA TGGACGCGTG GACGCAGGCA
601 CACTGGCAGC TTCCTTACGA CAAAACGGT GCAAAGGCGG CACAAGGCAA
651 CATATTGCCG CAACTGCTCG ACAGGCTGCT CGCCACCCG TATTTCGCAC
701 AACCACACCC TAAAGACAGC GGGCGCGAAC TGTTTGCCTT AAATTGGCTC
751 GAAACCTACC TTGACGCGCG CGAAAACCGA TACGACGTAT TGCGGACGCT
801 TTCCCGTTTT ACCGCGCAAA CCGTTTGCGA CGCGCTCTCA CACGACGCG
851 CAGATGCCCG TCAAATGTAC ATTTGCGGCG GCGGCATCCG CAATCCTGTT
901 TTAATGGCGG ATTTGGCAGA ATGTTTCGGC ACACGCGTTT CCCTGCACAG
951 CACCGCCGAC CTGAACCTCG ATCCGCAATG GGTGGAAGCC GCCGNATTG
1001 CGTGGTTGGC GCGGTGTTGG ATTAATCGCA TTCCCGGTAG TCCGCACAAA
1051 GCAACCGCGC CATCCAAACC GTGTATTCTG ANCGCGGGAT ATTATTATTG
1101 A

```

This corresponds to the amino acid sequence <SEQ ID 442; ORF 121-1>:

m121-1.pep

```

1  METQLYIGIM SGTSMGADA VLIRMDGGKW LGAEGHAFTP YPGRLLRQLL
51  DLQDTGADEL HSRILSQEL SRLYAQTAAE LLCSONLAPS DITALGCHGQ
101 TVRHAPEHGY SIQLADLPLL AERTRITVVG DFRSRDLAAG GQGAPLVPAF
151 HEALFRDNRE TRAVLNIGGI ANISVLPDA PAFGFDTPG NMLMDAWTQA
201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL
251 ETYLDGGENR YDVLRTLSRF TAQTVCDVAVS HAAADARQMY ICGGGIRNPV
301 LMADLAECFG TRVSLHSTAD LNLDPQWVEA AXFAWLAACW INRIPGSPHK
351 ATGASKPCIL XAGYYY*

```

m121-1/g121 95.6% identity in 366 aa overlap

10 20 30 40 50 60

```

m121-1.pep  METQLYIGIMSGTSMGDGADAVLIRMDGGKWLGAEGHAFTPYPGRLRRQLLDLQDTGADEL
              |||||
g121         METQLYIGIMSGTSMGDGADAVLVRMDGGKWLGAEGHAFTPYPDRLRRKLLDLQDTGTDEL
              10      20      30      40      50      60

              70      80      90      100     110     120
m121-1.pep  HRSRILSQELSRLYAQTAELLCSQNLAPSDITALGCHGQTVRHAPHEHGYSIQLADLPLL
              |||||
g121         HRSRILSQELSRLYAQTAELLCSQNLAPCDITALGCHGQTVRHAPHEHGYSIQLADLPLL
              70      80      90      100     110     120

              130     140     150     160     170     180
m121-1.pep  AERTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDNRETRAVLNIGGIANISVLPPDA
              |||||
g121         AELTRIFTVGDFRSRDLAAGGQGAPLVPFHEALFRDDRETRVVLNIGGIANISVLPPGA
              130     140     150     160     170     180

              190     200     210     220     230     240
m121-1.pep  PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLDRLLAHPYFAQPHPKST
              |||||
g121         PAFGFDTPGPNMLMDAWTQAHWQLPYDKNGAKAAQGNILPQLLGRLLAHPYFSQPHPKST
              190     200     210     220     230     240

              250     260     270     280     290     300
m121-1.pep  GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVCDVASHAAADARQMYICGGGIRNPV
              |||||
g121         GRELFALNWLETYLDGGENRYDVLRTLRSRFTAQTVWDVASHAAADARQMYICGGGIRNPV
              250     260     270     280     290     300

              310     320     330     340     350     360
m121-1.pep  LMDLAECFGRVSLHSTADLNLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              |||||
g121         LMDLAECFGRVSLHSTAEINLDPOWVEAAAFWLAACWINRIPGSPHKATGASKPCIL
              310     320     330     340     350     360

m121-1.pep  XAGYYYY
              |||||
g121         GAGYYYY

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 443>:

```

a121-1.seq
1  ATGGAACAC  AGCTTTACAT  CGGCATCATG  TCGGGAACCA  GCATGGACGG
51  GGCGGATGCC  GTACTGATAC  GGATGGACGG  CGGCAATGG  CTGGGCGCGG
101  AAGGGCAGCG  CTTTACCCCG  TACCCCGGCA  GGTACGCCG  CAAATTGCTG
151  GATTTGCAGG  ACACAGGCGC  GGACGAACTG  CACCGCAGCA  GGATGTTGTC
201  GCAAGAACTC  AGCCGCCTGT  ACGCGCAAAC  CGCCGCCGAA  CTGCTGTGCA
251  GTCAAAACCT  CGCGCCGTCC  GACATTACCG  CCCTCGGCTG  CCACGGGCAA
301  ACCGTCAGAC  ACGCGCCGGA  ACACAGTTAC  AGCGTACAGC  TTGCCGATTT
351  GCCGCTGCTG  GCGGAACGGA  CTCAGATTTT  TACCGTCGGC  GACTTCCGCA
401  GCCGCGACCT  TCGCGCCGGC  GGACAAGGCG  CGCCGCTCGT  CCCCCTTTT
451  CACGAAGCCC  TGTTCGCGCA  CGACAGGGAA  ACACGCGCGG  TACTGAACAT
501  CGCGCGGATT  GCCAACATCA  GCGTACTCCC  CCCCAGCGCA  CCGCCTTCG
551  GCTTCGACAC  AGGACCGGGC  AATATGCTGA  TGGACGCGTG  GATGCAGGCA
601  CACTGGCAGC  TTCCTTACGA  CAAAAACGGT  GCAAAGGCGG  CACAAGGCAA
651  CATATTGCCG  CAACTGCTCG  ACAGGCTGCT  CGCCACCCG  TATTTGCGAC
701  AACCCACCCC  TAAAGCACG  GGGCGCGAAC  TGTTTGCCCT  AAATTGGCTC
751  GAAACCTACC  TTGACGGCGG  CGAAAACCGA  TACGACGTAT  TCGCGACGCT
801  TTCCCGATTG  ACCGCGCAA  CCGTTTTCGA  CGCCGCTCTC  CACGACGCGG
851  CAGATGCCCG  TCAATGTAC  ATTTGCGGCG  GCGGCATCCG  CAATCCTGTT
901  TTAATGGCGG  ATTTGCGAGA  ATGTTTCGGC  ACACGCGTTT  CCCTGCACAG
951  CACCGCCGAA  CTGAACCTCG  ATCCGCAATG  GGTAGAAGCC  GCCGCGTTCC
1001  CATGGATGGC  GCGGTGTTGG  GTCAACCGCA  TTCCCGGTAG  TCCGCACAAA
1051  GCAACCGCGG  CATCCAAACC  GTGTATTCTG  GCGCGGGGAT  ATTATTATTG
1101  A

```

This corresponds to the amino acid sequence <SEQ ID 444; ORF 121-1.a>:

```

a121-1.pep
1  METQLYIGIM  SGTSMDGADA  VLIRMDGGKW  LGAEGHAFTP  YPGRLRRKLL
51  DLQDTGADEL  HRSRILSQEL  SRLYAQTAEE  LLCSQNLAPS  DITALGCHGQ
101  TVRHAPESY  SVQLADLPLL  AERTQIFTVG  DFRSRDLAAG  GQGAPLVPF
151  HEALFRDRE  TRAVLNIGGI  ANISVLPPDA  PAFGFDTPG  NMLMDAWMQA

```

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201 HWQLPYDKNG AKAAQGNILP QLLDRLLAHP YFAQPHPKST GRELFALNWL  
 251 ETYLDGGENR YDVLRTLSRF TAQTVFDAVS HAAADARQMY ICGGGIRNPV  
 301 LMADLAECFG TRVSLHSTAE LNLDPQWVEA AAFAWMAACW VNRIPGSPHK  
 351 ATGASKPCIL GAGYYY\*

m121-1/a121-1 96.4% identity in 366 aa overlap

	10	20	30	40	50	60
m121-1.pep	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRL	RRQLLDLQDTGADEL		
a121-1	METQLYIGIMSGTSM	GADAVLIRMDGGKWL	GAEGHAFTPYPGRL	RRQLLDLQDTGADEL		
	10	20	30	40	50	60
m121-1.pep	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQT	VRHAPEHGYSIQ	LADLPLL	
a121-1	HRSRILSQELSR	LYAQTAELLCSQNL	APSDITALGCHGQT	VRHAPEHSYSV	QLADLPLL	
	70	80	90	100	110	120
m121-1.pep	AERTRIFTVGDF	RSRDLAAGGQGAP	LVPAFHEALFRD	NRRETRAVLNIG	GIANISVLP	PPDA
a121-1	AERTQIFTVGDF	RSRDLAAGGQGAP	LVPAFHEALFRD	NRRETRAVLNIG	GIANISVLP	PPDA
	130	140	150	160	170	180
m121-1.pep	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRLL	AHPYFAQPHPK	ST
a121-1	PAFGFDTGPGN	MLMDAWTQAHWQ	LPYDKNGAKAAQ	GNILPQLLDRLL	AHPYFAQPHPK	ST
	190	200	210	220	230	240
m121-1.pep	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVCDASHAAAD	ARQMYICGGG	IRNPV
a121-1	GRELFALNWLE	TYLDGGENRYD	VLRTLSRFTAQ	TVCDASHAAAD	ARQMYICGGG	IRNPV
	250	260	270	280	290	300
m121-1.pep	LMADLAECFG	TRVSLHSTAD	NLDLPQWVEA	AXFAWLAACW	INRIPGSPHK	ATGASKPCIL
a121	LMADLAECFG	TRVSLHSTAD	NLDLPQWVEA	AXFAWLAACW	INRIPGSPHK	ATGASKPCIL
	310	320	330	340	350	360
m121-1.pep	XAGYYYY					
a121	GAGYYYY					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 445>:

g122.seq

```

1  ATGGCTTTAC TGAGCATCCG CAAGCTGCAC AAACAATACG GCAGCGTAAC
51  CGCCATCCAA TCCTTAGACT TGGACTTGA AAAAGGCGAA GtcatCGTAC
101 TGCTGGGCC gTccggtgc ggCAAATCCA CCCTcctgcg ctgcgtcaac
151 GGTTTGGAGC CGCACCAagg cgGCAGCATC GTGATGGACG GTgtcgCGA
201 ATTCggcAAA GACGTTTCCT GGCAAACCGC CCGGCAAAaA gtcggtatgg
251 tctttcaaag taacgAactg Tttgccaca tgaccgtcat cgAaaacatc
301 ttcttAggcC CGGTAAagga aCAAAcCgc gaccgtgccg aagcaGAGG
351 gCAAGCCGGC AAactGttgg aacgcgTCGG actgctAGAC CGCAAAAACG
401 CCTATCCGCG CGAACTTTCC GGCGGTCAGA AACAGCGCAT CGCCATTGTC
451 CGCGCCCTGT GCCTGAATCC GGAAGTCATC CTGCTGGACG AAATCACC GC
501 CGCACTTGAC CCCGAAATGG TGC CGAAGT CTGGAAGT GTTTTGAAC
551 TCGCCCGCGA AGGATGAGT ATGCTCATCG TAACCCACGA AATGGGGTTC
601 GCACGCAAAG TTGCCGACCG CATCGTCTTT ATGGACAAAG GCGGCATCGT
651 CGAATCGTCC GACCCCGAAA CCTTTTTTTC CGCACAAA AGCGAACGCG
701 CCCGCCAATT TCTGCGAGT ATGGA TACT GA

```

This corresponds to the amino acid sequence &lt;SEQ ID 446; ORF 122.ng&gt;:

1	MALLSIRKLEH	KQYGSVTAIQ	SLDLDLEKGE	VIVLLGPSGC	GKSTLLRCVN
51	GLEPHQGGSI	VMDGVGEFGK	DVSQATARQK	VGMVFQSNEL	FAHMTVIENI
101	FLGPVKEQNR	DRAEAEAQAG	KLLERVGLLD	RKNAYPRELS	GGQKQRIAYV
151	RALCLNPEVI	LDEITAAAL	PEMVRVLELV	VLELAREGMS	MLIVTHEMGF
201	ARKVADRIVF	MOKGIVESS	DPETFFSAPK	SERARQFLAG	MDY*

m122.seq

1	GTGTGCATGA	TTAAATCCG	CAATATCCAT	AAGACCTTTG	GCGAAACAC
51	TATTTTGC	GGCATCGATT	TGGATGTGTG	CAAAGGGCAG	GTGGTCGTCA
101	TCCTCGGGcC	TTCCGGCTCA	GGCAAAACGA	CGTTTCTGCG	ATGCCTTAAAC
151	GCGTTGGAAA	TGCCCGAAGA	CGGACAACAATC	GAGTTTCGACA	ACGAGCGGACC
201	CGTGAAAATC	GATTTTCTA	AAAAACCAAG	CAACACGAT	ATTTTGGCAC
251	TGCGCCGCAA	GATcAkGcAT	GTGTTTCAAC	AATACAAyCT	CTTTCCGCAC
301	AAAACCGCCT	TGGAAAACGT	AATGGAAGGA	CCGGTTGCCG	TACAgGGCAA
351	GCTGCGCGCC	CAAGCGCGCG	AAGAGGCTCT	GAAACTGCTG	GAAAAAGTCG
401	GCTTGGGCGA	CAAGATGGAT	TTGTATCCCT	ACACAGTCTTC	CGGCGGTCAG
451	CAGCAGCGCG	TCGGCATATG	CCGCGCATTG	GCGATTTCAG	CTGAACATGAT
501	GCTGTTTGAC	GAACCGACTT	CCGCGCTCGA	TCCTGAATTG	GTGCAAGATG
551	TTTTGGATmC	CATGAAGGAA	TTGGCGCAAG	AAGGCTGGAC	CATGGTTGTG
601	GTTACGCATG	AAATCAAGTT	CGCCTTAGAA	GTGGCAACCA	CCGwCGTCGT
651	GATGGACrGC	GGCCTTATTG	TCGAACAAGG	CAGCCCGCAA	GATTTGTTCG
701	ACCAACCCAA	ACACGAACGG	ACGCGGAGAT	TTTTAAGCCA	AATCCAATCT
751	ACCAAGATT	GA			

m122.pep

1	VVMIKIRNIH	KTFGENTILR	GIDLDVCKGQ	VVVILGPSGS	GKTTFLRCLN
51	ALEMPEDGQI	EFDNERPLKI	DFSKKPSKHD	ILALRRKSXM	VFQQYNLFPH
101	KTALENVMEG	PVAVQGKPA	QAREEALKLL	EKVLGDKVD	LYPYQLSGGQ
151	QQRVGIARAL	AIQPELMFLD	EPTSALDPEL	VQDVLDXMKE	LAQEGWTMNV
201	VTHEIKFALE	VATTXVMDX	GVIVEQGSQP	DLDFHPKHER	TRRFLSQQS
251	TKI*				

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 122 shows 47.2% identity over a 246 aa overlap with a predicted ORF (ORF 122.ng) from *N. gonorrhoeae*:

m122/q122

[illegible]

350

	180	190	200	210	220	230
		250				
m122.pep	TRRFLSQIQSTKIX					
	: : :					
g122	ARQFLAGMDYX					
	240					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 449>:

```

a122.seq
1   GTTGTTCATGA TTAAATCCG CAATATCCAT AAGACCTTCG GCAAAAATAC
51  CATTTCGCGC GGCATCAATT TGGATGTGTG CAAAGGGCAG GTGGTCGTCA
101 TCCTCGGGCC TTCCGGCTCA GGCAAAACGA CGTTTCTGCG ATGCCTAAAC
151 GCGTTGGAAA TGCCCGAAGA CGGACAAATC GAGTTCGACA ACGAGCGACC
201 GCTGAAAATC GATTTTCTA AAAACCAAG CAAACACGAT ATTTTGGCAC
251 TGCGCCGCAA ATCAGGCATG GTGTTTCAAC AATACACCT CTTCCGCAC
301 AAAACCGCCT TGGAAAACGT GATGGAAGGA CCGGTTGCCG TACAGGGCAA
351 GCCTGCCGCC CAAGCGCGCG AAGAGGCTCT GAAACTGCTG GAAAAAGTCG
401 GCTTGGGCGA CAAAGTGGAT TTGTATCCCT ACCAGCTTTC CGGCGGTCAG
451 CAGCAGCGCG TCGGCATTGC CCGAGCATTG GCGATTGAGC CCGAGCTGAT
501 GTTGTTCGAC GAACCCACTT CCGCGCTTGA CCCCAGTTG GTGCAAGACG
551 TGTGTAACGC CATGAAGGAA TTGGCGCGGG AAGGTTGGAC GATGGTCGTC
601 GTTACCCACG AAATCAAGTT CGCGCTGGAA GTTGCCACGA CCGTTGTCGT
651 GATGGACGGC GCGGTTATCG TAGAGCAGGG CAGCCCGAAA GAGTTGTTCC
701 ACCACCCCAA ACACGAACGG ACGCGGAGAT TTTTAAGCCA AATCCAATCT
751 ACCAAGATT GA

```

This corresponds to the amino acid sequence <SEQ ID 450; ORF 122.a>:

```

a122.pep
1   VVMIKIRNIH KTFGKNTILR GINLDVCKGQ VVVLGPGSGS GKTTFILRLN
51  ALEMPEDGQI EFDNERPLKI DFSKKPSKHD ILALRRKSGM VFQQYNLFPH
101 KTALENVMEG PVAVQGKPAA QAREEALKLL EKVLGDKVD LYPYQLSGGQ
151 QORVGIARAL AIQPELMLFD EPTSALDPEL VQDVNLAMKE LAREGWTMVV
201 VTHEIKFALE VATTVVVMDG GVIVEQGSFK ELFDHPKHER TRRFLSQIQS
251 TKI*

```

m122/a122 96.0% identity in 253 aa overlap

	10	20	30	40	50	60
m122.pep	VVMIKIRNIHKT	FGENTILRG	IDLDVCKGQ	VVVLGPGSG	GKTTFILRLN	ALEMPEDGQI
a122	VVMIKIRNIHKT	FGKNTILRG	INLDVCKGQ	VVVLGPGSG	GKTTFILRLN	ALEMPEDGQI
	10	20	30	40	50	60
m122.pep	EFDNERPLKID	FSKKPSKHD	ILALRRKSM	VFQQYNLFPH	KTALENVMEG	PVAVQGKPAA
a122	EFDNERPLKID	FSKKPSKHD	ILALRRKSG	MVFQQYNLF	PHKTALENV	MEGPVAVQGKPAA
	70	80	90	100	110	120
m122.pep	QAREEALKLLE	KVLGDKVD	LYPYQLSGG	QQORVGIAR	ALAIQPELM	LFDEPTSALDPEL
a122	QAREEALKLLE	KVLGDKVD	LYPYQLSGG	QQORVGIAR	ALAIQPELM	LFDEPTSALDPEL
	130	140	150	160	170	180
m122.pep	VQDVLDMKELA	QEGWTMVV	VTHEIKFALE	VATTXVVM	DXGVIVEQGS	PQDLFDHPKHER
a122	VQDVNLAMKE	LAREGWTMV	VVTHEIKFALE	VATTVVVMD	GGVIVEQGS	FKELFDHPKHER
	190	200	210	220	230	240
m122.pep	TRRFLSQIQST	KIX				
a122	TRRFLSQIQST	KIX				

a122                    |||||  
                          TRRFLSQIQSTKIX  
                          250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 451>:

g122-1.seq  
 1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACCATTTT  
 51 GCGCGGCATC GATTGGGATG TGGGCAAAGG GCAGGTGGTC GTCATCCTCG  
 101 GGCCTTCCGG CTCGGGTAAA ACAACATTTC TGCGCTGCCT AAACGCGTTG  
 151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGCGC GGCCGTTACG  
 201 CATTGATTTT TCCAAAAAAA CAAGCAAACA CGATATTTTG GCACTGCGCC  
 251 GCAAGTCCGG AATGGTATTC CAACAATACA ACCTCTTCCC GCATAAAACC  
 301 GTGTTGGAAC ACGTGATGGA AGGGCCGGTT GCCGTACAGG GCAAGCCTGC  
 351 CGCCCAAGCG CGCGAAGAGG CTTTGAAACT GCTGGAAAAA GTCGGCTTGG  
 401 GCGATAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG  
 451 CGTGTGCGTA TCGCCCGCGC ACTGGCGATT CAGCCTGAAT TGATGCTGTT  
 501 TGACGAACCC ACTTCCGCGC TGGACCCCGA GTTGGTGCAA GACGTGTTGG  
 551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC  
 601 CACGAAATCA AGTTCACGCT GGAAGTTGCC ACGAAGCTCG TCGTGATGGA  
 651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC  
 701 TCAAACACGA ACGGACGCGG AGATTTTAA GCCAATCCA ATCTGCCAAG  
 751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 452; ORF 122-1.ng>:

g122-1.pep  
 1 MIKIRNIHKT FGENTILRGI DLDVKGQV VILGPSGSGK TTFRLCLNAL  
 51 EMPEDGQIEF DNARPLRIDF SKKTSKHDIL ALRRKSGMVF QQYNLFPHKT  
 101 VLENVMEGPV AVQGKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ  
 151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDMKELA REGWTMVVVT  
 201 HEIKFTLEVA TNVVMDGGV IVEQSPKEL FDHLKHERTR RFLSQIQSAK  
 251 I\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 453>:

m122-1.seq  
 1 ATGATTAAAA TCCGCAATAT CCATAAGACC TTTGGCGAAA ACACATATTT  
 51 GCGCGGCATC GATTGGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG  
 101 GGCCTTCCGG CTCAGGCAAA ACGACGTTTC TGCGATGCCT AAACGCGTTG  
 151 GAAATGCCCG AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA  
 201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC  
 251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTCCC GCACAAAACC  
 301 GCCTTGGAAA ACGTAATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC  
 351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG  
 401 GCGACAAAGT GGATTTGTAT CCCTACCAGC TTTCCGCGCG TCAGCAGCAG  
 451 CGCGTCCGCA TTGCCGCGC ATTGGCGATT CAGCCTGAAC TGATGCTGTT  
 501 TGACGAACCG ACTTCCGCGC TCGATCCTGA ATTGGTGCAA GATGTTTGG  
 551 ATACCATGAA GGAATTGGCG CAAGAAGGCT GGACCATGGT TGTGCTTACG  
 601 CATGAAATCA AGTTCGCCTT AGAAGTGGCA ACCACCGTCG TCGTGATGGA  
 651 CGGCGGCGTT ATTGTGCAAC AAGGCAGCCC GCAAGATTG TTCGACCACC  
 701 CCAACACGA ACGGACGCGG AGATTTTAA GCCAATCCA ATCTACCAAG  
 751 ATTTGA

This corresponds to the amino acid sequence <SEQ ID 454; ORF 122-1>:

m122-1.pep  
 1 MIKIRNIHKT FGENTILRGI DLDVCKGQV VILGPSGSGK TTFRLCLNAL  
 51 EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT  
 101 ALENVMEGPV AVQGKPAQA REEALKLEK VGLGDKVDLY PYQLSGGQQQ  
 151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLDTMKELA QEGWTMVVVT  
 201 HEIKFALEVA TTVVMDGGV IVEQSPQDL FDHPKHERTR RFLSQIQSTK  
 251 I\*

m122-1/g122-1 94.8% identity in 251 aa overlap

	10	20	30	40	50	60
m122-1.pep	MIKIRNIHKTFGENTILRGIDLDVCKGQVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
g122-1	MIKIRNIHKTFGENTILRGIDLDVKGQV VILGPSGSGKTTFLRCLNALEMPEDGQIEF					



	10	20	30	40	50	60
m122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAAQA					
g122-1	70	80	90	100	110	120
	DNARPLRIDFSKKTSHDILALRRKSGMVFQQYNLFPHKTVLENVMEGPFVAVQGKPAAQA					
m122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSDPELVQ					
g122-1	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSDPELVQ					
m122-1.pep	190	200	210	220	230	240
	DVLDTMKELAQEGWMTMVVTHEIKFALEVATTVVMDGGVIVEQGSQDLFDHPKHHERTR					
g122-1	190	200	210	220	230	240
	DVLDAMKELAREGWMTMVVTHEIKFTLEVATNVVMDGGVIVEQGSQDLFDHLKHHERTR					
m122-1.pep	250					
	RFLSQIQSTKIX					
g122-1	250					
	RFLSQIQSAKIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 455>:

a122-1.seq

```

1  ATGATTAAAA TCCGCAATAT CCATAAGACC TTCGGCAAAA ATACCATTTT
51  GCCCGGCATC AATTGGGATG TGTGCAAAGG GCAGGTGGTC GTCATCCTCG
101 GGCCTTCCGG CTCAGGCCAA ACGACGTTTC TGCGATGCCT AAACGCGTTG
151 GAAATGCCCC AAGACGGACA AATCGAGTTC GACAACGAGC GACCGCTGAA
201 AATCGATTTT TCTAAAAAAC CAAGCAAACA CGATATTTTG GCACTGCGCC
251 GCAATCAGG CATGGTGTTC CAACAATACA ACCTCTTTCC GCACAAAACC
301 GCCTTGGAAA ACGTGATGGA AGGACCGGTT GCCGTACAGG GCAAGCCTGC
351 CGCCCAAGCG CGCGAAGAGG CTCTGAAACT GCTGGAAAAA GTCGGCTTGG
401 GCGACAAAGT GGATTGTAT CCCTACCAGC TTTCCGGCGG TCAGCAGCAG
451 CGCGTCGGCA TTGCCCGAGC ATTGGCGATT CAGCCCGAGC TGATGTTGTT
501 TGACGAACCC ACTTCCGCGC TTGACCCCGA GTTGGTGCAA GACGTGTTGA
551 ACGCCATGAA GGAATTGGCG CGGGAAGGTT GGACGATGGT CGTCGTTACC
601 CACGAAATCA AGTTCGCGCT GGAAAGTTGCC ACGACCGTTG TCGTGATGGA
651 CGGCGGCGTT ATCGTAGAGC AGGGCAGCCC GAAAGAGTTG TTCGACCACC
701 CCAAACACGA ACGGACGCGG AGATTTTAA GCCAAATCCA ATCTACCAAG
751 ATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 456; ORF 122-1.a>:

a122-1.pep

```

1  MIKIRNIHKT FGKNTILRGI NLDVCKGQVV VILGPSGSGK TFLRCLNAL
51  EMPEDGQIEF DNERPLKIDF SKKPSKHDIL ALRRKSGMVF QQYNLFPHKT
101 ALENVMEGPV AVQGKPAAQA REEALKLEK VLGDKVDLY PYQLSGGQQQ
151 RVGIARALAI QPELMLFDEP TSALDPELVQ DVLNAMKELA REGWMTMVVT
201 HEIKFALEVA TTVVMDGGV IVEQGSPEL FDHPKHHERTR RFLSQIQSTK
251 I*

```

a122-1/m122-1 97.2% identity in 251 aa overlap

	10	20	30	40	50	60
a122-1.pep	MIKIRNIHKTFGKNTILRGINLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
m122-1	MIKIRNIHKTFGKNTILRGIDLDVCKGQVVVILGPSGSGKTTFLRCLNALEMPEDGQIEF					
	10	20	30	40	50	60
a122-1.pep	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAAQA					
m122-1	70	80	90	100	110	120
	DNERPLKIDFSKKPSKHDILALRRKSGMVFQQYNLFPHKTALENVMEGPFVAVQGKPAAQA					
a122-1.pep	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSDPELVQ					
m122-1	130	140	150	160	170	180
	REEALKLLEKVLGDKVDLYPYQLSGGQQQRVGIARALAIQPELMLFDEPTSDPELVQ					

q125.seq

1	ATGTCGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCGCCGCCA	TCCGGCTGGT
51	TTGGTTCCGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TCGCCCCCTT	GGGCTGGCAG	CGCGGTCTGG	CGGCCCTGCT	TTTGGGTCAT
151	GCCGTCGGCG	GCGCGCTGTT	TTTTGCGGCG	GCGTATATCG	GCGCACTGAC
201	CGGACGCGAG	TCGATGGAAA	GTGTGCGCCT	GTGTTCCGGC	AAATGCGGTT
251	CAGTGCTGTT	TTCCGTGGCG	AATATGCTGC	AACTTCCCGG	CTGGACGGCG
301	GTGATGATT	ACGTCGGCGC	AacggtCAGC	TCGCTTTTGG	GCAAAAGTGT
351	GTGGGACggc	gaATCCTTTG	TCTGGTGGGC	ATTGGCAAAC	GGCGCACTGA
401	TCGTGCTGTG	GCTGGTTTTC	GGCGCACGCA	GAACGGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GCTTGCCGTG	TTGTGGTTGA	GCGTCGAAGT
501	GTTGCTTTCG	TCCGGCACAA	ACGCCGCGCC	CGCCGTTTCA	GACGGCATGA
551	CCTTCGGAAC	GGCAGTCGAA	CTGTCCGCGC	TCATGCCCGT	TTCTTGGCTC
601	CCGCTGGCCG	CCGACTACAA	GCGCCAAGCA	CGCCGCGCGT	TTGCGGCAAC
651	CCTGACGCGC	ACGCTCGCCT	ATACGCTGAC	GCGCTCTGCG	ATGATATGCT
701	TGGGTTTGGC	GGCGGCTCTG	TTTACCGGAG	AAACCGACGT	GGCGAAAAATC
751	CTGTTGGGCG	CGGGCTTGGG	CATAACGGGC	ATTCTGGCAG	TCGTCTCTCTC
801	CACCGTTACC	ACAACGTTTC	TCGATACCTA	TTCCGCCCGC	GCGAGTGCAG
851	ACAACATTTC	CGCGCGTTTT	GCGGAAATAC	CCGTGCTGT	CGGCGTTACC
901	CTGATccgca	ccgtgcttgc	cgtcatgctg	cccgttaccg	aatataaaaa
951	cttcctgctg	cttatccgct	cggatattgg	gccgatggcg	gggtggtttt
1001	attgccaact	TTTTtttctt	AAAACGGCGT	GA	

This corresponds to the amino acid sequence <SEQ ID 458: ORF 125.ng>:

m125.seq

1	ATGTCGGGGCA	ATGCCTCCTC	TCCTTCATCT	TCCTCCGCCA	TCGGGCTGAT
51	TTGGTTCGGC	GCGGCGGTAT	CGATTGCCGA	AATCAGCACG	GGTACGCTGC
101	TTGCGCCTTT	GGGCTGGCAG	CGCGGTCTGG	CGGCTCTACT	TTTGGGTCA
151	GCCGTCGGCG	GCGCGCTGTT	TTTTGCGGCG	GCGTATATCG	GCGCACTGAC
201	CGGACGCGAG	TCGATGGA	GCGTGCGCCT	GTCGTTCCGC	AAACGCGGTT
251	CAGTGCTGTT	TTCGCTGGCG	AAATAGTCTG	AACTGGCCGG	CTGGACGGCG
301	GTGATGATT	ACGCGCGCGC	AACGGTCAGC	TCGCGTTTGG	GCAAAGTGTT
351	GTGGGACGGC	GAATCTTTTG	TCTGTTGGGC	ATTGCAAAAC	GGCGCGCTGA
401	TTGTGCTGTG	GCTGGTTTTT	GGCGCACGCA	AAACAGGCGG	GCTGAAAACC
451	GTTTCGATGC	TGCTGATGCT	GTTGGCGGTT	CTGTGGCTGA	GTGCCGAAGT
501	CTTTCCACG	GCAGGCAGCA	CCGCGCACCA	GGTTTCAGAC	GGCATGAGTT
551	TCGGAACGGC	AGTCGAGCTG	TCCGCCGTGA	TGCCGCTTTC	CTGGCTGCCG
601	CTTGCCGCCG	ACTACACGGC	CCACGCGCGC	CGCCCGTTTG	CGGCAACCTT
651	GACGGCAACG	CTCGCCTACG	CGCTGACCGG	CTGCTGGATG	TATGCCTTGG
701	GTTTGGCAGC	GGCGTTTGTC	ACCGGACAAA	CCGACGTGGC	AAAAATCCAC
751	CTGGGCGCAr	GTTTGgGTGC	GGCAGGCATT	TTGGCGGTGC	TCCTCTCTTC
801	CGTTACCACA	ACGTTTCTCG	ATGCCTATT	CGCCGCGCGC	AGTGCGAACC

354

851 ACATTTCCGC GCGTTTTCG GAAACACCG TCGCTGTCrG CGTTACCCCTG  
 901 ATCGGCACGG TACTTGCCGT CATGCTGCCG GTTACCGAAT ATGAAAACCTT  
 951 CCTGCTGCTT ATCGGCTCGG TATTTGCGCC GATGGCGGgC GGTTTTGATT  
 1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

This corresponds to the amino acid sequence <SEQ ID 460; ORF 125>:

m125.pep  
 1 MSGNASSPSS SSAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH  
 51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSA NMLQLAGWTA  
 101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT  
 151 VSMLLMLLAV LWLSAEVFST AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP  
 201 LAADYTRHAR RPFATLTAT LAYTLTGCM YALGLAAALF TGETDVAKIL  
 251 LGAXLGAAGI LAVVLSTVTT TFLDAYSAGA SANNISARFA ETPVAVXVTL  
 301 IGTVLAVMLP VTEYENFLLL IGSVFAPMAG GFDCRLFRLE TA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 125 shows 92.1% identity over a 343 aa overlap with a predicted ORF (ORF 125.ng) from *N. gonorrhoeae*:

m125/g125

	10	20	30	40	50	60
m125.pep	MSGNASSPSSSSAIGLIWFGAAVSVIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA					
g125	MSGNASSPSSSSAIGLVWFGAAVSVIAEISTGTLLAPLGWQRLAALLLGHAVGGALFFAA					
	10	20	30	40	50	60
m125.pep	70	80	90	100	110	120
	AYIGALTGRSSMESVRLSFGKRGSVLFVANMLQLAGWTAVMIYAGATVSSALGKVLWDG					
g125	AYIGALTGRSSMESVRLSFGKCGSVLFVANMLQLAGWTAVMIYVAGATVSSALGKVLWDG					
	70	80	90	100	110	120
m125.pep	130	140	150	160	170	179
	ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLLMLLAVLWLSAEVFSTAGSTAAQ-VS					
g125	ESFVWWALANGALIVLWLVFGARRTGGLKTVSMLLMLLAVLWLSVEVFASSGTNAAPAVS					
	130	140	150	160	170	180
m125.pep	180	190	200	210	220	239
	DGMSFGTAVELSAVMPLSWPLAADYTRHARRPFAATLTATLAYTLTGCMYALGLAAL					
g125	DGMTFGTAVELSAVMPLSWPLAADYTRQARRPFAATLTATLAYTLTGCMYALGLAAL					
	190	200	210	220	230	240
m125.pep	240	250	260	270	280	299
	FTGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVT					
g125	FTGETDVAKILLGAGLGITGILAVVLSTVTTTFLDTYSAGASANNISARFAEIPVAVGVT					
	250	260	270	280	290	300
m125.pep	300	310	320	330	340	
	LIGTVLAVMLPVTEYENFLLIGSVFAPMAGGFDCRLFRLETAX					
g125	LIRTVLAVMLPVTEYKNFLLIRSVFPGPMAGGFDCRLFCLKTAX					
	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 461>:

a125.seq  
 1 ATGTCGGGCA ATGCCTCCTC TCCTTCATCT TCCGCCGCCA TCGGGCTGAT  
 51 TTGGTTCGGC GCGGCGGTAT CGATTGCCGA AATCAGCACG GGTACACTGC  
 101 TTGCGCCTTT GGGCTGGCAG CGCGGTCTGG CGGCTCTGCT TTTGGGTCAT

355

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151 GCCGTCGGCG GCGCGCTGTT TTTTGGCGCG GCGTATATCG GCGCACTGAC
201 CGGACGCAGC TCGATGGAAA GCGTGCGCCT GTCGTTCCGC AAACGCGGTT
251 CAGTGCTGTT TTCCGTGGCG AATATGCTGC AACTGGCCGG CTGGACGGCG
301 GTGATGATTT ACGCCGGCGC AACGGTCAGC TCCGCTTTGG GCAAAGTGTT
351 GTGGGACGGC GAATCTTTTG TCTGGTGGGC ATTGGCAAAC GCGCGCGTGA
401 TTGTGCTGTG GCTGGTTTTT GCGGCACGCA AAACAGGCGG GCTGAAAACC
451 GTTTCGATGC TGCTGATGCT GTTGGCGGTT CTGTGGCTGA GTGCCGAAGT
501 CTTTTCCACG GCAGGCAGCA CCGCCGCACA GGTTCAGAC GGCATGAGTT
551 TCGGAACGGC AGTCGAGCTG TCCGCCGTGA TGCCGCTTTC TTGGCTGCCG
601 CTGGCCGCCG ACTACACGCG CCACGCGCGC CGCCCGTTTG CGGCAACCCT
651 GACGGCAACG CTCGCCTACA CGCTGACCGG CTGCTGGATG TATGCCTTGG
701 GTTTGGCAGC GCGCTTGTTC ACCGGAGAAA CCGACGTGGC AAAATCCTG
751 CTGGGCGCAG GTTTGGGTGC GGCAGGCATT TTGGCGGTCG TCCTGTGCGC
801 CGTTACCAAC ACTTTTCTCG ATGCCTACTC CGCCGGCGTA AGTGCCAAACA
851 ATATTTCCGC CAAACTTTTC GAAATACCCA TCGCCGTTGC CGTCGCCGTT
901 GTCGGCACAC TGCTTGCCGT CCTCCTGCCC GTTACCGAAT ATGAAACTT
951 CCTGCTGCTT ATCGGCTCGG TATTGCGCC GATGGCG.GC GGTTTTGATT
1001 GCCGACTTTT TCGTCTTGAA ACGGCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 462; ORF 125.a>:

```

a125.pep
1 MSGNASSPSS SAAIGLIWFG AAVSIAEIST GTLLAPLGWQ RGLAALLLGH
51 AVGGALFFAA AYIGALTGRS SMESVRLSFG KRGSVLFSA NMLQLAGWTA
101 VMIYAGATVS SALGKVLWDG ESFVWWALAN GALIVLWLVF GARKTGGLKT
151 VSMMLMLLAV LWLSAEVFT AGSTAAQVSD GMSFGTAVEL SAVMPLSWLP
201 LAADYTRHAR RFAATLTAT LAYTLTGCWM YALGLAAALF TGETDVAKIL
251 LGAGLGAAGI LAVVLSTVTT TFLDAYSAGV SANNISAKLS EIPIAVAVAV
301 VGTLLAVLLP VTEYENFLLL IGSVFAPMAX GFDCRLFRLE TA*

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m125/a125 95.6% identity in 342 aa overlap

```

m125.pep      10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSVIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA
|||||:|||||
a125          10      20      30      40      50      60
MSGNASSPSSSSAIGLIWFGAAVSVIAEISTGTLLAPLGWQ RGLAALLLGHAVGGALFFAA

m125.pep      70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLF SVANMLQLAGWTAVMIYAGATVSSALGKVLWDG
|||||:|||||
a125          70      80      90      100     110     120
AYIGALTGRSSMESVRLSFGKRGSVLF SVANMLQLAGWTAVMIYAGATVSSALGKVLWDG

m125.pep     130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLMLLAVLWLSAEVFSTAGSTAAQVSD
|||||:|||||
a125         130     140     150     160     170     180
ESFVWWALANGALIVLWLVFGARKTGGLKTVSMLMLLAVLWLSAEVFSTAGSTAAQVSD

m125.pep     190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAALF
|||||:|||||
a125         190     200     210     220     230     240
GMSFGTAVELSAVMPLSWLPLAADYTRHARRPFAATLTATLAYTLTGCWMYALGLAAALF

m125.pep     250     260     270     280     290     300
TGETDVAKILLGAXLGAAGILAVVLSTVTTTFLDAYSAGASANNISARFAETPVAVXVTL
|||||:|||||
a125         250     260     270     280     290     300
TGETDVAKILLGAGLGAAGILAVVLSTVTTTFLDAYSAGVSANNISAKLSEIPIAVAVAV

m125.pep     310     320     330     340
IGTVLAVMLPVTEYENFLLLIGSVFAPMAGGFDCRLFRLETAX
:||||:|||||
a125         310     320     330     340
VGTLLAVLLPVTEYENFLLLIGSVFAPMAXGFDCRLFRLETAX

```

310                      320                      330                      340

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 463>:

```
g126.seq
  1  AtgccgtcTG AAaccCcaaa ggcACGCCGC CGGCTTTCAG ACGGCATCGC
 51  GTCCGACAAC CATACCAAAG AATCCATCAT GCTCACCctg tacggcGAAA
101  CTTTCCCTTC GCGGCTGCTg ctcggcacgG cggcctacCC GACCCCTGAA
151  ATCCTCAAAC AATCCGTCCG AACCGCCCGG CCCGCGATGA ttaccGTCTC
201  GCTGCGCCGC ACGGGATGCG GCGGCGAGGC GCACGGTCAG GGGTTTGTGT
251  CGCTGCTTCA AGAAACCGGC GTTCCCGTCC TGCCGAACAC GGCAGGCTGC
301  CAAAGCGTGC AGGAAGCGGT AACGACGGCG CAAATGGCGC GCGAAGTGTT
351  TGAAACCGAT TGGATAAAAT TGGAACTCAT CGGCGACGAC GACACCTTGC
401  AGCCGGACGT GTTCCAATC GTCGAAGCGG CGGAAATCCT GATTAAAGAC
451  GGCTTCAAAG TGCTGCCTTA TTGCACCGAA GACCTGATTG CCTGCCGCCG
501  CCTGCTCGAT GCGGGCTGTC AGGCGTTGAT GCCGTGGGCG GCTCCCATCG
551  GCACGGGTTT GGGGGCGGTT CACGCCTATG CGCTCAAAAT CCTGCGCGAA
601  CGCCTGCCCG ACACGCCGCT GATTATCGAC GCGGGCTTGG GTTTGCGCTT
651  CCAAGCGGCA CAAGTGATGG AATGGGGTTT TGACGGCGTA TTGTTAAACA
701  CCGCCGTTTC CCGCAGCGGC GACCCCGTCA ACATGGCGCG CGCCTTCGCA
751  CTCGCCGTCG AATCCGGACG GCTGGCATTG GAAGCCGGGC CGGTCGAAGC
801  GCGAACCAAA GCCCAAGCCA GCACGCCGAC AGTCGGACAA CCGTTTGTGG
851  ATTCGGCGGA ATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 464; ORF 126.ng>:

```
g126.pep
  1  MPSETPKARR RLSGDIASDN HTKESIMLTL YGETFPSRL LGTAAYPTPE
 51  ILKQSVRTAR PAMITVSLRR TCGGGEAHGQ GFWSLLQETG VVPLPNTAGC
101  QSVQEAHTTA QMAREVFETD WIKLELIGDD DTLQPDVFQL VEAAILIKD
151  GFKVLPYCTE DLIACRRLLD AGCQALMPWA APIGTGLGAV HAYALKILRE
201  RLPDTPLIID AGLGLPSQAA QVMEWGFQDV LLNTAVSRSG DPNVNMARAF
251  LAVESGRALF EAGPVEARTK AQAAPTPTVGQ PFWHSAEY*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 465>:

```
m126.seq (partial)
  1  ..CACTATACAA AGGAACCCAT TATGCTCACC CTATACGGCG AAACTTTCCC
 51  CTCGCGGCTG CTGCTCGGCA CGGCTGCCTA CCCGACCCCG GAAATCCTCA
101  AACAATCCAT CCAAACCGCC CAGCCTGCGA TGATTACCGT CTCGCTGCGC
151  CGCGCGGGAA GCGGCGGCGA GCGCGACGGT CAGGGGTTTT GGTGCTGCT
201  TCAAGAAACC GCGGTTCCCG TCCTGCCGAA CACGGCAGGC TGCCAAAGCG
251  TGCAGGAAGC GGTAACGACG GCGCAAATGG CGCGCGAAGT GTTTGAAACC
301  GATTGGATAA AATTGGAAC TATCGGAGAT GACGACACCT TGCAGCCGGA
351  TGTGTTCCAG CTGTGCGAAG CGGCGGAAAT CCTGATTAAA GACGGCTTCA
401  AAGTGCTGCC TTATTGCACC GAAGACCTGA TTGCCTGCCG CCGCCTGCTC
451  GACGCGGGCT GTCAGGCGTT GATGCCGTGG GCGGCCCGA TCGGCACGGG
501  TTTGGGCGCG GTTACGCCTT ACGCGTTGAA CGTCTGCGC GAACGCCTGC
551  CCGACACGCC GCTGATTATC GACGCGGGCT TGGGTTTGCC CTCACAGGCG
601  GCACAAGTGA TGAATGGGG CTTTGACGGC GTGCTTTTGA ATACTGCCGT
651  TTCCCGCAGC GCGGATCCGG TCAATATGGC ACGGCGCTTC GACTCGCCG
701  TCGAATCCGG ACGGCTGGCA TTTGAAGCCG GACCGGTGCA AGCAGCGAC
751  AAAGCGCAAG CCAGCACGCC GACAGTCGGA CAACCGTTTT GGCATTGCGC
801  GGAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 466; ORF 126>:

```
m126.pep (partial)
  1  ..HYTKEPIMLT LYGETFPSRL LLGTAAYPTP EILKQSIQTA QPAMITVSLR
 51  RAGSGGEAHG QGFWSLLQET GVPVLPNTAG CQSVQEAHTT AQMAREVFET
```

```

101 DWIKLELIGD DDTLQPDVFQ LVEAAEILIK DGFKVLPYCT EDLIACRRLI
151 DAGCQALMPW AAPIGTGLGA VHAYALNVLR ERLPDTPLII DAGLGLPSQA
201 AQVMEWGFDG VLLNTAVSRS GDPVNMAF ALAVESGRLA FEAGPVEARD
251 KQASTPTVG QPFWHSAEY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 126 shows 95.9% identity over a 269 aa overlap with a predicted ORF (ORF 126.ng) from *N. gonorrhoeae*:

m126/g126

```

                                10      20      30      40
m126.pep      .  HYTKPEIMLTLYGETFPSRLLLGTAAAYPTPEILKQSIQTAQ
                  ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      MPSETPKARRRLSDGIASDNHTKESIMLTLYGETFPSRLLLGTAAAYPTPEILKQSVRTAR
                  10      20      30      40      50      60

                                50      60      70      80      90      100
m126.pep      PAMITVSLRRAGSGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      PAMITVSLRRTGCGGEAHGQGFWSLLQETGVPVLPNTAGCQSVQEAVTTAQMAREVFETD
                  70      80      90      100      110      120

                                110      120      130      140      150      160
m126.pep      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      WIKLELIGDDDTLQPDVFQ LVEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWA
                  130      140      150      160      170      180

                                170      180      190      200      210      220
m126.pep      APIGTGLGAVHAYALNVLRERLPDTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      APIGTGLGAVHAYALKILRERLPDTPLIIDAGLGLPSQAAQVMEWGFDGVLLNTAVSRSG
                  190      200      210      220      230      240

                                230      240      250      260      270
m126.pep      DPVNMAFALAVESGRLA FEAGPVEARDKQASTPTVGQPFWHSAEYX
                  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g126      DPVNMAFALAVESGRLA FEAGPVEARTKQASTPTVGQPFWHSAEYX
                  250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 467>:

a126.seq

```

1  TTGTTAATCC ACTATACAAA GGAACCCATT ATGCTCACCC TGTACAGCGA
51  AACTTTCCT TCGCGGCTGC TGCTCGGCAC AGCCGCTAC CCGACCCCTG
101 AAATCCTCAA ACAATCCGTC CGAACC GCCCGCGAT GATTACCGTC
151 TCGCTGCGCC GCGCGGGATG CCGCGGCGAG GCGCACGGTC AGGGGTTTGT
201 GTCGCTGCTT CAAGAAACCG GCGTTCCTCGT CCTGCCGAAC ACGGCAGGCT
251 GCCAAGCGT GCAGGAAGCG GTAACGACGG CGCAAATGGC GCGCGAAGTG
301 TTTGAAACCG ATTGGATTAA ACTCGAACTC ATCGGCGACG ACGACACCTT
351 GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC GCGGGAATC CTGATTAAAG
401 ACGGCTTCAA AGTGCTGCCT TATTGCACCG AAGACCTGAT TGCCTGCCGC
451 CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG ATGCCGTGGG CGGCCCGAT
501 CGGCACGGGT TTGGGCGCGG TTCACGCCTA CGCGTTGAAC GTCCTGCGCG
551 AACGCTGCC CGACACGCGG CTGATTATCG ACGCGGGCTT GGGTTTGCCG
601 TCACAGCGCG CACAAGTGAT GGAATGGGGC TTGACGGCG TGCTTTTGAA
651 TACTGCCGTT TCCCGCAGCG GCGATCCGGT CAATATGGCA CGCGCTTCG
701 CACTCGCGT CGAATCCGGA CGGCTGGCAT TTGAAGCCGG ACCGGTCGAA
751 GCACGCGACA AAGCGCAAGC CAGCAGCCG ACAGTCGGAC AACCGTTTTG
801 GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 468; ORF 126.a>:

```
a126.pep
1  LLIHYTKEPI MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV
51 SLRRAGCGGE AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV
101 FETDWIKLEL IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR
151 RLLDAGCQAL MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP
201 SQAAQVMWEG FDGVLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE
251 ARDKAQASTP TVGQPFWSHA EY*
```

m126/a126 98.1% identity in 269 aa overlap

```

              10      20      30      40      50
m126.pep      HYTKEPIMLTLYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGE
              |||||
a126           LLIHYTKEPIMLTLYSETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRAGCGGE
              10      20      30      40      50      60

              60      70      80      90      100     110
m126.pep      AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              |||||
a126           AHGQGFWSLLQETGVPVLPNTAGCQSVQEA VTTAQMAREVFETDWIKLELIGDDDTLQPD
              70      80      90      100     110     120

              120     130     140     150     160     170
m126.pep      VFQVLEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              |||||
a126           VFQVLEAAEILIKDGFKVLPYCTEDLIACRRLLDAGCQALMPWAAPIGTGLGAVHAYALN
              130     140     150     160     170     180

              180     190     200     210     220     230
m126.pep      VLRERLPDTP LIIDAGLGLPSQAAQVMWEGFDGVLNTAVSRSGDPVNMA RAFALAVESG
              |||||
a126           VLRERLPDTP LIIDAGLGLPSQAAQVMWEGFDGVLNTAVSRSGDPVNMA RAFALAVESG
              190     200     210     220     230     240

              240     250     260     270
m126.pep      RLAFEAGPVEARDKAQASTPTVGQPFWSHA EYX
              |||||
a126           RLAFEAGPVEARDKAQASTPTVGQPFWSHA EYX
              250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 469>:

```
g126-1.seq
1  ATGCTCACCC TGTACGGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51  GGCCGCTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACC GCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCACGGGATG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTGCTGCTT CAAGAAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAATC
301 ATCGGCGACG ACGACACCTT GCAGCCGGAC GTGTTC AAC TCGTCGAAGC
351 GGCGGAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC CGCCTGCTCG ATGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCTCCCAT CGGCACGGGT TTGGGGGCGG TTCACGCCTA
501 TCGGCTCAAA ATCCTGCGCG AACGCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTGCTT TCCCAAGCGG CACAAGTGAT GGAATGGGGT
601 TTTGACGGCG TATTGTTAAA CACCGCCGTT TCCCGCAGCG GCGACCCCGT
651 CAACATGGCG CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG GCCGGTCGAA GCGCGAACCA AAGCCCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTGT GCATTGCGCG GAATATTGA
```

This corresponds to the amino acid sequence <SEQ ID 470; ORF 126-1.ng>:

```
g126-1.pep
1  MLTLYGETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRTGCGGE
```

```

51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALK ILRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARTKAQASTP
251 TVGQPFWSHA EY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 471>:

m126-1.seq

```

1 ATGCTCACCC TATACGGCGA AACTTTCCCC TCGCGGCTGC TGCTCGGCAC
51 GGCTGCCTAC CCGACCCCGG AAATCCTCAA ACAATCCATC CAAACCGCCC
101 AGCCTGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGAAG CGGCGGCGAG
151 GCGCACGGTC AGGGGTTTGT GTCGCTGCTT CAGAGAACCG GCGTTCCCGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATAAA ATTGGAACCTC
301 ATCGGAGATG ACGACACCTT GCAGCCGGAT GTTTCAGC TTGTCGAAGC
351 GGCGGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCTT TATTGCACCG
401 AAGACCTGAT TGCCTGCCGC GCGCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CCGCCCCGAT CCGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CCGCTTGAAC GTCCTGCCGC AACGCTGCCG CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCAGCGCG
751 ACAGTCGGAC AACCGTTTGT GCATTGCGG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 5; ORF 126-1>:

m126-1.pep

```

1 MLTYGETFP SRLLLGTAAY PTPEILKQSI QTAQPAMITV SLRRAGSGGE
51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQVLEAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCQAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWSHA EY*

```

m126-1/g126-1 96.9% identity in 262 aa overlap

	10	20	30	40	50	60
m126-1.pep	MLTYGETFP SRLLLGTAAYPTPEILKQSIQTAQPAMITVSLRRAGSGGEAHGQGFWSLL					
g126-1	MLTYGETFP SRLLLGTAAYPTPEILKQSVRTARPAMITVSLRRTGCGGEAHGQGFWSLL					
	10	20	30	40	50	60
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
g126-1	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
	70	80	90	100	110	120
m126-1.pep	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
g126-1	QETGVPVLPNTAGCQSVQEA VTTAQMAREV FETDWIKLELIGDDDTLQPDVFQVLEAAEI					
	70	80	90	100	110	120
m126-1.pep	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALNVLRERLPDTP					
g126-1	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALKILRERLPDTP					
	130	140	150	160	170	180
m126-1.pep	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALNVLRERLPDTP					
g126-1	LIKDGFKVLPYCTEDLIACRRLDAGCQALMPWAAPIGTGLGAVHAYALKILRERLPDTP					
	130	140	150	160	170	180
m126-1.pep	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
g126-1	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
m126-1.pep	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
g126-1	LIIDAGLGLPSQAAQVMEWGF DGVLLNTAVSRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
m126-1.pep	ARDKAQASTPTVGQPFWSHA EYX					
g126-1	ARTKAQASTPTVGQPFWSHA EYX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 473>:

a126-1.seq

```

1 ATGCTCACCC TGTACAGCGA AACTTTCCCT TCGCGGCTGC TGCTCGGCAC
51 AGCCGCTTAC CCGACCCCTG AAATCCTCAA ACAATCCGTC CGAACCGCCC
101 GGCCCGCGAT GATTACCGTC TCGCTGCGCC GCGCGGGATG CGGCGGCGAG

```



360

```

151 GCGCACGGTC AGGGGTTTTG GTCGCTGCTT CAAGAAACCG GCGTTCCTGT
201 CCTGCCGAAC ACGGCAGGCT GCCAAAGCGT GCAGGAAGCG GTAACGACGG
251 CGCAAATGGC GCGCGAAGTG TTTGAAACCG ATTGGATTAA ACTCGAACTC
301 ATCGCGGACG ACGACACCTT GCAGCCGGAT GTGTTCCAAC TTGTCGAAGC
351 GCGCGAAATC CTGATTAAAG ACGGCTTCAA AGTGCTGCCT TATTGCACCG
401 AAGACCTGAT TGCCTGCCCG CGCCTGCTCG ACGCGGGCTG TCAGGCGTTG
451 ATGCCGTGGG CGGCCCCGAT CGGCACGGGT TTGGGCGCGG TTCACGCCTA
501 CGCGTTGAAC GTCCTGCGCG AACGCCTGCC CGACACGCCG CTGATTATCG
551 ACGCGGGCTT GGGTTTGCCC TCACAGGCGG CACAAGTGAT GGAATGGGGC
601 TTTGACGGCG TGCTTTTGAA TACTGCCGTT TCCCGCAGCG GCGATCCGGT
651 CAATATGGCA CGCGCCTTCG CACTCGCCGT CGAATCCGGA CGGCTGGCAT
701 TTGAAGCCGG ACCGGTCGAA GCACGCGACA AAGCGCAAGC CAGCACGCCG
751 ACAGTCGGAC AACCGTTTTG GCATTCGGCG GAATATTGA

```

This corresponds to the amino acid sequence <SEQ ID 474; ORF 126-1.a>:

```

a126-1.pep
  1 MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE
 51 AHGQGFWSLL QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL
101 IGDDDTLQPD VFQLVAAEI LIKDGFKVLP YCTEDLIACR RLLDAGCOAL
151 MPWAAPIGTG LGAVHAYALN VLRERLPDTP LIIDAGLGLP SQAAQVMEWG
201 FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE ARDKAQASTP
251 TVGQPFWWSA EY*

```

a126-1/ml26-1 98.14 identity in 262 aa overlap

	10	20	30	40	50	60
a126-1.pep	MLTLYSETFP SRLLLGTAAY PTPEILKQSV RTARPAMITV SLRRAGCGGE AHGQGFWSLL					
	:     :     :     :     :					
m126-1	MLTLYGETFP SRLLLGTAAY PTPEILKQSIQTAQPAMITV SLRRAGSGGE AHGQGFWSLL					
	10	20	30	40	50	60
	70	80	90	100	110	120
a126-1.pep	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	:     :     :     :     :					
m126-1	QETGVPVLPN TAGCQSVQEA VTTAQMAREV FETDWIKLEL IGDDDTLQPD VFQLVAAEI					
	70	80	90	100	110	120
	130	140	150	160	170	180
a126-1.pep	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	:     :     :     :     :					
m126-1	LIKDGFKVLP YCTEDLIACR RLLDAGCQAL MPWAAPIGT GLGAVHAYALN VLRERLPDTP					
	130	140	150	160	170	180
	190	200	210	220	230	240
a126-1.pep	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	:     :     :     :     :					
m126-1	LIIDAGLGLP SQAAQVMEWG FDGVLLNTAV SRSGDPVNMA RAFALAVESG RLAFEAGPVE					
	190	200	210	220	230	240
	250	260				
a126-1.pep	ARDKAQASTP TVGQPFWWSA EYX		:     :			
	:     :					
m126-1	ARDKAQASTP TVGQPFWWSA EYX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 475>:

g127.seq

```

  1 ATGGAATAT GGAATATGTT GAACACTTGG CCCGATGCCG TCCCGATACG
 51 CGCGGAGGCG GCCGAATCCG TGGCGGCGGT CGCGGCTTTG CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAGAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGGTTTTT GGTGCCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCAAATT CAAACGCTGG
251 CTTTGTGCGAT GTTTCGGTG GCGGCGCGG TCGTCGTGGC GACAAAAGAA
301 CTGATTATGT GTCTGTGCGG CAGTATTTTA aggtctGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAATCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TTCCCAACA GCCTGTTGTT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA

```

```

551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 TCAGCGGTAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGGCC GCGCGTTACC CCGGTACCGT ACGACGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCCTC CCCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TCGCGTACA ATACCGCTG TTAAATCATC
851 CCGCCGgctc cgAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 476; ORF 127.ng>:

g127.pep

```

1 MEIWNMLNTW PDAVPIRAEA AESVAAVAAL LLARALLNI HFRRHDPFGI
51 ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAUVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 477>:

m127.seq

```

1 ATGGAATAT GGAATATGTT GGACACTTGG CTCGGTGCCG TCCCGATACG
51 TGCGGAGGCG GTCGAATCCG TGGCGGCGGT TGCGGCTTGT CTGCTGGCGC
101 GCGCCCTTCT GTTGAATATC CACTTCAAAC GGCATCCGGA TTTCGGCATC
151 GAAAGCAAGC GCGGTTTTTT GGTGCGCAGC CGCAATATAA CGCTGCTTTT
201 GGTGCTGTTT TCGCTGGCAT TTATCTGGTC GCGCAAATC CAAACGCTGG
251 CTTTGTGAT GTTTCGGTG GCGGCGCGG TCGTCGTGGC GACGAAGGAA
301 CTGATTATGT GTCTGTCCGG CAGTATTTTA AGGTCTGCCA CCCAGCAATA
351 CTCGGTCGGC GACTATATCG AAATCAACGG CCTGCGCGGG CGCGTGGTCG
401 ACATCAACCT GTTGAACACG CTGATGATGC AGGTCGGTCC GAACCCCTTG
451 GTCGGACAGC TTGCGGGAAC CACCGTTTCT TCCCCAACA GCCTGTGTGT
501 GAGCCACCCC GTGCGCCGCG ACAATATTTT GGGCGACTAT GTCATCCATA
551 CGGTCGAAAT CCCCGTTCCC ATCCATTGG ATTCCGATGA AGCCGTATGC
601 CGTCTGAAAG CCGTACTCGA GCCCTTGTGC GCGCCCTACA TCCCCGCCAT
651 CCAACGGsAT TTGGAACG TGCAGGCGGA AAAACTGTTT ATCAGCCCCG
701 CCGCCAGACC GCGCGTTACC CCGTGCCGT ACGATGACAA GGCATACCGC
751 ATCATCGTCC GCTTCGCTTC CCCGTTTCA AAGCGGCTGG AAATCCAACA
801 GGCGGTTATG GACGAATTTT TCGCGTACA ATACCGCTG TTAAATCACC
851 CCGCCGCTC CGAAACACTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 478; ORF 127>:

m127.pep

```

1 MEIWNMLDTW LGAVPIRAEA VESVAAVAAL LLARALLNI HFKRHDPFGI
51 ESKRRFLVAS RNITLLLVLF SLAFIWSAQI QTLALSMFAV AAUVVATKE
101 LIMCLSGSIL RSATQQYSVG DYIEINGLRG RVVDINLLNT LMMQVGNPL
151 VGQLAGTTVS FPNSLLLSHP VRRDNILGDY VIHTVEIPVP IHLDSDEAVC
201 RLKAVLEPLC APYIPAIQRY LENVQAEKLF ITPAARPRVT RVPYDDKAYR
251 IIVRFASPVS KRLEIQQAVM DEFLRVQYRL LNHPAGSETL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 127 shows 97.9% identity over a 290 aa overlap with a predicted ORF (ORF 127.ng) from *N. gonorrhoeae*:

m127/g127

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAAVAALLARALLNIHFKRHDPFGIESKRRFLVAS					
	:       :       :       :       :       :       :       :					
g127	MEIWNMLNTWPDVPIRAEAAESVAAVAALLARALLNIHFRRHDPFGIESKRRFLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAUVVATKELIMCLSGSILRSATQQYSVG					
	:       :       :       :       :       :       :       :					
g127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAUVVATKELIMCLSGSILRSATQQYSVG					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
g127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGQLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
g127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRYLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
g127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 479>:

a127.seq	1	ATGGAAATAT	GGAATATGTT	GGACACTTGG	CTCGGTGCCG	TCCCGATACG
	51	TGCGGAGGCG	GTCGAATCCG	TGCGGTGGT	CGCGGCTTTG	CTGCTGGCGC
	101	GCGCCCTTCT	GTTGAATATC	CACTTCAAAC	GGCATCCGGA	TTTCGGCATC
	151	GAAAGCAAGC	GGCGGTTTTT	GGTGCCAGC	CGCAATATAA	CGCTGCTTTT
	201	GGTGCTGTTT	TCGCTGGCAT	TTATCTGGTC	GGCGCAAATC	CAAACGCTGG
	251	CTTTGTCGAT	GTTTGCGGTG	GCGGCGGCGG	TCGTCTGGC	GACGAAGGAA
	301	CTGATTATGT	GTCTGTCGGG	CAGCATTTTA	AGGTCTGCCA	CCCAGCAATA
	351	CTCGGTCGGC	GACTATATCG	AAATCAACGG	CCTGCGCGGG	CGCGTGGTCG
	401	ACATCAACCT	GTTGAACACG	CTGATGATGC	AGGTCGGTCC	GAACCCCTTG
	451	GTCGGACAGC	TTGCGGGAAC	CACCGTTTCT	TTCCCAACA	GCCTGTTGTT
	501	GAGCCACCCC	GTGCGCCGCG	ACAATATTTT	GGGCGACTAC	GTCATCCATA
	551	CGGTCGAAAT	CCCGGTTCCC	ATCCATTTGG	ATTCTGGATG	AGCCGTATGC
	601	CGTCTGAAAG	CCGTACTCGA	GCCCTTGTGC	GCGCCCTACA	TCCCGGCCAT
	651	CCAACGGCAT	TTGGAACACG	TGCAGGCGGA	AAAACGTTT	ATCACGCCCG
	701	CCGCCAAACC	GCGCGTTACC	CGCGTGCCGT	ACGATGACAA	GGCATAACGC
	751	ATCATCGTCC	GCTTCGCCTC	CCCCGTTTCA	AAGCGGCTGG	AAATCCAACA
	801	GGCGGTTATG	GACGAATTTT	TGCGCGTACA	ATACCGCCTG	TTAAATTACC
	851	CCGCCGGCTC	CGAAACACTT	TAA		

This corresponds to the amino acid sequence <SEQ ID 480; ORF 127.a>:

a127.pep	1	MEIWNMLDTW	LGAVPIRAEA	VESVAVVAAL	LLARALLNI	HFKRHPDFGI
	51	ESKRRLVAS	RNITLLLVLF	SLAFIWSAQI	QTLALSMFAV	AAAVVVATKE
	101	LIMCLSGSIL	RSATQQYSVG	DYIEINGLRG	RVVDINLLNT	LMMQVGNPL
	151	VGQLAGTTVS	FPNSLLLSHP	VRRDNILGDY	VIHTVEIPVP	IHLDSEAVC
	201	RLKAVLEPLC	APYIPAIQRH	LENVQAEKLF	ITPAKPRVT	RVPYDDKAYR
	251	IIVRFASPV	KRLEIQQAVM	DEFLRVQYRL	LNYPAGSETL	*

m127/a127 98.6% identity in 290 aa overlap

	10	20	30	40	50	60
m127.pep	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
a127	MEIWNMLDTWLGAVPIRAEAVESVAVVAALLARALLNIHFKRHPDFGIESKRRLVAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m127.pep	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVVATKELIMCLSGSILRSATQQYSVG					
a127	RNITLLLVLFSLAFIWSAQIQTALSMFAVAAAVVVATKELIMCLSGSILRSATQQYSVG					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m127.pep	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
a127	DYIEINGLRGRVVDINLLNTLMMQVGNPLVGLAGTTVSFPNSLLLSHPVRRDNILGDY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m127.pep	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRXLENVQAEKLFITPAARPRVT					
a127	VIHTVEIPVPIHLDSEAVCRLKAVLEPLCAPYIPAIQRHLENVQAEKLFITPAARPRVT					
	190	200	210	220	230	240
	250	260	270	280	290	
m127.pep	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
a127	RVPYDDKAYRIIVRFASPVSKRLEIQQAVMDEFLRVQYRLNHPAGSETLX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 481>:

g128.seq

1	atgattgaca	acgCActgct	ccacttgggc	gaagaaccCC	GTTTaatca
51	aatccaaacc	gaagACatca	AACCCGCCGT	CCAAACCGCC	ATCGCCGAAG
101	CGCGCGGACA	AATCGCCGCC	GTCAAAGCGC	AAACGCACAC	CGGCTGGCGG
151	AACACCGTCG	AGCGTCTGAC	CGGCATCACC	GAACGCGTCG	GCAGGATTTG
201	GGGCGTCGTG	TCCCATCTCA	ACTCCGTCGT	CGACACGCCC	GAACCTGCGG
251	CCGTCTATAA	CGAACTGATG	CCTGAAATCA	CGGTCTTCTT	CACCGAAATC
301	GGACAAGACA	TGAACTGTGA	CAACCGCTTC	AAAACCATCA	AAAATTCCCC
351	CGAATTTGCA	ACGCTTTCCC	CCGCACAAAA	AACCAAGCTC	GATCACGACC
401	TGCGCGATTT	CGTATTGAGC	GGCGCGGAAC	TGCCGCCCCA	ACGGCAGGCA
451	GAACTGGCAA	AACCTGCAAA	CGAAGGCGCG	CAACTTTCCG	CCAAATTCTC
501	CCAAAACGTC	CTAGACGCGA	CCGACGCGTT	CGGCATTTC	TTTGACGATG
551	CCGCACCGCT	TGCCGCGCAT	CCCAGAAGAC	CGCTCGCCAT	GTTTGCCGCC
601	GCCGCGCAAA	GCGAAGGCAA	AACAGGTTAC	AAAATCGGCT	TGCAGATTCC
651	GCACTACCTT	GCCGTTATCC	AATACGCCGG	CAACCGCGAA	CTGCCGGAAC
701	AAATCTACCG	CGCCTACGTT	ACCCGTGCCA	GCGAACTTTC	AAACGACGGC
751	AAATTCGACA	ACACCGCCAA	CATCGACCGC	ACGCTCGAAA	ACGCATTGAA
801	AACCGcctaa	cTGCTCGGCT	TTAAAAATTA	CGCCGAATTG	TCGCTGGCAA
851	CCAAAATGGC	GGACACGCCC	GAACAGGTTT	TAAACTTCCT	GCACGACCTC
901	GCCCCCGCG	CCAAACCCTA	CGCCGAAAAA	GACCTCGCCG	AAGTCAAAGC
951	CTTCGCCCGC	GAACACCTCG	GTCTCGCCGA	CCCGCAGCCG	TGGGACTTGA
1001	GCTACGCCGG	CGAAAAACTG	CGCGAAGCCA	AATACGCATT	CAGCGAAACC
1051	GAAGTCAAAA	AATACTTCCC	CGTCGGCAAA	GTTCTGGCAG	GCCTGTTCCG
1101	CCAAATCAAA	AAACTCTACG	GCATCGGATT	CGCCGAAAAA	ACCGTTCCCC
1151	TCTGGCACA	AGACGTGCGC	TATTTTGAAT	TGCAACAAAA	CGGCAAAACC
1201	ATCGGCGGCG	TTTATATGGA	TTTGTACGCA	CGCGAAGGCA	AACGCGGCGG
1251	CGCGTGGATG	AACGACTaca	AAGGCCGCGG	CCGCTTTGCC	GACGgcacGC
1301	TGCAACTGCC	CACCGCCTAC	CTCGTCTGCA	ACTTCGCCCC	GCCCCGTCCG
1351	GGCAAAGAAG	CGCGTTTAAG	CCACGACGAA	ATCCTCACCC	TCTTCCACGA
1401	AacCGGCCAC	GGACTGCACC	ACCTGCTTAC	CCAAGTGGAC	GAAGTGGGCG
1451	TGTCCGGCAT	CAAcggcgta	GAATGGGACG	CGGTGGAAGT	GCCACGCCAG
1501	TTTATGGAAA	ACTTCGTTTG	GGAATACAAT	GTATTGGCAC	AAATGTCCGC
1551	CCACGAAGAA	AccgGCGAGC	CCCTGCCGAA	AGAACTCTTC	GACAAAATGC
1601	TcgcCGCCAA	AAACTTCCAG	CGCGGTATGT	TCCTCGTCCG	GCAAAATGGAG
1651	TTCGCCCTCT	TCGATATGAT	GATTTACAGT	GAAAGCGACG	AATGCCGTCT
1701	GAAAACTGG	CAGCAGGTTT	TAGACAGCGT	GCGCAAAGAA	GTcGCCGTCA
1751	TCCAACCGCC	CGAATACAAC	CGCTTCGCCA	ACAGCTTCGG	CCacatctTC
1801	GcgggcGGCT	ATTCCGACGG	CTATTACAGC	TACGCATGGG	CCGAAAGTCCt
1851	cAGCACCGAT	GCCTACGCCG	CCTTTGAAGA	AAGcGACGac	gtcGCCGCCA
1901	CAGGCAACCG	CTTCTGGCAA	GAAAtccttg	ccgtcggcgg	ctCCCCGACG
1951	gcgGCGGAAT	CCTTCAAAGC	CTTCCGCGGA	CGCGAACCGA	GCATAGACGC

2001 ACTGCTGCGC CAAagcggtT TCGACAACGC gGcttgA

This corresponds to the amino acid sequence <SEQ ID 482; ORF 128.ng>:

g128.pep

```

1 MIDNALLHLG EEPFRNQIQT EDIKPAVOTA IAEARGQIAA VKAQTHTGWA
51 NTVERLTGIT ERVGRIWGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVGK VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTLQLPTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHHLLTQVD ELGVSGINGV EWDAAVELPSQ
501 FMENFVWEYN VLAQMSAHEB TGEPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS ESDECRLKNW QQVLDSVRKE VAVIQPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSTD AYAAFEESDD VAATGKRWFQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR QSGFDNAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 483>:

m128.seq (partial)

```

1 ATGACTGACA ACGCACTGCT CCATTGCGG GAAGAACCCC GTTTTGATCA
51 AATCAAAACC GAAGACATCA AACCGGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCTG AACCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTGCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCCGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTCGAC ACCCTCTCCC CCGCACAAA AACCAACTC AACCAC
1 TACGCCAGCG AAAAAGTGGC CGAAGCCAAA TACGCGTTCA GCGAAACCGA
51 wGTCAAAAAA TAyTTCcCyG TCGGCAAwGT ATTAACCGGA CTGTTGCCCC
101 AAmTCAAAAA ACTmTACGGC ATCGGATTTA CCGAAAAAAC yGTCCCCGTC
151 TGGCACAAAG ACGTGCGCTA TTKTGAATTG CAACAAAACG GCGAAmCCAT
201 AGGCGGCGTT TATATGGATT TGTACGCACG CGAAGGCAAA CGCGGCGGCG
251 CGTGGATGAA CGACTACAAA GGCCGCCGCC GTTTTTCAGA CGGCACGCTG
301 CAAYTGCCCA CGCCTACCT CGTCTGCAAC TTCGCCCCAC CCGTCGGCGG
351 CAGGGAAGCC CGCyTGAGCC ACGACGAAAT CCTCATCTC TTCCACGAAA
401 CCGGACACGG GCTGCACCAC CTGCTTACCC AAGTGGACGA ACTGGGCGTA
451 TCCGGCATCA ACGGCGTAKA ATGGGACGCG GTCGAACTGC CCAGCCAGTT
501 TATGGAAAAT TTCGTTTGGG AATACAATGT CTGGGCACAA mTGTCAGCCC
551 ACGAAGAAAC CGGcgTTCCC yTGCCGAAAG AACTCTTsGA CAAAwTGCTC
601 GCCGCCAAAA ACTTCCAAaG CGGCATGTTC yTsGTCCGGC AAwTGAGTT
651 CGCCCTCTTT GATATGATGA TTTACAGCGA AGACGACGAA GGCCGTCTGA
701 AAAACTGGCA ACAGGTTTTA GACAGCGTGC GCAAAAAAGT CGCCGTCATC
751 CAGCCGCCCG AATACAACCG CTTCGCCTTG AGCTTCGGCC ACATCTTCGC
801 AGGCGGCTAT TCCGCAGCTn ATTACAGCTA CGCGTGGGCG GAAGTATTGA
851 GCGCGGACGC ATACGCCGCC TTTGAAGAAA GCGACGATGT CGCCGCCACA
901 GGCAAACGCT TTTGGCAGGA AATCCTCGCC GTCGGGGnAT CGCGCAGCGG
951 nGCAGAAATCC TTCAAAGCCT TCCGCGGCCG CGAACCAGC ATAGACGCAC
1001 TCTTGCGCCA CAGCGGTTTC GACAACGCGG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 484; ORF 128>:

m128.pep (partial)

```

1 MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRIWGVV SHLNCVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NH

```

//

```

1 YASEKLREAK YAFSETXVKK YFPVGXVLNG LFAQXKKLYG IGFTEKTPVP
51 WHKDVRYXEL QONGEXIGGV YMDLYAREGK RGGAWMNDYK GRRRFSDGTL
101 QLPTAYLVCN FAPPVGGREA RLSDHEILIL FHETGHGLHH LLTQVDELGV
151 SGINGVXWDA VELPSQFMEN FVWEYNVLAQ XSAHEETGVP LPKELKDKKL
201 AAKNFQXGMF XVRQXEFALF DMMIYSEDDE GRLKNWQQLV DSVRKKVAVI
251 QPPEYNRFAL SFGHIFAGGY SAAXYSYAWA EVLSADAYAA FEESDDVAAT

```

301 GKRFWQEILA VGXSRGAES FKAFRGREPS IDALLRHS GF DNAV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 128 shows 91.7% identity over a 475 aa overlap with a predicted ORF (ORF 128.ng) from *N. gonorrhoeae*:

m128/g128

	10	20	30	40	50	60
g128.pep	MIDNALLHLGEEPRFNQIQTEDIKPAVQTAIAEARGQIAAVKAQHTGWANTVERLTGIT					
m128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g128.pep	ERVGRIWGVVSHLSNVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA					
m128	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130	140	150	160	170	180
g128.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEALQTEGAQLSAKFSQNVLDATDAFGIY					
m128	TLSPAQKTKLNH					
	130					
	//					
			340	350	360	
g128.pep	YAGEKLREAKYAFSETEVKKYFPVGKVLG					
m128	YASEKLREAKYAFSETXVKYFPVGXVLNG					
			10	20	30	
	370	380	390	400	410	420
g128.pep	LFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIGGVYMDLYAREGKRGGAWMNDYK					
m128	LFAQXKKLYGIGFTEKTVPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWMNDYK					
	40	50	60	70	80	90
	430	440	450	460	470	480
g128.pep	GRRRFADGTLQLPTAYLVCNFAPPVGGKEARLSHDEILTLFHETGHGLHLLTQVDELGV					
m128	GRRRFSGDTLQLPTAYLVCNFAPPVGGREARLSHDEILILFHETGHGLHLLTQVDELGV					
	100	110	120	130	140	150
	490	500	510	520	530	540
g128.pep	SGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGEPLPKELFDKMLAAKNFQXGMF					
m128	SGINGVXWDAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKKLAAKNFQXGMF					
	160	170	180	190	200	210
	550	560	570	580	590	600
g128.pep	LVRQMEFALFDMMIYSEDECRLKNWQQVLDVSRKEVAVIQPPEYNRFANSFGHIFAGGY					
m128	XVRQXEFALFDMMIYSEDDEGRKNWQQVLDVSRKKVAVIQPPEYNRFALSFGHIFAGGY					
	220	230	240	250	260	270
	610	620	630	640	650	660
g128.pep	SAGYYSYAWAEVLSTDAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRGREPS					
m128	SAAXYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRGREPS					
	280	290	300	310	320	330

	670	679
g128.pep	IDALLRQSGFDNAAX	
	:     :	
m128	IDALLRHSGFDNAVX	
	340	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 485>:

```

a128.seq
1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTGGTG TCGCACCTCA ACTCCGTCAC CGACACGCCC GAACTGCGCG
251 CGGCCTACAA TGAATTAATG CCCGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAATC AACCCAGATC
401 TGC GCGATT T CGTCCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTTGACGATG
551 CCGCACCGCT TGCCGCGATT CCCGAAGACG CGCTCGCCAT GTTTGCCGCT
601 GCCGCGCAAA GCGAAGGCAA AACAGGCTAC AAAATCGGTT TGCAGATTCC
651 GCACTACCTC GCCGTCAATC AATACGCGA CAACCGCAAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGCGCCA GCGAGCTTTC AGACGACGGC
751 AAATTCGACA ACACGCGCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 AACCGCCAAA CTGCTCGGCT TCAAAACTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCCC GAACAAGTTT TAAACTTCCT GCACGACCTC
901 GCCCGCCGCG CCAAACCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTGCGCCGC GAAAGCCTCG GCCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCGG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAAA GTATTAAACG GACTGTTCCG
1101 CCAAATCAAA AAACCTCTACG GCATCGGATT TACCGAAAAA ACCGTCCCCG
1151 TCTGGCACAA AGACGTGCGC TATTTTGAAT TGCAACAAAA CGGCGAAACC
1201 ATAGGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCCGCGC CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAATC GCCCAGTCAG
1501 TTTATGGAAT ATTTGTTTGG GGAATACAAT GTCTTGGCGC AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCGGCCAA AAACCTTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAGAA GTCGCGCTCG
1751 TCCGACCGCC CGAATACAAC CGCTTCGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCGCGAGG CTATTACAGC TACGCGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCCG CCTTTGAAGA AAGCGACGAT GTCGCGCCCA
1901 CAGGCAAACG CTTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAA CTTTCAAAGC CTTCGCGGGA CGCGAACC GAATAGACGC
2001 ACTCTTGC GC CACAGCGGCT TCGACAACGC GGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 486; ORF 128.a>:

```

a128.pep
1  MTDNALLHLG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGWA
51  NTVEPLTGIT ERVGRWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGKTYG KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
451 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMDATP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVGK VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSINGV EWDAVELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME

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551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF  
 601 AGGYSAGYYS YAWAEVLSAD AYAFAEESDD VAATGKRFWQ EILAVGGSRS  
 651 AAESFKAFRG REPSIDALLR HSGFDNAA\*

## m128/a128 66.0% identity in 677 aa overlap

	10	20	30	40	50	60
m128.pep	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
a128	MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIKAQHTGTWANTVEPLTGIT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m128.pep	ERVGRIWGVVSHLNCVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	:       :					
a128	ERVGRIWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD					
	70	80	90	100	110	120
	130					
m128.pep	TLSPAQKTKLNH-----					
a128	TLSHAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
m128.pep	-----					
a128	FDDAAPLAGIPEDALAMFAAAQSEGKTGYKIGLQIPHYLAVIQYADNRKLREQIYRAYV					
	190	200	210	220	230	240
m128.pep	-----					
a128	TRASELSDDGKFDNTANIDRTLENALQTAIKLLGFKNYAELSLATKMADTPEQVLNLFHDL					
	250	260	270	280	290	300
m128.pep	-----					
				140	150	
m128.pep	-----YASEKLREAKYAFSETXVKKYFPVGX					
	:					
a128	ARRAKPYAEKDLAEVKAFARESGLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGK					
	310	320	330	340	350	360
m128.pep	160	170	180	190	200	210
	VLNGLFAQXKKLYGIGFTEKTPVWHKDVRYXELQONGEXIGGVYMDLYAREGKRGGAWM					
a128	VLNGLFAQIKKLYGIGFTEKTPVWHKDVRYFELQONGETIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
m128.pep	220	230	240	250	260	270
	NDYKGRRRFSDGTLQLPTAYLVCNFAAPPVGGREARLSHDEILILFHETGHLHLLTQVD					
a128	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD					
	430	440	450	460	470	480
m128.pep	280	290	300	310	320	330
	ELGVSGINGVXWDAAVELPSQFMENFVWEYNVLAQXSAHEETGVPLPKELXDKXLAAKNFQ					
a128	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540
m128.pep	340	350	360	370	380	390
	XGMFXVRQXEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKKVAVIQPPEYNRFALSFGHIF					
a128	RGMFLVRQMEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF					
	550	560	570	580	590	600



368

```

          400      410      420      430      440      450
m128.pep  AGGYSAA XSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGXSRSGAESFKAFRG
          |||||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
          610      620      630      640      650      660

          460      470
m128.pep  REPSIDALLRHSGFDNAVX
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a128      REPSIDALLRHSGFDNAAX
          670

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 487>:

g128-1.seq (partial)

```

1  ATGATTGACA ACGCACTGCT CCACTTGGGC GAAGAACCCC GTTTTAATCA
51  AATCAAAACC GAAGACATCA AACCCGCCGT CCAAACCGCC ATCGCCGAAG
101 CGCGCGGACA AATCGCCGCC GTCAAAGCGC AAACGCACAC CGGCTGGGCG
151 AACACCGTCG AGCGTCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG
201 GGGCGTCTGT TCCCATCTCA ACTCCGTCGT CGACACGCCC GAACGCGCGC
251 CCGTCTATAA CGAACTGATG CCTGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAACTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGTGA ACGCTTTCCC CCGCACAAAA AACCAAGCTC GATCAGGACC
401 TGGCGGATTT CGTATTGAGC GCGCGGAAC TGCCGCCCGA ACGGCAGGCA
451 GAACGCGCAA AACTGCAAA CAAAGGCGCG CAACTTTCOG CCAAATTCTC
501 CCAAACGCTC CTAGACGCGA CCGACGCGTT CGGCATTTC TTTGACGATG
551 CCGCACCGCT TGCCGGCATT CCGAAGACG CGCTCGCCAT GTTGCCGCC
601 GCCGCGCAAA GCGAAGGCAA AACAGGTAC AAAATCGGCT TGCAGATTCC
651 GCACTACCTT GCGTTATCC AATACGCGG CAACGCGGAA CTGCGCGAAC
701 AAATCTACCG CGCTACGTT ACCCGTGCCA GCGAACTTTC AAAACGCGGC
751 AAATTCGACA ACACCGCAA CATCGACCGC ACGCTCGAAA ACGCATTGAA
801 AACCGCCAAA CTGCTCGGCT TTAATAATTA CGCCGAATTG TCGCTGGCAA
851 CCAAATGGCG GGACACGCCC GAACAGGTTT TAACTTCCT GCAAGACCTC
901 GCCCGCGCGC CCAAACCTTA CGCGAAAAAA GACCTCGCGG AAGTCAAAGC
951 CTTCGCGCGC GAACACCTCG GTCTCGCCGA CCCGCGCCG TGGGACTTGA
1001 GCTACGCGCG CGAAAACTG CGCGAAGCCA AATACGCATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTTCTGGCAG GCCTGTTCGC
1101 CCAAATCAAA AACTCTACG GCATCGGATT CGCCGAAAAA ACCGTTCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CGGCAAAACC
1201 ATCGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACGCGGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGCTTTGCC GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCGCCCC GCCCGTCGGC
1351 GGCAAGAAG CGCGTTTAAG CCACGACGAA ATCCTCACC TCTTCCACGA
1401 AACCGGCCAC GGACTGCACC ACCTGCTTAC CCAAGTGAC GAACTGGGCG
1451 TGTCCGGCAT CAACGGCGTA AAA

```

This corresponds to the amino acid sequence <SEQ ID 488; ORF 128-1.ng>:

g128-1.pep (partial)

```

1  MIDNALLHLG EPRFNQIKT EDIKPAVQTA IAEARGQIAA VKAQHTGWA
51  NTVERLTGIT ERVGRINGVV SHLNSVVDTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFA TLSPAQKTKL DHDLRDFVLS GAELPPERQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSEGTGY KIGLQIPHYL AVIQYAGNRE LREQIYRAYV TRASELSNDG
251 KFDNTANIDR TLENALKTAK LLGFKNYAEI SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR EHLGLADPQP WDLSYAGEKL REAKYAFSET
351 EVKKYFPVKG VLAGLFAQIK KLYGIGFAEK TVPVVHKDVR YFELQONGKT
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFA DGTQLPLTAY LVCNFAPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLTQVD ELGVSGINGV K

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 489>:

m128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGGGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATCGCCGAAG
101 CGCGCGAACA AATCGCCGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCG AACCCCTGAC CGGCATCACC GAACGCGTCG GCAGGATTTG

```

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201 GGGCGTGGTG TCGCACCTCA ACTCCGTCGC CGACACGCCC GAACTGCGCG
251 CCGTCTATAA CGAACTGATG CCGGAAATCA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAATTCCCC
351 CGAATTGAC ACCCTCTCCC CCGCACAAAA AACCAAACTC AACCAAGATC
401 TGGCGGATTT CGTCTCAGC GGCGCGGAAC TGCCGCCCGA ACAGCAGGCA
451 GAACTGGCAA AACTGCAAAC CGAAGGCGCG CAACTTTCCG CCAAATTCTC
501 CCAAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTATC TTTGACGATG
551 CCGCACCGCT TCGCGGCATT CCGAAGACG CGCTCGCCAT GTTTGCCGCC
601 GCCGCGCAAA GCGAAAGCAA AACAGGCTAC AAAATCGGCT TGCAGATTCC
651 AACTACCTC GCCGTCATCC AATACGCCGA CAACCGCGAA CTGCGCGAAC
701 AAATCTACCG GCGCTACGTT ACCCGCGCCA GCGAACTTTC AGACGACGGC
751 AAATTCGACA ACACCGCCAA CATCGACCGC ACGCTCGCAA ACGCCCTGCA
801 AACC GCCAAA CTGCTCGGCT TCAAAAAC TA CCGCGAATTG TCGCTGGCAA
851 CCAAAATGGC GGACACGCCC GAACAAGTTT TAAACTTCTT GCACGACCTC
901 GCCCGCCGCG CCAAAACCTA CGCCGAAAAA GACCTCGCCG AAGTCAAAGC
951 CTTCCGCCGC GAAAGCCTGA ACCTCGCCGA TTTGCAACCG TGGGACTTGG
1001 GCTACGCCAG CGAAAAAC TG CGGAAGCCA AATACGCGTT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAACG GACTGTTCCG
1101 CCAAAATCAA AACTCTACG GCATCGGATT TACCGAAAAA ACCGTCGCCG
1151 TCTGGCACA AGACGTGCGC TATTTTGAAT TGCAACAAAA CCGCGAAACC
1201 ATAGGCGCGG TTTATATGGA TTTGTACGCA CGCGAAGGCA AACCGCGCGG
1251 CGCGTGGATG AACGACTACA AAGGCGCGCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCTTAC CTCGTCTGCA ACTTCGCCCC ACCGTCGGCG
1351 GGCAGGGAAG CCCGCTGAG CCACGACGAA ATCTCTATCC TCTTCCACGA
1401 AACC GGACAC GGGCTGCACC ACCTGCTTAC CCAAGTGGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CGTTCGAACT GCCCAGCCAG
1501 TTTATGGAAT ATTTCGTTTG GGAATACAAAT GTCTTGGCAG AAATGTCAGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAAATGC
1601 TCGCGGCCAA AAACCTTCAA CGCGGCATGT TCCTCGTCCG GCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAAAAA GTCGCCGTCA
1751 TCCAGCGGCC CGAATACAAC CGCTTCGCCT TGAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TAGCGGTGGG CGGAAGTATT
1851 GAGCGGGGAC GCATACGCGG CCTTTGAAGA AAGCGACGAT GTCGCCGCCA
1901 CAGGCAAAAC CTTTGGCAG GAAATCCTCG CCGTCGCGCG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGC CGCGAACCGA GCATAGACGC
2001 ACTCTTGGCG CACAGCGGTT TCGACAACGC GGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 490; ORF 128-1>:

m128-1.pep.

```

1 MTDNALLHLG EEPRFDQIKT EDIKPALQTA IAEAREQIAA IKAQTHTGWA
51 NTVEPLTGIT ERVGRINGVV SHLNSVADTP ELRAVYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSPAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAQSESKTGY KIGLQIPHYL AVIQYADNRE LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLNALQTAQ LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLNLADLPQ WDLGYASEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVVHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFAPPVG
451 GREARLSHDE ILILFHETGH GLHLLLTQVD ELGVSGINGV EWDDELPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNFQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLEKNW QQVLDVSRKK VAVIQPPEYN RFALSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAAPESDD VAATGKRFWQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAV*

```

m128-1/g128-1 94.5% identity in 491 aa overlap

```

          10      20      30      40      50      60
g128-1.pep MIDNALLHLGEEPRFNQIKTEDIKPAVQTAIAEARGQIAAVKAQTHTGWANTVERLTGIT
m128-1      MTDNALLHLGEEPRFDQIKTEDIKPALQTAIAEAREQIAAIIKAQTHTGWANTVEPLTGIT
          10      20      30      40      50      60

          70      80      90     100     110     120
g128-1.pep ERVGRINGVVSHLNSVVDTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFA
m128-1      ERVGRINGVVSHLNSVADTPELRAVYNELMPEITVFFTEIGQDIELYNRFKTIKNSPEFD
          70      80      90     100     110     120

```

370

	130	140	150	160	170	180
g128-1.pep	TLSPAQKTKLDHDLRDFVLSGAELPPERQAEIAKLQTEGAQLSAKFSQNVLDATDAFGIY					
m128-1	TLSPAQKTKLNHDLRDFVLSGAELPPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIY					
	130	140	150	160	170	180
g128-1.pep	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYAGNRELREQIYRAYV					
m128-1	FDDAAPLAGIPEDALAMFAAAAQSEKGTGYKIGLQIPHYLAVIQYADNRELREQIYRAYV					
	190	200	210	220	230	240
g128-1.pep	TRASELSNDGKFDNTANIDRTLENALKTAKLGLGFKNYAELSLATKMADTPEQVNLFLHDL					
m128-1	TRASELSDDGKFDNTANIDRTLANALQTAKLGLGFKNYAELSLATKMADTPEQVNLFLHDL					
	250	260	270	280	290	300
g128-1.pep	ARRAKPYAEKDIAEVKAFAREHLGLADPQWDLGYASEKLREAKYAFSETEVKKYFPVVGK					
m128-1	ARRAKPYAEKDIAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVVGK					
	310	320	330	340	350	360
g128-1.pep	VLNGLFAQIKKLYGIGFAEKTVPVWHKDVRYFELQONGKTIIGGVYMDLYAREGKRGGAWM					
m128-1	VLNGLFAQIKKLYGIGFTEKTVPVWHKDVRYFELQONGKTIIGGVYMDLYAREGKRGGAWM					
	370	380	390	400	410	420
g128-1.pep	NDYKGRRRFADGTLQLPTAYLVCNFAFPVGGKEARLSHDEILTLFHETGHGLHLLTQVD					
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFAFPVGGREARLSHDEILTLFHETGHGLHLLTQVD					
	430	440	450	460	470	480
g128-1.pep	ELGVSINGVVK					
m128-1	ELGVSINGVWEVDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ					
	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 491>:

a128-1.seq

```

1  ATGACTGACA ACGCACTGCT CCATTGCGC GAAGAACCCC GTTTTGATCA
51  AATCAAAACC GAAGACATCA AACCCGCCCT GCAAACCGCC ATTGCCGAAG
101 CGCGCGAACA AATCGCGGCC ATCAAAGCCC AAACGCACAC CGGCTGGGCA
151 AACACTGTCT AACCCTGAC CGGCATCACC GAACGCGTCT GCAGGATTGT
201 GCGCGTGGTG TCGCACCTCA ACTCCGTCA CACACGCCC GAAGTGGCG
251 CCGCTACAA TGAATTAATG CCGGAAATTA CCGTCTTCTT CACCGAAATC
301 GGACAAGACA TCGAGCTGTA CAACCGCTTC AAAACCATCA AAAACTCCCC
351 CGAGTTCGAC ACCCTCTCCC ACGCGCAAAA AACCAAACTC AACCAAGATC
401 TGCGCGATTT CGTCTCAGC GCGCGGAAC TGCGCGCGA ACAGCAGGCA
451 GAATTGGCAA AACTGCAAA CAAAGGCGCG CAACTTTCCT CCAAATTCTC
501 CCAAACGTC CTAGACGCGA CCGACGCGTT CGGCATTAC TTGACGATG
551 CGCACCGCT TGCGCGCAT CCGAAGACG CGCTCGCAT GTTTGCGCT
601 GCGCGCAAA GCGAAGCAA AACAGGCTAC AAAATCGGT TGCAGATTCC
651 GCACTACCTC GCGTCATCC AATACGCCA CAACGCAAA CTGCGCGAAC
701 AAATCTACG CGCTACGTT ACCCGCGCA GCGAGCTTC AGACGACGGC
751 AAATTCGACA ACACCGCAA CATCGACCGC ACGCTCGAAA ACGCCCTGCA
801 ACGCGCAAA CTGCTCGCT TCAAAACTA CGCGAATTG TCGCTGGCAA
851 CCAAATGGC GGACACCCC GAACAAGTTT TAACTTCTT GCACGACCTC
901 GCGCGCGCG CCAAACCTA CGCCGAAAA GACCTCGCG AAGTCAAAGC
951 CTTCGCGCG GAAAGCCTG GCCTCGCGA TTTGCAACG TGGGACTTGG
1001 GCTACGCGG CGAAAACTG CGCGAAGCCA AATACGATT CAGCGAAACC
1051 GAAGTCAAAA AATACTTCCC CGTCGGCAA GTATTAAAC GACTGTTTCG
1101 CCAAATCAA AACTCTACG GCATCGGATT TACCGAAAA ACCGTCCCCG
1151 TCTGGCACA AGACGTGCGC TATTTGAAT TGCAACAAA CCGCGAAACC
1201 ATAGCGGCG TTTATATGGA TTTGTACGCA CGCGAAGCA AACGCGCGG

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1251 CGCGTGGATG AACGACTACA AAGGCGCCG CCGTTTTTCA GACGGCACGC
1301 TGCAACTGCC CACCGCCTAC CTCGTCTGCA ACTTCACCCC GCCCGTCGGC
1351 GGCAAAGAAG CCCGCTTGAG CCATGACGAA ATCCTCACCC TCTTCCACGA
1401 AACCGGACAC GGCCTGCACC ACCTGCTTAC CCAAGTCGAC GAACTGGGCG
1451 TATCCGGCAT CAACGGCGTA GAATGGGACG CAGTCGAACT GCCCAGTCAG
1501 TTTATGGAAA ATTTCTGTTG GGAATACAAT GTCTTGCGCG AAATGTCCGC
1551 CCACGAAGAA ACCGGCGTTC CCCTGCCGAA AGAACTCTTC GACAAAATGC
1601 TCGCCGCCAA AAACCTCCAA CGCGGAATGT TCCTCGTCCG CCAAATGGAG
1651 TTCGCCCTCT TTGATATGAT GATTTACAGC GAAGACGACG AAGGCCGTCT
1701 GAAAACTGG CAACAGGTTT TAGACAGCGT GCGCAAGAA GTCCGCCGTCG
1751 TCCGACCGCC CGAATACAAC CGCTTGCCA ACAGCTTCGG CCACATCTTC
1801 GCAGGCGGCT ATTCCGCAGG CTATTACAGC TACCGGTGGG CGGAAGTATT
1851 GAGCGCGGAC GCATACGCGG CCTTTGAAGA AAGCGACGAT GTCCGCCGCA
1901 CAGGCAACG CTTTGGCAG GAAATCCTCG CCGTCGGCGG ATCGCGCAGC
1951 GCGGCAGAAT CCTTCAAAGC CTTCCGCGGA CGGAACCGA GCATAGACGC
2001 ACTCTTGCGC CACAGCGGCT TCGACAACGC GGCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 492; ORF 128-1.a>:

**a128-1.pep**

```
1 MTDNALLHLHG EEPFRDQIKT EDIKPALQTA IAEAREQIAA IKAQHTGTWA
51 NTVEPLTGIT ERVGRIWGVV SHLNSVTDTP ELRAAYNELM PEITVFFTEI
101 GQDIELYNRF KTIKNSPEFD TLSHAQKTKL NHDLRDFVLS GAELPPEQQA
151 ELAKLQTEGA QLSAKFSQNV LDATDAFGIY FDDAAPLAGI PEDALAMFAA
201 AAGSEKGTGY KIGLQIPHYL AVIQYADNRK LREQIYRAYV TRASELSDDG
251 KFDNTANIDR TLENALQTAK LLGFKNYAEL SLATKMADTP EQVLNFLHDL
301 ARRAKPYAEK DLAEVKAFAR ESLGLADLQP WDLGYAGEKL REAKYAFSET
351 EVKKYFPVKG VLNGLFAQIK KLYGIGFTEK TVPVWHKDVR YFELQONGET
401 IGGVYMDLYA REGKRGGAWM NDYKGRRRFS DGTLLQLPTAY LVCNFTPPVG
451 GKEARLSHDE ILTLFHETGH GLHLLLTQVD ELGVSGINGV EWDAVELEPSQ
501 FMENFVWEYN VLAQMSAHEE TGVPLPKELF DKMLAAKNPQ RGMFLVRQME
551 FALFDMMIYS EDDEGRLLKNW QQVLDSVRKE VAVVRPPEYN RFANSFGHIF
601 AGGYSAGYYS YAWAEVLSAD AYAFAESDD VAATGKRFPQ EILAVGGSRS
651 AAESFKAFRG REPSIDALLR HSGFDNAA*
```

m128-1/a128-1 97.8% identity in 677 aa overlap

	10	20	30	40	50	60
a128-1.pep	MTDNALLHLG	EEPRFDQIKT	EDIKPALQTA	IAEAREQIAA	IKAQHTGTWA	NTVEPLTGIT
m128-1	MTDNALLHLG	EEPRFDQIKT	EDIKPALQTA	IAEAREQIAA	IKAQHTGTWA	NTVEPLTGIT
	70	80	90	100	110	120
a128-1.pep	ERVGRIWGVV	SHLNSVTDTP	PELRAAYNELM	PEITVFFTEI	GQDIELYNRF	KTIKNSPEFD
m128-1	ERVGRIWGVV	SHLNSVADTP	PELRAAYNELM	PEITVFFTEI	GQDIELYNRF	KTIKNSPEFD
	130	140	150	160	170	180
a128-1.pep	TLSHAQKTKL	NHDLRDFVLS	GAELPPEQQA	ELAKLQTEGA	QLSAKFSQNV	LDATDAFGIY
m128-1	TLSPAQKTKL	NHDLRDFVLS	GAELPPEQQA	ELAKLQTEGA	QLSAKFSQNV	LDATDAFGIY
	190	200	210	220	230	240
a128-1.pep	FDDAAPLAGI	PEDALAMFAA	AAQSEKGTGY	KIGLQIPHYL	AVIQYADNRK	LREQIYRAYV
m128-1	FDDAAPLAGI	PEDALAMFAA	AAQSEKGTGY	KIGLQIPHYL	AVIQYADNRK	LREQIYRAYV
	250	260	270	280	290	300
a128-1.pep	TRASELSDDG	KFDNTANIDR	TLENALQTAK	LLGFKNYAEL	SLATKMADTP	EQVLNFLHDL
m128-1	TRASELSDDG	KFDNTANIDR	TLENALQTAK	LLGFKNYAEL	SLATKMADTP	EQVLNFLHDL
	310	320	330	340	350	360
a128-1.pep	ARRAKPYAEK	DLAEVKAFAR	ESLGLADLQP	WDLGYAGEKL	REAKYAFSET	EVKKYFPVKG

m128-1	ARRAKPYAEKD LAEVKAFARESLNLADLPWDLGYASEKLREAKYAFSETEVKKYFPVGK
	310 320 330 340 350 360
a128-1.pep	VLNGLFAQIKKLYGIGFTEKTPVWVHKDVRYPFELQQNGETIGGVYMDLYAREGKRGGAWM
m128-1	VLNGLFAQIKKLYGIGFTEKTPVWVHKDVRYPFELQQNGETIGGVYMDLYAREGKRGGAWM
	370 380 390 400 410 420
a128-1.pep	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
m128-1	NDYKGRRRFSDGTLQLPTAYLVCNFTPPVGGKEARLSHDEILTLFHETGHLHLLTQVD
	430 440 450 460 470 480
a128-1.pep	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
m128-1	ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAAKNFQ
	490 500 510 520 530 540
a128-1.pep	RGMFLVRQMEFALFDMMIYSEDDEGRLEKNWQVLDVSRKEVAVVRPPEYNRPFANSFGHIP
m128-1	RGMFLVRQMEFALFDMMIYSEDDEGRLEKNWQVLDVSRKEVAVVRPPEYNRPFANSFGHIP
	550 560 570 580 590 600
a128-1.pep	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
m128-1	AGGYSAGYYSYAWAEVLSADAYAAFEESDDVAATGKRFWQEILAVGGSRSAAESFKAFRG
	610 620 630 640 650 660
a128-1.pep	REPSIDALLRHSGFDNAAX
m128-1	REPSIDALLRHSGFDNAVX
	670 679

## a128-1/ P44573

sp|P44573|OPDA\_HAEIN OLIGOPEPTIDASE A >gi|1075082|pir||C64055 oligopeptidase A (prlc) homolog  
 - Haemophilus influenzae (strain Rd KW20)  
 >gi|1573174 (U32706) oligopeptidase A (prlc) [Haemophilus influenzae Rd] Length = 681  
 Score = 591 bits (1507), Expect = e-168  
 Identities = 309/677 (45%), Positives = 415/677 (60%), Gaps = 4/677 (0%)

Query: 4 NALLHLGEEPRFDQIKTEDIKPALQTXXXXXXXXXXXXXXXXXXTHGTWANTVEPLTGITERV 63  
 N LL++ P F QIK E I+PA++ H W N + PLT +R+

Sbjct: 5 NPLLNIQGLPFPFSQIKPEHIRPAVEKLIQDCRNTIEQVLKQPHFTWENFILPLTETNDRL 64

Query: 64 GRWGVVSHLNSVTDTPELRAAYNELMPEITVFFTEIGQDIELYNRFTIKNSPEFDTLS 123  
 R W VSHLNSV ++ ELR AY +P ++ + T +GQ LYN + +KNS EF S

Sbjct: 65 NRAWSPVSHLNSVKNSTELREAYQTCLPILLSEYSTWVGQHKGLYNAYLALKNSAEFADYS 124

Query: 124 HAQKTKLNHDLRDFVLSGAEPLPEQQAELAKLQTEGAQLSAKFSQNVLDATDAFGIYFDD 183  
 AQK + + LRDF LSG L E+Q ++ ++L+++FS NVLDAT + ++

Sbjct: 125 IAQKKAIEENSLRDFELSGIGLSEKQORYGEIVARLSELNSQFSNNVLDATMGWEKLIEN 184

Query: 184 AAPLAGIPEDALAMFAAAQSEGKTYKIGLQIPHYLAVIQYADNRKLRQIYRAYVTRA 243  
 A LAG+PE AL +A+S+G GY+ L+IP YL V+ Y +NR LRE++YRAY TRA

Sbjct: 185 EAELAGLPESALQAAQQAESKGLKGYRFTLEIPSYLPVMTYCENRALREEMYRAYATRA 244

Query: 244 SELSDD-GKFDNTANIDRTLENALQTAKLIGFKNYAELSLATKMDTPEQVLNFLHDLAR 302  
 SE + GK+DN+ ++ L ++ AKLIGF Y ELSLATKMA+ P+QVL+FL LA

Sbjct: 245 SEQGPNAGKWDNSKVMEEILTLRVELAKLLGPNITYELSLATKMAENPQQVLDLDFLDHLAE 304

Query: 303 RAKPYAEKD LAEVKAFARESLGLADLPWDLGYAGEKLREAKYAFSETEVKKYFPVGKVL 362  
 RAKP EK+L E+K + + G+ +L PWD+G+ EK ++ YA ++ E++ YFP +V+

Sbjct: 305 RAKPQGEKELQELKGYCEKEFGVTELPWDIGFYSEKQKQHLAYAINDEELRPYPFENRVI 364

Query: 363 NGLFAQIKKLYGIGFTE-KTVPVWHKDVRYFEL-QQNETIGGVYMDLYAREGKRGAWM 420  
 +GLF IK+++ I E K V WHKDVR+F+L +N + G Y+DLYARE KRGAWM  
 Sbjct: 365 SGLFELIKRIFNIRAVRKGVDTHWKDVRFFDLIDENDQLRGSFYLDLYAREHKRGAWM 424

Query: 421 NDYKRRRFSDDTLQLPTAYLVNFTPPVGGKEARLSHDEIXXXXXXXXXXXXXXXXXXQVD 480  
 +D GR+R DG+++ P AY L CNF P+G K A +H+E+ Q+D  
 Sbjct: 425 DDCIGRKRRLDGSJETPVAYLTCNFPNAPIGNKPALFTHNEVTTLFHEFGHGIHMLTQID 484

Query: 481 ELGVSGINGVEWDAVELPSQFMENFVWEYNVLAQMSAHEETGVPLPKELFDKMLAANKFQ 540  
 V+GINGV WDAVELPSQFMEN+ WE LA +S H.ETG PLFKE ++L AKNFQ  
 Sbjct: 485 VSDVAGINGVWDAVELPSQFMENWCWEEALAFISGHYETGEPLPKEKLTQLLKAKNFQ 544

Query: 541 RGMFLVRQMEFALFDMMIYSEDDEGRLLKNWQQVLDSVRKEVAVVRPPEYNRFANSFGHIF 600  
 MP++RQ+EF +FD ++ D + L SV+ +VAV++ ++ R +SF HIF  
 Sbjct: 545 AAMFILRQLEFGIFDFRLHHTFDAEKTNIQILDTLKSVKSQVAVIKGVNWARAPHSFSHIP 604

Query: 601 XXXXXXXXXXXXXWAEVLSADAYAAFEESDDV-AATGKRFWQEILAVGGSRSAAESPKAFR 659  
 WAEVLSADAY+ FEE TKG F EIL GGS E FK FR  
 Sbjct: 605 AGGYAAGYYSYLWAEVLSADAYSRFEEGIFNPITGKSFLDEILTRGGSEPMELFKRFR 664

Query: 660 GREPSIDALLRHSGFDN 676  
 GREP +DALLRH G N  
 Sbjct: 665 GREPQLDALLRHKGIMN 681

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 493>:

g129.seq  
 1 ATGCTTTCAC CTCCTCGGCG TAAACGGCG GCACATCAAT CAAGCCGTCT  
 51 TTCATTGCG TGCGGAAAAA ATGCGGCGTG TTGCCGTGAT CAAATCAAT  
 101 ATCGTGCAGC ATCCAGCCCA AATCGCGGTT TGCCTCGCTT TCCGATAACG  
 151 CCGACGGCGG CAGCGGTTCA CCCTTATCCG CGCTTTCGCC ATTTGCCCTT  
 201 TCAGGCTGCG GGCATAGGGG CGGAACAGGC GCGGTCGAA TCCTGTTTCA  
 251 TCCGACAAA CGCGTTGGCA GTCGAAAAT CCGGCCGGCC GTGTCAAATA  
 301 ATGCGTTACT TTGGCCGGGT CTTGTCCTTT GTAAGCGCG GTCTTTTTTT  
 351 GCGCGCCATC CGCATCTGTT TGGGCGCATG GCAAACGGCG GCTGCCGTAC  
 401 AATCAAAATG TTTGGCGATT TCATGCAGAC AGGCATCCGG ATGCCGCCCG  
 451 ACATATCGAG CCGTTTTTGT CCTATCCGAT TTGGCGCAT TTAGGCCGGT  
 501 AACTTGA

This corresponds to the amino acid sequence <SEQ ID 494; ORF 129.ng>:

g129.pep  
 1 MLSPRRKTA AHQSSRLSFA CGKNAACCRD QNQYRAASSP NRGLPRFPIT  
 51 PTAAAVHPYP RFRHLPFOAA GIGAEQAAVE SCFIRTNALA VGKSGRPCQI  
 101 MRYFGRVLSF VSGGLFLRAI RICLGAWQTA AAVQSKCLAI SCRQASGCRP  
 151 TYRAGFCLSD LAAFRPVT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 495>:

m129.seq (partial)  
 1 ..TATCTGCGCT TTCACTATTT GCCCTTTCAG GCTGCGGGCA TAGGGACGGA  
 51 ACAGGTAGCG GTCAAATCCT GTTTCATCCA AATAAACACG TTGGTAGTCG  
 101 GAAATTCGG CCGGCTGTGT CAAATAATGC GTTACTTTGG CCGGGTCTTG  
 151 TTCTTTGTAA GTGGTGGTCT TTTTTCGCG GTTATCCCCA TCTGTTTGAG  
 201 TGCATAGCAA ATGGTGGCTG CCGTACAATC AAAATGTTTG GCGATTTCAT  
 251 GCAGATAGGC ATCCGGGTGT TGCCCAACAT ATTGAGCCGG TTTTTCCTA  
 301 TCCGATTGA CGGCATTTAG ACCGGTAACT TGA

This corresponds to the amino acid sequence <SEQ ID 496; ORF 129>:

m129.pep (partial)  
 1 ..YLRFHYPFQ AAGIGTEQVA VKSCFIQINT LVVGKFGRLC QIMRYFGRVL  
 51 FVSGGLFLR VIPICLSAXQ MVAQVSKCL AISCRXASGC CPTYXAGFCL  
 101 SDLTAFRPVT \*

Computer analysis of this amino acid sequence gave the following results:

m129/g129

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 497>:

This corresponds to the amino acid sequence <SEQ ID 498; ORF 129.a>:

**m129/a129 98.2% identity in 110 aa overlap**

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 499>:

g130.seq

```
1 ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51 TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAAGC
101 TGGCGGGGCA TGGATCGTTC GGCATGTCTG ATGCCACTAC GGAAGCGGCA
151 ACCGAGACCC GCATCCAGCC TGTCGGACAA TTGACCATGG GTGACGGGCT
201 CCCCCTCGGC GAAGCCCAAG GCGAACAGAT TTTCGGGCAA ATCTGTATCC
```

```

251 AATGCCACGC GCGGACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGACT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTGCCA
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGCAG
401 ACCTGACCGA TCAGGAATC AAACGGGCGA TTACCTACAT GGCGAATAAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACAATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTGCAC AAACATGCCC TTGAAGGCTT TAACGCGATG
751 CCGGCCAAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 500; ORF 130.ng>:

```

g130.pep
  1 MKQLRDNKAQ GSAFLTVLSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
 51 TQTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFQHAL NGFNAMPAKG GAADLTQDEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAPAVGVVDG
201 KKVFEATCQV CHGGSIPGIP GIGKDDWAP RIKKGKETLH KHALEGPNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 501>:

```

m130.seq (partial)
  1 ..GGCGAACAGA TTTTCGGCAA AATCTGTATC CAATGCCACG CCGCGGACAG
 51 CAATGTGCCG AACGCTCCGA AACTGGAACA CAACGGCGAT TrGGCACC GC
101 GTATCGGCAA GGCTTCGATA CCTTGTGCCA ACACGCGCTG AACGGCTTTA
151 ACGCCATGCC TGCAAAAGGC GGTGCGGCAG ACCTGACCGA TCAGGAACCTT
201 AAACGGGCGA TTACTTACAT GGCGAACAAA AGCGGCGGTT CTTTCCCGAA
251 TCCTGATGAG GCTGCGCCTG CCGACAATGC CGCTTCAGGA ACAGCTTCTG
301 CTCCTGCCGA TAGTGAGCT CCGGCAGAAG CGAAGGCAGA AGACAAGGGT
351 GCGGCACCCC TGCGGTCGGC GTTGACGGTA AAAAAAGTCTT CGAAGCAACC
401 TGTCAGGTGT GCCACGGCGG TTCGATTCCC GGTATTCCCG GCATAGGCAA
451 AAAAGACGAT TGGGCACCGC GTATCAAAAA AGGCAAAGAA ACCTTGACACA
501 AACACGCCCT TGAAGGCTTT AACGCGATGC CTGCCAAAG CGCAATGCA
551 GGTTTGAGCG ATGACGAAGT CAAAGCGGCT GTTGACTATA TGGCAAACCA
601 ATCCGGTGCA AAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 502; ORF 130>:

```

m130.pep (partial)
  1 ..GEQIFGKICI QCHAADSNVP NAPKLEHNGD XAPRIQGFDT LFOHALNGFN
 51 AMPAKGGAAD LTDQELKRAI TYMANKSGGS FPNPDEAAPA DNAASGTASA
101 PADSAPAEA KAEDKGAAPA VGVDGKKVFE ATCQVCHGGS IPGIPGIGKK
151 DDWAPRIKKG KETLHKHALE GFNAMPAXKG NAGLSDEVK AAVDYMANQS
201 GAKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 130 shows 98.1% identity over a 206 aa overlap with a predicted ORF (ORF 130.ng) from *N. gonorrhoeae*:

```

m130/g130
m130.pep
          10      20      30
          GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||
g130      DATTEAATQTRIQPVGQLTMDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90     100

          40      50      60      70      80      89
m130.pep  XAPRI-QGFDTLFOHALNGFNAMPAKGGGAADLTQELKRAITYMANKSGGSFPNPDEAAP
          |||
g130      WAPRIAQGFDTLFOHALNGFNAMPAKGGGAADLTQELKRAITYMANKSGGSFPNPDEAAP
          110     120     130     140     150     160

```



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```

          90      100      110      120      130      140
m130 . pep  ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||
g130        ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130 . pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDDEVKAAVDYMANQSGAKFX
          |||
g130        KKDDWAPRIKKGKETLHKHALEGFNAMPKGGNAGLSDDDEVKAAVDYMANQSGAKFX
          230      240      250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 503>:

```

a130 . seq
1  ATGAAACAAC TCCGCGACAA CAAAGCCCAA GGCTCTGCAC TGTTTACCCT
51  TGTGAGCGGT ATCGTTATTG TTATTGCAGT CCTTTATTTC CTGATTAAGC
101 TGGCGGGCAG CGGCTCGTTC GGCGATGTCG ATGCCACTAC GGAAGCAGCA
151 ACGCAGACCC GTATCCAGCC TGTCCGACAA TTGACGATGG GCGACGGCAT
201 CCCGTCGGC GAACGCCAAG GCGAACAGAT TTTCCGCCAA ATCTGTATCC
251 AATGCCACGC GCGGCACAGC AATGTGCCGA ACGCTCCGAA ACTGGAACAC
301 AACGGCGATT GGGCGCCGCG TATCGCGCAA GGCTTCGATA CCTTGTTCCT
351 ACACGCGCTG AACGGCTTTA ACGCCATGCC TGCCAAAGGC GGTGCGGTAG
401 ACCTGACCGA TCAGGAATC AAACGGGCGA TTAATTACAT GGCGAACAA
451 AGCGGCGGTT CTTTCCCGAA TCCTGATGAG GCTGCGCCTG CCGACATGC
501 CGCTTCAGGA ACAGCTTCTG CTCCTGCCGA TAGTGCAGCT CCGGCAGAAG
551 CGAAGGCAGA AGACAAGGCT GCGGCAGCCC CTGCGGTCGG CGTTGACGGT
601 AAAAAAGTCT TCGAAGCAAC CTGTCAAGTG TGCCACGGCG GTTCGATTCC
651 CGGTATTCCC GGCATAGGCA AAAAAGACGA TTGGGCACCG CGTATCAAAA
701 AAGGCAAAGA AACCTTGCAC AAACACGCCC TTGAAGGCTT TAACGCCATG
751 CCTGCCAAG GCGGCAATGC AGGTTTGAGC GATGACGAAG TCAAAGCGGC
801 TGTGACTAT ATGGCAAACC AATCCGGTGC AAAATTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 504; ORF 130.a>:

```

a130 . pep
1  MKQLRDNKAQ GSALFTLVSG IVIVIAVLYF LIKLAGSGSF GDVDATTEAA
51  QTTRIQPVGQ LTMGDGIPVG ERQGEQIFGK ICIQCHAADS NVPNAPKLEH
101 NGDWAPRIAQ GFDTLFOHAL NGFNAMPAKG GAVDLTDQEL KRAITYMANK
151 SGGSFNPDE AAPADNAASG TASAPADSAA PAEAKAEDKG AAAPAVGVDG
201 KKVFEATCQV CHGGSIPGIP GIGKKDDWAP RIKKGKETLH KHALEGFNAM
251 PAKGGNAGLS DDEVKAAVDY MANQSGAKE*

```

m130/a130 97.6% identity in 206 aa overlap

```

          10      20      30
m130 . pep  GEQIFGKICIQCHAADSNVPNAPKLEHNGD
          |||
a130        DATTEAATQTRIQPVGQLTMGDGIPVGERQGEQIFGKICIQCHAADSNVPNAPKLEHNGD
          50      60      70      80      90      100

          40      50      60      70      80      89
m130 . pep  XAPRI-QGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFFNPDEAAP
          |||
a130        WAPRIAQGFDTLFQHALNGFNAMPAKGGAADLTDQELKRAITYMANKSGGSFFNPDEAAP
          110      120      130      140      150      160

          90      100      110      120      130      140
m130 . pep  ADNAASGTASAPADSAAPAEAKAEDKGAA-PAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          |||
a130        ADNAASGTASAPADSAAPAEAKAEDKGAAAPAVGVDGKKVFEATCQVCHGGSIPGIPGIG
          170      180      190      200      210      220

          150      160      170      180      190      200
m130 . pep  KKDDWAPRIKKGKETLHKHALEGFNAMPKXGNAGLSDDDEVKAAVDYMANQSGAKFX

```

a130  
KKDDWAPRIKKGKETLHKHALEGFNAMPAKGGNAGLSDDDEVKAAVDYMANQSGAKFX  
230 240 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 505>:

```
g132.seq
1  ATGGAAGCCT TCAAAACCCT AATTGGATT ATTAATATTA TTCCGCTTT
51  GGCCGTATC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACCTT CGGATCGGGA AGCGGCAGCG CGCAAGGCGT ATTCGGCTCT
151 GCCGGCAACG CCAACTTctt CAgccGCTCG AccGccGTTG CAGCAACAtt
201 tttctttGca acctgcAtgg gctatggTgt atattcacac CCACACGACA
251 AAACACGGTT TGGACTtcag caacataCGA CAGACTCAGC AagcACCCAA
301 ACCcgtAAGC AATACCGAAC CTTCTGCCCC TGTTCTCTAG CAGCAGAAAT
351 AACagtTTTT CAAATgccga caTGgtga
```

This corresponds to the amino acid sequence <SEQ ID 506; ORF 132.ng>:

g132.pep

```
1  MEAFKTLIWI INIISALAVI VLVLLQHGKG ADAGATFGSG SGSAQGVFGS
51  AGNANFLSRs TAAVATFFFA TCMGYGVYSH PHDKTRFGLQ QHTTDSASTQ
101 TRKQYRTFCP CSSAAEITVF QMPTW*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 507>:

```
m132.seq (partial)
1 ATGGAACCCCT TCAAAACCTT AATTTGGATT GTTAATTTAA TTTCCGCTTT
51 GGCCGTCTTC GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTT CGGA...
```

This corresponds to the amino acid sequence <SEQ ID 508; ORF 132>:

m132.pep (partial)  
1 MEPPFKTLIWI VNLISALAVF VLVLLQHGKG ADAGATFG...

**Computer analysis of this amino acid sequence gave the following results:**

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 132 shows 89.5% identity over a 38 aa overlap with a predicted ORF (ORF 132.ng) from *N. gonorrhoeae*:

```

m132/g132
      10      20      30
m132.pep  MEPPFKTLIWIIVNLISALAVFVLVLLQHKGKADAGATFG
          |||||||:|||||:|||||:|||||:|||||:
g132      MEAPFKTLIWIINIISALAVIVLVLLQHKGKADAGATFGSGSGSAQGVFGSAGNANFLSRS
          10      20      30      40      50      60

```

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 509>:

```

a132.seq
1  ATGGAAGCCT TCAAAACCCT AATTGGATT GTTAATATAA TTTCCGCTTT
51  GGCCGTATCT GTGTTAGTAT TGCTCCAACA CGGCAAAGGC GCGGATGCCG
101 GCGCGACTTC CGGATCGGGA AGCGGCAGCG CGCAAGCGTG ATTCCGGCTCT
151 GCGCGCAACG CTAACTTCCT CAGCCGCTCG ACCGCGGTG CAGCAACATT
201 TTTCTTTGCA ACCTGCATGg GCTATGGTGT ATATTACAC CCACACGACA
251 AAACACGGTT TGGACTTCAG CAACGTACAA CAAACTCAGC AAGCACCCAA
301 ACCCGTAAGC AATACCGAAC CTTCTGCCCC TGTTCTCAG CAGCAGAAAT
351 AACAGTTTTT CAAATGCCGA CATGGTGA

```

This corresponds to the amino acid sequence <SEO ID 510: ORF 132.a>:

a132.pep

1	MEAFKTLIWI	VNIISALAVI	VLVLLQHGKG	ADAGATFGSG	SGSAQGVFGS
51	AGNANFLSR	TAVAAFFFFA	TCMGYGVYSH	PHDKTRFGLQ	QRTTNSASTQ
101	TRKOYRTFCP	CSSAAEITVF	OMPTW*		

**m132/a132 92.1% identity in 38 aa overlap**

	10	20	30	
m132.pep	MEPFKTLIWIIVNLISALAVFVLVLLQHGKGADAGATFG			
	:     :			
a132	MEAFKTLIWIIVNIIISALAVIVLVLLQHGKGADAGATFGSGSGSAQGVFGSAGNANFLSRS			
	10	20	30	40 50 60

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 511>:

g134.seq

```

1 ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51 CATCTCCAC CCCGATGCGG GTAAAACCAC GCTGACCAG AAACCTGCTGC
101 TGTTTTCGGG CGCGATTCAA AGCGCAGGCA CGGTGAAAGG TAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTACAAAGAC CACACCGTCA
251 ACCTCTTGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTAACCG CAGTGGACAG CGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCGATA
401 CGCCGATTGT TACCTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCT
451 TTGGAACCTT TGGACGAAGT GGAAGACATC CTGCAATCC GCTGCGCGCC
501 CGTTACCTGG CCGATCGGTA TGGGCAAAAA CTTCAAGGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCCTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATAAAC AATCCCGAAT TGAACAACG
651 CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAATTTAAT CTCGacgaAT TTCTCGccgG CGAACTCACG
751 CCAGTGTCT TCGGCTCTGC GATTAAACAAC TTCGGCATTC AGGAAATCCT
801 CAATTCATTG ATTGACTGGG CACCCGCACC GAAACCGCGC GACGCGACCA
851 TGCGCATGGT CGGGCCGGAC GAGCCGAAAT TTTCCGATT TATCTTTAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATCG CCTTCTTGCG
951 CGTCTGCTCC GGTAAATTCG AGCGCGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTAG TAACCTTCAT GTCGCACGAC
1051 CGCGAAGTGG CGGAAGAAGC CTACGCCGGC GACATCATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTTACCGG CATCCCATTC TTGCGGCCCG AACTGTTCCG CAGCGTCCGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACTG CAAAAGGTT TGCAACAAC
1251 CGGCGAAGAA GGTGCGGTTC AAGTATTCAA ACCGATGAGC GGC GCGGATT
1301 TGATTTTGGG TGGCGTCCGC GTGTTGCAGT TTGAAGTCGT AACCTCACGC
1351 CTCGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAACTG GCGGAATTTG
1451 AAAAAGCCAA CGCAGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGG TTGACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAACA TTCGGTCAAA CTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 512; ORF 134.ng>:

g134.pep

```

1 MSQEILDQVR RRRTFAIISH PDAGKTLTE KLLLFSGAIQ SAGTVKGKKT
51 GKFATSDWMD IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREV RDS
151 LELLDEVEDI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDIIKGIN NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFPGSAINN FGIQEILNSL IDWAPAPKPR DATMRMVGPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351 RELAEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQLGEE GAVQVFKPMS GADLILGAVG VLOFEVTSR
451 LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTOERNPDIV FHETREHSVK L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 513>:

m134.seq

```

1 ATGTCCCAAG AAATCCTCGA CCAAGTGC GC CGCCGCCGCA CGTTTGCCAT
51 CATCTCCAC CCTGACGAG GTAAAACCAC GTTGACTGAA AAACCTTGC
101 TGTTTTCGGG CGCGATTCAAG AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACTTCCGA CTGGATGGAA ATCGAGAAGC AGCGCGGCAT

```

```

201  TTCGGTGGCA TCAAGTGTGA TGCAGTTCGA TTACAAAGAC CACACCGTCA
251  ACCTCTTGGA CACGCCGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301  GTTTTAACCG CCGTGGACAG CGCATTAAATG GTCATCGACG CGGCAAAGG
351  CGTGAAGCG CAAACCATCA AGCTCTTAAA CGTCTGCCGC CTGCGCGATA
401  CACCGATTGT TACGTTTATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451  CTGGAACTTT TGGACGAAGT GGAAAACATT TTAATAATCC GCTGCGCGCC
501  CGTTACCTGG CCGATCGGTA TGGGCAAAA CTTCAAGGGC GTGTACCACA
551  TCCTGAACGA TGAAATTTAT CTCTTTGAAG CTGGCGGCGA ACGCCTGCCG
601  CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCTGAAT TGGAACAACG
651  CTTTCCGTTG GAAATCCAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701  CGGCTTCCAA CGAGTTTAAT CTCGACGAAT TCCTCGCCGG CGAACTCAGC
751  CCCGTATTCT TCGGCTCTGC GATTAACAAC TTCGGTATTG AGGAAATCCT
801  CAATTCAATG ATTGACTGGG CGCCCGCGCC GAAACCGCGC GACGCGACCG
851  TACGTATGGT CGAGCCGAC GAGCCGAAGT TTTCGGGATT TATCTTCAAA
901  ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CTTTCTTGCG
951  CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAGATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCGGCC TCCAGCGTGG TTACCTTCAT GTGCGAGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGCG GACATTATCG GCATCCCGAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACCTG
1151 CGTTCACCGG CATCCCATTC TTCGCACCGG AACTGTTCCG CAGCGTACGC
1201 ATCAAAAACC CGCTGAAAAT CAAACAACCTG CAAAAGGCT TGCAACAGCT
1251 CGGCGAAGAA GCGCGGGTGC AGGTGTTCAA ACCGATGAGC GGCGCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTCGCCAACG AATACGGCGT AGAAGCCGTG TTCGACAGCG CATCCATCTG
1401 GTCGCGCGCG TGGGTATCGT GCGACGACAA GAAAAAAGT GCTGAATTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCAGGCGG CAACCTCGCC
1501 TACCTCGCCC CCAACCGCGT GAATTTGGGA CTCACGCAAG AACGTTGCC
1551 GGACATCGTG TTCCAGGAAA CACGCGAACA TTCGGTCAAA CTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 514; ORF 134>:

```

m134 . pep
1  MSQEILDQVR RRRRTFAIISH PDAGKTTLTE KLLLFSGAIQ SAGTVKGKKT
51  GKFATSDWME IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSEDYR
101  VLTAVDSALM VIDAAGVEA QTIKLLNVCR LRDTPIVTFM NKYDREVRDS
151  LELLDEVENI LKIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201  HEFDIIKGID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251  PVFFGSAINN FGIQEILNSL IDWAPAPKPR DATVRMVEPD EPKFSGFIFK
301  IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVTFMSHD
351  RELVEEAYAG DIIGIPNHGN IQIGDSFSEG EQLAFTGIPF FAPELFRSVR
401  IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451  LANEYGVAV FDSASIWSAR WVSCDDKKKL AEFKANAGN LAIDAGGNLA
501  YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 134 shows 98.7% identity over a 531 aa overlap with a predicted ORF (ORF 134.ng) from *N. gonorrhoeae*:

m134/g134

```

               10      20      30      40      50      60
m134 . pep  MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWME
              |||||
g134        MSQEILDQVRRRRRTFAIISHPDAGKTTLTEKLLLFSGAIQSAGTVKGKKTGKFATSDWMD
              |||||
               70      80      90     100     110     120
m134 . pep  IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGVEA
              |||||
g134        IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSEDYRVLTAVDLSALMVIDAAGVEA
              |||||
               70      80      90     100     110     120
               130     140     150     160     170     180

```

380

m134 . pep	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVENILKIRCAPVTWPIMGKKNFKG
g134	QTIKLLNVCRLRDTPIVTFMKNKYDREVRDSLELLLDEVEDILQIRCAPVTWPIMGKKNFKG
	130 140 150 160 170 180
m134 . pep	VYHILNDEIYLF EAGGERLPHEFDIIKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN
g134	VYHILNDEIYLF EAGGERLPHEFDIIKGINNPELEQRFPLEIQQLRDEIELVQAASNEFN
	190 200 210 220 230 240
m134 . pep	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPDEPKFSGFIFK
g134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATMRMVGPDPEPKFSGFIFK
	250 260 270 280 290 300
m134 . pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELVEEAYAG
g134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVTFM SHDRELAEAYAG
	310 320 330 340 350 360
m134 . pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIQQLQKGLQQLGEE
g134	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIQQLQKGLQQLGEE
	370 380 390 400 410 420
m134 . pep	GAVQVFKPMMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL
g134	GAVQVFKPMMSGADLILGAVGVQLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL
	430 440 450 460 470 480
m134 . pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
g134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX
	490 500 510 520 530

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 515>:

```

a134 . seq
1  ATGTCCCAAG AATCCTCGA CCAAGTGCGC CGCCGCCGCA CGTTTGCCAT
51  CATCTCCAC  CCTGACGCAG GTAAAACCAC GTTGACTGAA AAACCTCTGC
101 TGTTTTCAGG TGCATTCAA AGCGCGGGTA CGGTAAAAGG CAAGAAAACC
151 GGCAAATTCG CCACCTCCGA CTGGATGGAC ATCGAGAAGC AGCGCGGCAT
201 TTCCGTGGCA TCAAGCGTGA TGCAGTTCGA CTATAAAGAC CACACCGTCA
251 ACCTTTTGGA CAGCCCGGGA CACCAAGACT TCTCCGAAGA CACCTACCGC
301 GTTTTGACCG CCGTCGATAG TGCCTTGATG GTCATCGACG CGGCAAAAGG
351 CGTGGGAAGCG CAAACCATCA AACTCTTGAA CGTCTGCCGC CTGCGCAATA
401 CGCCGATTGT TACGTTTCATG AACAAATACG ACCGCGAAGT GCGCGATTCC
451 CTGGAATTGC TGGACGAAGT GGAAAACATC CTGCAAATCC GCTGCGCGCC
501 CGTAACCTGG CCGATCGGCA TGGGCAAAAA CTTCAAAGGC GTGTACCACA
551 TCCTGAACGA CGAAATCTAT CTCTTTGAAG CGGGCGGCGA ACGCTTGCCG
601 CACGAGTTCG ACATCATCAA AGGCATCGAT AATCCCGAAT TGAACAACG
651 CTTTCCGTTA GAAATACAGC AGTTGCGCGA CGAAATCGAA TTGGTGCAGG
701 CGGCTTCCAA CGAGTTCAAT CTCGACGAAT TCCTCGCCGG CGAACTCAGC
751 CCCGTATTCT TCGGCTCTGC GATTAAACAAC TTCGGTATTC AGGAAATCCT
801 CAATTCATTG ATTGAATGGG CGCCCGCGCC GAAACCACGC GATGCGACCG
851 TCGGTATGGT CGAGCCGGAC GAGCCGAAGT TTCCGGATT TATCTTCAAA
901 ATCCAAGCCA ATATGGACCC GAAACACCGC GACCGTATTG CCTTCTTGCG

```

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951 CGTCTGCTCC GGCAAATTCG AGCGCGGCAT GAAAATGAAA CACCTGCGTA
1001 TCAACCGCGA AATCGCCGCC TCCAGCGTGG TAACCTTCAT GTCCACACGAC
1051 CGCGAGCTGG TTGAAGAAGC CTACGCCGGC GACATTATCG GTATCCCAAA
1101 CCACGGCAAC ATCCAAATCG GCGACAGCTT CTCCGAAGGC GAACAACTGA
1151 CGTTTACCGG CATCCCATTG TTCGCGCCCG AACTGTTCCG CAGCGTTCGC
1201 ATCAAAAACC CGCTGAAAAT CAAGCAACTG CAAAAGGTT TGCAACAGCT
1251 TGGCGAAGAA GGTGCGGTGC AGGTGTTCAA ACCAATGAGC GGC GCGGATT
1301 TGATTTTGGG CGCGGTCGGC GTGTTGCAGT TTGAAGTCGT TACCTCGCGC
1351 CTTGCCAACG AATACGGCGT GGAAGCCGTG TTCGACAACG CATCCATCTG
1401 GTCGGCGCGC TGGGTATCGT GCGACGACAA GAAAAAAGT GCGGAATTTG
1451 AAAAAGCCAA CGCGGGCAAC CTCGCCATCG ACGCGGGCGG CAACCTCGCC
1501 TACCTCGCCC CTAACCGCGT GAATCTGGA CTACGCAAG AACGCTGGCC
1551 GGACATCGTG TTCCACGAAA CGCGCGAGCA TTCGGTCAA CTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 516; ORF 134.a>:

```

a134.pep
1 MSQEILDQVR RRTFAIISH PDAGKTTL TEKLLFSGAIQ SAGTVKGKKT
51 GK FATS DWM D IEKQRGISVA SSVMQFDYKD HTVNLLDTPG HQDFSED TYR
101 VLTAVDSALM VIDAAGVEA QTIKLLNVCRLRNTPIVTFM NKYDREVRDS
151 LELLDEVENI LQIRCAPVTW PIGMGKNFKG VYHILNDEIY LFEAGGERLP
201 HEFDI IKGID NPELEQRFPL EIQLRDEIE LVQAASNEFN LDEFLAGELT
251 PVFFGSAINN FGIQEILNSL IEWAPAPKPR DATVRMVEPD EPKFSGFIFK
301 IQANMDPKHR DRIAFLRVCS GKFERGMKMK HLRINREIAA SSVVT FMSHD
351 RELVEEAYAG DIIIGIPNHGN IQIGDSFSEG EQLTFTGIPF FAPELFRSVR
401 IKNPLKIKQL QKGLQQLGEE GAVQVFKPMS GADLILGAVG VLQFEVVTSR
451 LANEYGEAV FDNASIWSAR WVSCDDKKKL AEFEKANAGN LAIDAGGNLA
501 YLAPNRVNLG LTQERWPDIV FHETREHSVK L*

```

m134/a134 98.9% identity in 531 aa overlap

	10	20	30	40	50	60
m134.pep	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLFSGAIQSAGTVKGKKTGKFATS DWM					
a134	MSQEILDQVRRRTFAIISHPDAGKTTLTEKLLFSGAIQSAGTVKGKKTGKFATS DWM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m134.pep	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSED TYRVLTAVDSALMVIDAAGVEA					
a134	IEKQRGISVASSVMQFDYKDHTVNLLDTPGHQDFSED TYRVLTAVDSALMVIDAAGVEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m134.pep	QTIKLLNVCRLRDTPIVTFM NKYDREVRDSLELLDEVENILKIRCAPVTWP IGMGKNFKG					
a134	QTIKLLNVCRLRNTPIVTFM NKYDREVRDSLELLDEVENILQIRCAPVTWP IGMGKNFKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m134.pep	VYHILNDEIYLF EAGGERLPHEFDI IKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
a134	VYHILNDEIYLF EAGGERLPHEFDI IKGIDNPELEQRFPLEIQQLRDEIELVQAASNEFN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m134.pep	LDEFLAGELTPVFFGSAINNFGIQEILNSLIDWAPAPKPRDATVRMVEPD EPKFSGFIFK					
a134	LDEFLAGELTPVFFGSAINNFGIQEILNSLIEWAPAPKPRDATVRMVEPD EPKFSGFIFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m134.pep	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVT FMSHDRELVEEAYAG					
a134	IQANMDPKHRDRIAFLRVCSGKFERGMKMKHLRINREIAASSVVT FMSHDRELVEEAYAG					
	310	320	330	340	350	360

382

	370	380	390	400	410	420
m134 .pep	DIIGIPNHGNIQIGDSFSEGEQLAFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	:					
a134	DIIGIPNHGNIQIGDSFSEGEQLTFTGIPFFAPELFRSVRIKNPLKIKQLQKGLQQLGEE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m134 .pep	GAVQVFKPMSGADLILGAVGVLQFEVVT SRLANEYGV EAVFDSASIWSARWVSCDDKKKL					
	:					
a134	GAVQVFKPMSGADLILGAVGVLQFEVVT SRLANEYGV EAVFDNASIWSARWVSCDDKKKL					
	430	440	450	460	470	480
	490	500	510	520	530	
m134 .pep	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	:					
a134	AEFEKANAGNLAIDAGGNLAYLAPNRVNLGLTQERWPDIVFHETREHSVKLX					
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 517>:

g135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCG
51  TTCGGACgGC AGCCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCTG CAGGGTTCGG CGCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC TGCCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCGATTCCC ATCATCAATG
401 AAAACGACAC GGTTCGGTT GAGGAGTTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTTCGGC AAACGGCACG GGCGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATCGCCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCACTCAA ACCCGATTCA TTGGCCGAAG CCGCCGAACA TCAGGCGGAC
751 GGCTCGTTT TCGTcccCcg tgCCAAAGGT TTGCGGACAC AGAAGCAATG
801 GctggCGTTC TATTCCgaaa gcggGGgcag cgttTatgtg gacgaaagtg
851 cggaacacgc tTgtccgaa caagggaaag cctgCTGA

```

This corresponds to the amino acid sequence <SEQ ID 518; ORF 135.ng>:

g135.pep

```

1  MKYKRIVFKV GTSSITRSDG SLRSGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQORRAIP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIEM
201 AGSGSGSANGT GGMLTKIKAA TIAAESGVPV YICSSLKPDs LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESgGSVYV DESAEHALSE QGKAC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 519>:

m135.seq

```

1  ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCTGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCCGT CGGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCGCAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CGGCGCACTT TCCGTGCTGC TGCAACGCCG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGGTT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGCTGCT

```

```

501 GACCGACATA GACGGTCTTT ACACGGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCAGC GCGGGTATGC TGACCAAAAT
651 CAAAGCGGCA ACCATGCGCG CCGAATCCGG CGTACCGGTG TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTTGCCGAAG CTGCCGAACA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCCGAAA GCCGGGGCAG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGGAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TCCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCCC TGGGCAAAGG GCGCGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATCGCGTA AGGCGAAAGG CGTGTTTCATC
1051 CATCGGACG ACTGGATTTC CATCACGCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 520; ORF 135>:

```

m135.pep
  1 MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TCQLAALHHA GHELVLVSSG
 51 AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAPV IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGPNPS NPDAVRLDKI EHHINHEIEM
201 AGSGSGSANGT GGMLTKIKAA TIAESGVPV YICSSLKPDA LAEAAEHQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGSVYV DEGAEHALSE QGKSLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KSRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 135 shows 97.6% identity over a 294 aa overlap with a predicted ORF (ORF 135.ng) from *N. gonorrhoeae*:

m135/g135

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
g135	MKYKRIVFKVGTSSITRSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQIILSRADFADKRRYQNAGGAL					
g135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQIILSRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
m135.pep	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
g135	SVLLQRRAPVIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGPNPS					
	130	140	150	160	170	180
m135.pep	NPDAVRLDKIEHHINHEIEMAGSGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPDA					
g135	NPDAVRLDKIEHHINHEIEMAGSGSGSANGTGGMLTKIKAATIAESGVPVYICSSLKPD					
	190	200	210	220	230	240
m135.pep	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLMSGI					
g135	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESGSVYVDESAEHALSEQKACX					
	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESRGSVYVDEGAEHALSEQGKSLMSGI					
g135	LAEAAEHQADGSGFFVPRAKGLRTQKQWLAFYSESGSVYVDESAEHALSEQKACX					
	310	320	330	340	350	360



m135.pep

AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFSGAAAEDLLKSRKAKGVFIHRDDWISITP

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 521>:

a135.seq

```

1   ATGAAATACA AAAGAATCGT ATTTAAAGTC GGCACATCTT CGATTACCCA
51  TTCGGACGGC AGTCTCTCGC GCGGCAAAAT CCAAACCATC ACCCGCCAGC
101 TTGCCGCATT GCATCATGCG GGACACGAGC TGGTCTTGGT GTCTTCCGGC
151 GCGGTTGCGG CAGGGTTCGG TGCGCTGGGT TTCAAAAAC GTCCGGTCAA
201 AATCGCCGAC AAACAGGCTT CCGCCGCGGT CCGGCAGGGG CTGCTGATGG
251 AAGAATATAC GGCAAACCTG TCTTCAGACG GCATCGTGTC CGCACAAATC
301 CTGCTCAGCC GCGCCGACTT TGCCGACAAA CGCCGCTACC AAAATGCCGG
351 CCGCGCACTT TCCGTGCTGC TGCAACGCGG CGCCGTCCCC ATCATCAATG
401 AAAACGATAC GGTTCGCGT GAGGAATTGA AAATCGGCGA CAACGACACA
451 TTGAGTGCGC AAGTGGCGGC GATGATACAG GCAGACCTCT TGGTGTCTGT
501 GACCGACATA GACGGTCTTT ACACCGGCAA CCCGAACAGC AATCCCGATG
551 CCGTACGGCT GGACAAAATC GAACACATCA ACCATGAAAT CATCGAAATG
601 GCGGGCGGCT CGGGTTCGGC AAACGGCACA GCGGGTATGC TGACTAAAT
651 CAAAGCGGCG ACGATTGCGA CCGAGTCCGG CGTACCGGTC TATATCTGTT
701 CCTCGCTCAA ACCCGATGCA CTGCGGAAG CGGCAGATAA TCAGGCGGAC
751 GGCTCGTTTT TCGTCCCCCG TGCCAAAGGT TTGCGGACGC AGAAGCAATG
801 GCTGGCGTTC TATTCGAAA GCAGGGGCGG CGTTTATGTG GACGAAGGTG
851 CGGAACACGC TTTGTCCGAA CAGGGAAAAA GCCTGCTGAT GTCGGGCATT
901 GCCGGAATCG AAGGGCATT TTTCCGTATG GACACCGTAA CCGTGTACAG
951 CAAGGCAACC AAACAGCCTT TGGGCAAAGG GCGAGTCCTG TTCGGCTCTG
1001 CCGCCGCCGA AGACCTGCTC AAATTGCGTA AGGCGAAAGG CGTGTTCATC
1051 CATCGGGACG ACTGGATTTC CATCACGCCC GAAATACGCC TGCTTCTGAC
1101 CGAATTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 522; ORF 135.a>:

a135.pep

```

1   MKYKRIVFKV GTSSITHSDG SLSRGKIQTI TRQLAALHHA GHELVLVSSG
51  AVAAGFGALG FKKRPVKIAD KQASAAVGQG LLMEEYTANL SSDGIVSAQI
101 LLSRADFADK RRYQNAGGAL SVLLQRRAVP IINENDTVSV EELKIGDNDT
151 LSAQVAAMIQ ADLLVLLTDI DGLYTGNPNS NPDAVRLDKI EHNHEIEM
201 AGSGSANGT GGMLTKIKAA TIATESGVFV YICSSLKPDA LAEADNQAD
251 GSFFVPRAKG LRTQKQWLAF YSESRGGVYV DEGAERHALSE QGKSLLMSGI
301 AGIEGHFSRM DTVTVYSKAT KQPLGKGRVL FGSAAAEDLL KLRKAKGVFI
351 HRDDWISITP EIRLLLTEF*

```

m135/a135 98.4% identity in 369 aa overlap

	10	20	30	40	50	60
m135.pep	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITCQLAALHHAGHELVLVSSGAVAAGFGALG					
a135	MKYKRIVFKVGTSSITHSDGSLSRGKIQTITRQLAALHHAGHELVLVSSGAVAAGFGALG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m135.pep	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
a135	FKKRPVKIADKQASAAVGQGLLMEEYTANLSSDGIVSAQILLRADFADKRRYQNAGGAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m135.pep	SVLLQRRAVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
a135	SVLLQRRAVPIINENDTVSVEELKIGDNDTLSAQVAAMIQADLLVLLTDIDGLYTGNPNS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m135.pep	NPDAVRLDKIEHNHEIEMAGSGSANGTGGMLTKIKAATIAESGVFVYICSSLKPDA					
a135	NPDAVRLDKIEHNHEIEMAGSGSANGTGGMLTKIKAATIAESGVFVYICSSLKPDA					
	190	200	210	220	230	240

385

	250	260	270	280	290	300
m135.pep	LAEAAEHQADGSFFVPRAKGLRTQKQWLAFYSESRGVSYYVDEGAEHALSEQGKSLMSGI					
a135	LAEAADNQADGSFFVPRAKGLRTQKQWLAFYSESRGGVYVDEGAEHALSEQGKSLMSGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m135.pep	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAAEDLLKSRKAKGVFIHRDDWISITP					
a135	AGIEGHFSRMDTVTVYSKATKQPLGKGRVLFGSAAAEDLLKLRKAKGVFIHRDDWISITP					
	310	320	330	340	350	360
	370					
m135.pep	EIRLLLTEFX					
a135	EIRLLLTEFX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 523>:

g136.seq

```

1  ATGGAAATCC GGTTCAGAC AGCATTTTTC CGTTTGGTTC AGatgAAAC
51  AAACGCTtca aTCTTaccg caACACGCCT TGTATTTCCT GccgCTGCCG
101 CACGGACAGG GATCGTTCCT GCCGgtTTTT TCCCCTTCCC TGCGGACGGT
151 TTGCGGTTTG TTGATGACCG CCTGCCAGTA GCGGTAGATG Tctgccagcg
201 cgTAAGGcag tTCGGAcgca agttccgcca gctcgcttc ggTGAATTGC
251 AGgcgataa cgccgtttTC CTCTCGTCg taaatgccgc ccactgccat
301 cacgGGGTAA AACAGCTCTT CAAACGCTTC ATCATCGGCG GCTTCAAACC
351 AATCGGTCGG CACAATGTCC AAACCGTAAA GATAGGCGTT GCACCAAGTG
401 TAAAAATCGC TGCCGCCCTC GCCGTCGTCG TAGAGCCACA AATCGGGCAG
451 CTTTTTATCC GACATCGCGG CGGTTGTTTC CATCGCCATT GCCAAAACCA
501 GCCGTTTCGAT TCGGAACGT TCGGCGGCGG TAAATTGCGA TTCGTCGCCC
551 AACACTTCGG GCAGCCAGTC GAGCGGTGCC AATTGTCCG GCCCGCTCAA
601 CAGCGCCGTC ATAAACCTT GAACCTCGTC GCAACGCATC GTGTTGCCTT
651 GTTCGCTTTT GGCATCCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 524; ORF 136.ng>:

g136.pep

```

1  MEIRFQTAFL RLVQMKTNAS ILTATRLVFP AAAARTGIVP AGFFPPPADG
51  LRFVDDRLPV AVDVCQVRVQ FGRKFRQLAF GELQADNAVF LfVVNAAHCH
101 HGVKQLFKRF IIGGFKPIGR HNVQTVKIGV APSVKIAAAL AVVVEPQIGQ
151 LFIRHRGGCF HRHCQNQPF DFGTFGGGKLR FVAQHFGQPV ERCQFVRPAQ
201 QRRHKTNLV ATHRVALFAF GIQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 525>:

m136.seq

```

1  ATGGAAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC
51  CGCTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTTTC GCCTTCCCTG
101 CGGACGGTTT GCGGTTTGTG GATGACTGCC TGCCAGTAGC GGTAGATATC
151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCTTCTG
201 TGAATTGCAG ACGGATAGCG CCGTTTTCTT CTTCGTCGTA AATACCGCCC
251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC
301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC
351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTTCATA CAGCCACAAA
401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTTCCA TCGCCATTGC
451 CAAAACACAG CGTTCGATT CCGAACGTTT GCGGCGGTA AATTGCGATT
501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC
551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT
601 GTTGCTTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG
651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTTT CAAATGGGTT
701 TTGCGCCCTA TTATCGCCGC AATGCCGTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 526; ORF 136>:

386

m136.pep  
 1 METNASILTA TRLVFSAAAA RTGIVPACFF AFPADGLRFV DDCLPVAVDI  
 51 RQCIRQLGFQ FRQLAFCELQ TDSAVFLFVV NTAQCHDGIK QLFKRFIIDG  
 101 FKPIGRHNIQ TVKISIAPCV KIAAAVFVFI QPQIGQFFIR HRGGCFHRHC  
 151 QNQPFDFGTF GGGKLRFVAQ HFGQPVERCQ FVRPAQQRH KTLNLVATHR  
 201 VALFAFGIQQ FAQPPFGCFG KFSGIHHFPF QMGFAPYYRR NAV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 136 shows 85.6% identity over a 209 aa overlap with a predicted ORF (ORF 136.ng) from *N. gonorrhoeae*:

m136/g136

	10	20	30	40
m136.pep	METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPV			
g136	MEIRFQTAFRLRLVQMKTNASILTATRLVFPAAAARTGIVPAGFFFPFADGLRFVDDRLPV			
	10	20	30	40
	50	60	70	80
m136.pep	AVDIRQCIRQLGFQFRQLAFCELQ TDSAVFLFVVNTAQCHDGIKQLFKRFIIDGFKPIGR			
g136	AVDVCQVRVQFGRKFRQLAFGELQADNAVFLFVVNAACHHGKQLFKRFIIGGFKPIGR			
	70	80	90	100
	110	120	130	140
m136.pep	HNIQTVKISIAPCVKIAAAVFVFIQPQIGQFFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
g136	HNVQTVKIGVAPSVKIAAALAVVVEPQIGOLFIRHRGGCFHRHCQNQPFDFGTFGGGKLR			
	130	140	150	160
	170	180	190	200
m136.pep	FVAQHFGQPVERCQFVRPAQQRHKTNLVATHRVALFAFGIQQFAQPPFGCFGKFSGIH			
g136	FVAQHFGQPVERCQFVRPAQQRHKTNLVATHRVALFAFGIQX			
	190	200	210	220
	230	240		
m136.pep	HFPFQMGFAPYYRRNAVX			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 527>:

a136.seq  
 1 ATGGAACAA ACGCTTCAAT TCTTACCGCA ACACGCCTTG TATTTTCTGC  
 51 CGTGCCGCA CGGACAGGGA TCGTTCCTGC CTGTTTTC TCCTCCCTG  
 101 CGGACGGTT GCGGCTTGT GATGACCGCC TGCCAGTAGC GGTAGATATC  
 151 CGCCAATGCA TAAGGCAACT CGGATTCCAG TTCCGCCAGC TCGCCTTCTG  
 201 TGAATTGCAG ACGGATAGTG CCGTTGTCCT CTTGTCGTA AATACCGCCC  
 251 AATGCCATGA TGGGATAAAA CAACTCTTCA AACGCTTCAT CATCGACGGC  
 301 TTCAAACCAA TCGGTCGGCA CAATATCCAA ACCGTAAAGA TAAGCATTGC  
 351 ACCATGTGTA AAAATCGCTG CCGCCGTCTT CGTTTTATA CAGCCACAAA  
 401 TCGGGCAGTT TTTTATCCGA CATCGCGGCG GTTGTTCCTA TCGCCATTGC  
 451 CAAAACCAGC CGTTCGATT CGGAACGTT GCGGCGGTA AATTGCGATT  
 501 CGTCGCCCAA CACTTCGGGC AGCCAGTCGA GCGGTGTCAA TTTGTCCGGC  
 551 CCGCTCAACA GCGCCGTCAT AAAACCTTGA ACCTCGTCGC AACGCATCGT  
 601 GTTGCCTTGT TCGCTTTTGG CATCCAACAA TTCGCTCAAC CGCCGTTTGG  
 651 ATGCTTCGGT AAATTTTCGG GAATCCATCA TTTTCCTTT CCAATGGGTT  
 701 TTGCGCCCTA TTATAGTGGA TTAAATTAA ATCAGGACAA GGCGACGAAG  
 751 CCGCAGACAG TACAAATAGT ACGGCAAGGC GAGGCAACGC CGTACTGGTT  
 801 TAAATTTAAT CCACTATATC GCCGCAATGC CGTCTGA

This corresponds to the amino acid sequence <SEQ ID 528; ORF 136.a>:

a136.pep

```

1  METNASILTA  TRLVFSAAAA  RTGIVPACFF  AFPADGLRLV  DDRLPVAVDI
51  RQCIRQLGFQ  FRQLAFCELO  TDSAVVLFV  NTAQCHDGIK  QLFKRFIIDG
101 FKPIGRHNIQ  TVKISIAPCV  KIAAAVFVFI  QPQIGQFFIR  HRGGCFHRHC
151 QNQPFDFGTF  GGGKLRFVAQ  HFGQPVERCQ  FVRPAQORRH  KTLNLVATHR
201 VALFAFGIOQ  FAQPPFGCFG  KFSGIHHFPF  PMGFAPYYS  LNLNQDKATK
251 PQTQVIVRQG  EATPYWFKFN  PLYRRNAV*

```

m136/a136 98.3% identity in 238 aa overlap

```

          10      20      30      40      50      60
m136.pep  METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRFVDDCLPVAVDIRQCIRQLGFQ
          |||
a136      METNASILTATRLVFSAAAAARTGIVPACFFAFPADGLRLVDDRLLPVAVDIRQCIRQLGFQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m136.pep  FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          |||
a136      FRQLAFCELOTD SAVVLFVVNTAQCHDGIKQLFKRFIIDGFKPIGRHNIQTVKISIAPCV
          70      80      90     100     110     120

          130     140     150     160     170     180
m136.pep  KIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
          |||
a136      KIAAAVFVFIQ P QIGQFFIRHRGGCFHRHCQNQPFDFGTGGGKLRFVAQHFGQPVERCQ
          130     140     150     160     170     180

          190     200     210     220     230     240
m136.pep  FVRPAQORRHKT LNLVATHRVALFAFGIOQFAQPPFGCFGKFSGIHHFPFQMGFAPYYRR
          |||
a136      FVRPAQORRHKT LNLVATHRVALFAFGIOQFAQPPFGCFGKFSGIHHFPFPMGFAPYYSG
          190     200     210     220     230     240

m136.pep  NAVX
a136      LNLNQDKATKPQTQVIVRQGEATPYWFKFNPLYRRNAVX
          250     260     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 529>:

```

g137.seq
1  ATGATTATCC  ATCACcaATT  CGATCCCGTC  CTCATCAGTA  TCGGCCCGCT
51  TGCCGTCCGC  TGGTATGCCT  TAAGCTACAT  CCTCGGATTT  ATTCTTTTTA
101 CCTTCTCGG  CAGAAGGCGC  ATCGCGCAAG  GCTTGTCGGT  TTTTACCAAA
151 GAATCGCTCG  ACGACTTCCT  GACATGGGGC  ATTTTGGGCG  TGATTTTGGG
201 CGGACGCTTG  GGCTATGTCC  TGTTTTACAA  ATTCTCCGAC  TACCTCGCCC
251 ATCCGCTTGA  TATTTTCAAG  GTATGGGAAG  GCGGAATGTC  GTTCCACGGC
301 GGCTTTTGG  GTGTAGTIAT  TGCCATATGG  TTGTTAGCC  GCAAGCACGG
351 CATCGGCTTC  CTCAAACCTGA  TGGACACGGT  CGCGCCGCTC  GTTCCGCTGG
401 GTCTCGCTTC  GGGACGTATC  GGCAACTTTA  TCAACGGCGA  ACTTTGGGGA
451 CGCATTACCG  ACATTAAACGC  ATTTTGGGCA  ATGGGCTTCC  CGCAAGCCCA
501 TTACGAAGAT  GCCGAAGCCG  CCGCGCACAA  TCCGCTTTGG  GCAGAATGGC
551 TGCAACAATA  CGGTATGCTG  CCGCGTCATC  CCTCGCAGCT  TTATCAGTTT
601 GCCCTTGAAG  GCATCTGCCT  GTTCGCCGTC  GTTTGGCTGT  TTTCCAAAAA
651 ACCGCGCCCG  ACCGGGCAGA  CTGCCGCGCT  TTTTCTCGGC  GGCTACGGCG
701 TGTTCGCTT  TATTGCGGAA  TTTGCGCGCC  AACCCGACGA  CTATCTCGGG
751 CTGCTGACCT  TGGGGCTGTC  GATGGGGCAA  TGGTTGAGCG  TCCCAGATGAT
801 TGTTTGGGT  ATCGTCGGCT  TTGTCGGTT  CGGCATGAAA  AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 530; ORF 137.ng>:

g137.pep

```

1  MIIHHQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIW LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RITDINAFWA MGFPQAHYED AAAAAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFAV VWLFSSKKPRP TGQTAALFLG GYGVFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 531>:

m137.seq

```

1  ATGATTACCC ATCCCAATT CGATCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCG TAAGCTACAT CCTCGGATT ATTCTTTTGA
101 CCTTCTCCG CAGAAAGCGC ATCGCGCAAG GCTTGTCCGT TTTTACAAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC ATTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGG GTGTAGTTAT TGCCATACGG TTGTTCGGCC GCAAACACGG
351 CATCGGCTTC CTCAAACTGA TGGATACGGT CGCACCGCTC GTTCCGCTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAT CCGGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGAATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGCT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTACCGTTC ATTTGGCTGT TCTCTAAAAA
651 ACAGCGGTCG ACCGGACAAG TCGCCTCGCT CTTCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTCGCACGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCCGGTT CGGCATGAAA AAACAGCACT
851 GA

```

This corresponds to the amino acid sequence <SEQ ID 532; ORF 137>:

m137.pep

```

1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTK
51  ESLDDFLTGW ILGVILGGRL GYVLFYKFSY YLAHPLDIFK VWEGGMSFHG
101 GFLGVVIAIR LFSRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINGELWG
151 RVTDINAFWA MGFPQARYED AAAAAHNPLW AEWLQOYGML PRHPSQLYQF
201 ALEGICLFTV IWLFSKKQRS TGQVASLFLG GYGVFRFIAE FARQPDYDLG
251 LLTLGLSMGQ WLSVPMIVLG IVGFVRFGMK KQH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 137 shows 95.4% identity over a 283 aa overlap with a predicted ORF (ORF 137.ng) from *N. gonorrhoeae*:

m137/g137

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
g137	MIIHHQFDPVLISIGPLAVRWYALSYILGFILFTFLGRRRIAQGLSVFTKESLDDFLTGW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m137.pep	ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIRLFSRKHGIGF					
g137	ILGVILGGRLGYVLFYKFSYLAHPLDIFKVWEGGMSFHGGFLGVVIAIWLFSRKHGIGF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m137.pep	LKLMDTVAPLVPLGLASGRIGNFINGELWGRVTDINAFWAMGFPQARYEDAAAAHNPLW					
g137	LKLMDTVAPLVPLGLASGRIGNFINGELWGRI TDINAFWAMGFPQAHYEDAAAAHNPLW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m137.pep	AEWLQOYGMLPRHPSQLYQFALEGICLFTVIWLFSKKQRSTGQVASLFLGGYGVFRFIAE					

```

a137.seq
1  ATGATTACCC ATCCCCAATT CGACCCCGTC CTTATCAGTA TCGGCCCGCT
51  TGCCGTCCGC TGGTATGCCC TAAGCTACAT CCTCGGATTA ATTCCTTTTA
101 CCTTTCTCGG CAGAAGCGCG ATCGCGCAAG GCTTGTCCGT TTTTACCAA
151 GAATCGCTCG ACGACTTCCT GACATGGGGC GTTTTGGGCG TAATTTTGGG
201 CGGGCGTTTG GGTTACGTCC TGTTTTACAA GTTTTCCGAC TACCTCGCCC
251 ATCCGCTTGA TATTTTCAAG GTATGGGAAG GCGGAATGTC GTTCCACGGC
301 GGCTTTTGGG GTGTAGTTAT TGCCATATGG TTGTTCCGGT GCAAACACGG
351 CATCGGCTTC CTCAACTGA TGGACACGGT CGCACCCTGC GTTCCACTGG
401 GTCTCGCTTC GGGACGTATC GGCAACTTCA TCAACGGCGA ACTTTGGGGA
451 CGCGTTACCG ACATCAACGC ATTTTGGGCA ATGGGCTTCC CGCAGGCGCG
501 TTACGAAGAC CTCGAAGCCG CCGCGCACAA TCCGCTTTGG GCAGATGGC
551 TGCAACAATA CGGTATGCTG CCGCGTCATC CCTCGCAGT TTATCAGTTT
601 GCACTTGAAG GCATCTGCCT GTTCGCGCTC GTTTGGCTGT TCTCTAAAA
651 ACAGCGGGCG ACCGGACAAG TCGCCTCACT CTTCTCGGC GGCTACGGCA
701 TATTCCGCTT CATTGCCGAA TTTGCAGGCC AACCCGACGA CTATCTCGGG
751 CTGCTGACCT TGGGGCTGTC GATGGGGCAA TGGTTGAGCG TCCCGATGAT
801 TGTTTTGGGT ATCGTCGGCT TTGTCGGGTT CGGCATGAAA AAACAGCACT
851  GA

```

```

a137.pep
1  MITHPQFDPV LISIGPLAVR WYALSYILGF ILFTFLGRRR IAQGLSVFTTK
51  ESLDDFLTWG ILGVILGGRL GYVLFYKFS D YLAHPLDIFK VWEGGSFHHG
101 GFLGVVIAIW LFGRKHGIGF LKLMDTVAPL VPLGLASGRI GNFINDELWG
151 RVTDINAFWA MGFPQARYD LEAAAHNPLW AEWLQQYQML PRHPSQLYQF
201 ALEGICLFAV WLSFSKKQRP TQGVASLFLG GYGFIRFIAE FARQPDDYLG
251 LTLGLSMGQ VWSVPMIVLG IGVFVRFGMK KGH*

```

	10	20	30	40	50	60
m137.pep	MITHPQFDPVLISIGPLAVRWYALS YILGFILEFTFLGRRRIAQGLSVFTKESLDDFLTGWG					
a137	MITHPQFDPVLISIGPLAVRWYALS YILGFILEFTFLGRRRIAQGLSVFTKESLDDFLTGWG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m137.pep	ILGVILGGRLGYVLFYKFS DYLAHPLDIFK VWEGGMSFHGGFLGVVIAIRLFG RKHGIGF					
a137	ILGVILGGRLGYVLFYKFS DYLAHPLDIFK VWEGGMSFHGGFLGVVIAIWLFGRKHGIGF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m137.pep	LKLMDTVAPLVP LGLASGRIGNFINGELWGRVTDINAFWAMGF PQARYEDAEAAAHNPLW					
a137	LKLMDTVAPLVP LGLASGRIGNFINGELWGRVTDINAFWAMGF PQARYEDLEAAAHNPLW					
	130	140	150	160	170	180
	190	200	210	220	230	240
m137.pep	AEWLQQYGMLPRHPSQLYQFALEGICLFTVIWLF SKKQ RSTGQVASLFLGGYGIFRFIAE					
a137	AEWLQQYGMLPRHPSQLYQFALEGICLFAVWVLF SKKQ RPTGQVASLFLGGYGIFRFIAE					

	190	200	210	220	230	240
	250	260	270	280		
m137 . pep	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQH	X				
a137	FARQPDDYLGLLTLGLSMGQWLSVPMIVLGIVGFVRFGMKKQH	X				
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 535>:

```

g138.seq
1  ATGGAGTTTG AAAACATTAT TTCCGCCGCC gaCAAGGCGC GTATCCTTGC
51  CGAAGCACTG CCTTACATcc gccgGTTTTC CGGTTCCGTC GCCGTCATCA
101 AGTATGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GCGAATTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGAC GATGGATATT
301 GTCGAAATGG TATTGGGCGG GCACGTCAAC AAGGAAATCG TGTCGATGAT
351 TAACACATAT GGAGGGCACG CGGTCGGCGT GAGCGGGCGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGGTCGATA CGCCCGAACA GAATAGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGCGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 TTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT GGCAGGCAAA
601 TTGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAAtatcgc
651 cgGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC acgCCGAAAC
701 GGATTGATGG GCTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCcgccgtc aACGGTGTGA AAGCCACGCA
801 CATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGGTCGATG ATTTTAGGCA GAGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 536; ORF 138.ng>:

```

g138.pep
1  MEFENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKETMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LVDTPEQNSV
151 DIGQVGTVES IDTGLVKGLI ERGCI PVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMMTNIAGVM DKTGNLLTKL TPKRIDGLIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGRGEDA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 537>:

```

m138.seq
1  ATGGAGTCTG AAAACATTAT TTCCGCCGCC GACAAGGCGC GTATCCTTGC
51  CGAAGCGCTG CCTTACATCC GCCGGTTTTC CGGTTCCGTC GCCGTCATCA
101 AATACGGCGG CAACGCGATG ACCGAACCTG CCTTGAAAGA AGGGTTTGCC
151 CGCGATGTCG TGCTGCTGAA GCTGGTCGGC ATTCATCCCG TCATCGTTCA
201 CGGCGGCGGG CCGCAGATCA ATGCGATGCT TGAAAAAGTC GGCAAAAAGG
251 GTGAGTTTGT CCAAGGAATG CGCGTTACCG ACAAAGAGGC GATGGATATT
301 GTCGAAATGG TGTGGGCGG GCATGTCAAT AAAGAAATCG TGTCGATGAT
351 TAACACATAT GGCGGACACG CGGTCGGCGT AAGCGGACGC GACGACCATT
401 TCATTAAGGC GAAGAACTT TTGATCGATA CGCCCGAACA GAATGGCGTG
451 GACATCGGAC AGGTCGGTAC GGTGGAAGC ATCGATACCG GTTTGGTTAA
501 AGGGCTGATA GAACGTGGCT GCATTCCCGT CGTCGCCCCC GTCGGCGTAG
551 TTGAAAAAGG CGAAGCGTTC AACATCAACG CCGATTGGT AGCAGGCAAA
601 GTGGCGGAAG AATTGAACGC CGAAAACTC TTGATGATGA CGAATATCGC
651 CGGTGTGATG GACAAAACGG GCAATCTGCT GACCAAATC ACGCCGAAAC
701 GGATTGATGA ACTGATTGCC GACGGCACGC TGTATGGCGG TATGCTGCCG
751 AAAATCGCTT CTGCGGTCGA AGCCGCGGTC AACGGTGTGA AAGCCACGCA
801 TATCATCGAC GGCAGGTTGC CCAACGCGCT TTTGCTGGAA ATCTTTACCG
851 ATGCCGGTAT CGGTTGATG ATTTTGGGCG GTGGGGAAGA TGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 538; ORF 138>:

```

m138.pep
1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA

```

```

51  RDVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDKAEMDI
101 VEMVLGGHVN KEIVSMNTYV GGHAVGVSGR DDHFIAKAKKL LIDTPEQNGV
151 DIGQGVGTVES IDTGLMNGLI ERGCI PVVAV VGVGKEGEAF NINADLVAGK
201 LAELNAEKL LMTNTIAGVM DKGTNLLTKL TPKRIDELIA DGTLYGGMPL
251 KIASAVEAAV NGVKATHIID GRLPNALLLE IFTDAGIGSM ILGGGDA*

```

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 138 shows 98.0% identity over a 298 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

m138/g138

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
g138	MEFENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGKKGEFVQGMRVTDKEAMDIVEMVLGGHVNKEIVSMINTY					
g138	IHPVIVHGGGPQINAMLEKVGKKGEFVQGMRVTDKETMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
g138	GGHAVGVSGRDDHFIKAKLLVDTPQNSVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLLMMTNIAGVMDKTGNLLTKLTPKRIDELIA					
g138	VGVGEKGEAFNINADLVAGKLAELNAEKLLMMTNIAGVMDKTGNLLTKLTPKRIDGLIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMPLPKIASAVEAAVGVKATHIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
g138	DGTLYGGMPLPKIASAVEAAVGVKATHIDGRLPNALLLEIFTDAGIGSMILGRGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 539>:

**a138.seq**

1	ATGGAGTCTG	AAAACATTAT	TTCGCGCGCC	GACAAGCGCG	GTATCCTTGC
51	CGAAGCGCTG	CCTTACATCC	GCCGGTTTTC	CGGTTGCGTC	GCCGTCATCA
101	AATACGGCGG	CAACGCGATG	ACCGAACTTG	CCTTGAAAGA	AGGGTTTGCC
151	CGCGATGTGG	TGCTGCTGAA	GCTGGTCGCG	ATTTCATCCG	TCATCGTTCA
201	CGCGCGCGGG	CGCGAGATCA	ATGCGATGCT	TGAAAAAGTC	GGCAAAAAAGG
251	GTGAGTTTGT	CCAAGGAATG	CGCGTTACCG	ACAAAGAGGC	GATGGATATT
301	GTGAAATGG	TGTTGGGCGG	GCATGTCAAT	AAAGAAATCG	TGTCGATGAT
351	TAACACATAT	GGCGGACACG	CGGTCGGCGT	AAGCGGACGC	GACGACCATT
401	TCAATTAAGC	GAAGAAACTT	TTGATCGATA	CGCCCCAACA	GAATGGCGTG
451	GACATCGGAC	AGGTCCGTAC	GGTGGAAGAAG	ATCGATACCG	GTTTGGTTAA
501	AGGCGTGATA	GAACGTGGCT	GCATTTCCCGT	CGTCGCCCCC	GTCGGCGTAG
551	GTGAAAAAGG	CGAAGCGTTC	AACATCAACG	CGGATTTGGT	AGCAGGCAAA
601	TTGGCGGAAG	AATTGAACGC	CGAAAAACTC	TTGATGATGA	CGAATATCGC
651	CGGTGTGATG	GACAAAACGG	GCAATCTGCT	GACCAAACCT	ACGCCGAAAC
701	GGATTGATGA	ACTGATTGCC	GACGGCAGCG	TGTATGGCGG	TATGCTGCCG
751	AAATATCGTT	CTCGGTCGA	AGCGCCCGTC	AAGCGCGTGA	AATCTTACCG
801	TATCATCGAC	GGCAGGGTGC	CCAACGCGCT	TTTGCTGGAA	ATCTTTACGA
851	ATGCCGGTAT	CGGTTGATG	ATTTTGGGCG	GTGGGGAAGA	TGCCTGA



This corresponds to the amino acid sequence <SEQ ID 540; ORF 138.a>:

```
a138.pep
1  MESENIISAA DKARILAEAL PYIRRFSGSV AVIKYGGNAM TEPALKEGFA
51  RDVVLLKLVG IHPVIVHGGG PQINAMLEKV GKKGEFVQGM RVTDEAMDI
101 VEMVLGGHVN KEIVSMINTY GGHAVGVSGR DDHFIKAKKL LIDTPEQNGV
151 DIGQVGTVES IDTGLVKGLI ERGCIPVVAP VGVGEKGEAF NINADLVAGK
201 LAEELNAEKL LMTNIAAGVM DKTGNLLTKL TPKRIDELIA DGTLYGGMLP
251 KIASAVEAAV NGVKATHIID GRVPNALLLE IFTDAGIGSM ILGGGEDA*
```

m138/a138 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m138.pep	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
a138	MESENIISAADKARILAEALPYIRRFSGSVAVIKYGGNAMTEPALKEGFARDVVLLKLVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m138.pep	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDEAMDIVEMVLGGHVNKEIVSMINTY					
a138	IHPVIVHGGGPQINAMLEKVGGKGEFVQGM RVTDEAMDIVEMVLGGHVNKEIVSMINTY					
	70	80	90	100	110	120
	130	140	150	160	170	180
m138.pep	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
a138	GGHAVGVSGRDDHFIKAKKLLIDTPEQNGVDIGQVGTVESIDTGLVKGLIERGCIPVVAP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m138.pep	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAAGVMDKTGNLLTKLTPKRIDELIA					
a138	VGVGEKGEAFNINADLVAGKLAELNAEKLMMTNIAAGVMDKTGNLLTKLTPKRIDELIA					
	190	200	210	220	230	240
	250	260	270	280	290	299
m138.pep	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRLPNALLLEIFTDAGIGSMILGGGEDAX					
a138	DGTLYGGMLPKIASAVEAAVNGVKATHIIDGRVPNALLLEIFTDAGIGSMILGGGEDAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 541>:

```
g139.seq
1  ATGCGAACCA CCTCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
51  GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAggc ggcggcggag
101 gcGGCACTTC TGCTCCCGAC TTTAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACGATAGC GGAATCAGCA GCAGTATCTT ACGCCGGTAT
201 AAAAAACGAA ATGTGCAAG ACAGAAGCAT GCTCTGTGCC GGTCCGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAAAGCCCC CCGAATCTGC
301 ATACCGGAGA CTTTTCAAAC CCAAATGACC AATATTAAGA ATATGATCAA
351 CCTCAAACCT GCAATTGAAG CAGGCTATAC AGGACGCGGG GTAGAGGTAG
401 GTATCGTCGA TACAGGCGAA TCCGTCGGCA GCATATCCTT TCCCGAAGT
451 TATGGCAGAA AAGAACACGG CTATAACGAA AATTACAAAA ACAAAATTACA
501 AAAACTATAC GCGGTATATG CGGAAGGAAG CGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 542; ORF 138.ng>:

```
g139.pep
1  MRTTSTFPTK TFKPAAMALA VATTLSACLG GGGGTSAPD FNAGGTGIGS
51  NSRATIAESA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKIKAPRIC
101 IPETFQTQMT NIKNMINLKP AIEAGYTGRG VEVGIVDTGE SVGSISFPPEL
151 YGRKEHGYNE NYKNKLQKLY GVYAEGSA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 543>:

```
m139.seq
  1 ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGACTGCCAT
 51 GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGTACCGG TATCGGCAGC
151 AACAGCAGAG CAACAACAGC GAAATCAGCA GCAGTATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTGCGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCAGAAC
301 TGCATACCGG AGACTTTCCA AACCCAAATG ACGCATACA AGAATTTGAT
351 CAACCTCAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTACG AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 544; ORF 138>:

```
m139.pep
  1 MRTTPTFPTK TFKPTAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
 51 NSRATTAKSA AVSYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI
101 CIPETFTQTM THYKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSI SFPE
151 LYGRKEHGYN ENYEKLYGVY AEGSA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 138 shows 92.2% identity over a 179 aa overlap with a predicted ORF (ORF 138.ng) from *N. gonorrhoeae*:

```
m139/g139
      10      20      30      40      50      60
m139.pep MRTTPTFPTKTFKPTAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA
g139      MRTTSTFPTKTFKPAAMALAVATTLSACLGGGGGTSAPDFNAGGTGIGSNSRATIAESA
      10      20      30      40      50      60
      70      80      90     100     110     120
m139.pep AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFTQTMTHYKNLINLK
g139      AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKIKAP-RICIPETFTQMTNINKMINLK
      70      80      90     100     110
      130     140     150     160     170
m139.pep PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENY----EKLYGVYAEGSAX
g139      PAIEAGYTGRGVEVGIVDTGESVGSISFPPELYGRKEHGYNENYKNKLQKLYGVYAEGSAX
      120     130     140     150     160     170
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 545>:

```
a139.seq
  1 ATGCGAACGA CCCCAACCTT CCCTACAAAA ACTTTCAAAC CGGCTGCCAT
 51 GCGGTTAGCT GTTGCAACAA CACTTTCTGC CTGCTTAGGC GGCGGCGGAG
101 GCGGCACTTC TGCGCCCGAC TTCAATGCAG GCGGCACCGG TATCGGCAGC
151 AACAGCAGGG CAACAACAGC GAAATCAGCA GCAATATCTT ACGCCGGTAT
201 CAAGAACGAA ATGTGCAAAG ACAGAAGCAT GCTCTGTGCC GGTGCGGATG
251 ACGTTGCGGT TACAGACAGG GATGCCAAAA TCAATGCCCC CCCCAGAAC
301 TGCATACCGG AGACTTTACA AACCCAAATG ACGCATACA AGAATTTGAT
351 CAACCTCAA CCTGCAATTG AAGCAGGCTA TACAGGACGC GGGGTAGAGG
401 TAGGTATCGT CGACACAGGC GAATCCGTCG GCAGCATATC CTTTCCCGAA
451 CTGTATGGCA GAAAAGAACA CGGCTATAAC GAAAATTAC. AAAAATAATA
501 CGGCGTATAT GCGGAAGGAA GCGCCTGA
```

This corresponds to the amino acid sequence <SEQ ID 546; ORF 139.a>:

```
a139.pep
  1 MRTTPTFPTK TFKPAAMALA VATTLSACLG GGGGGTSAPD FNAGGTGIGS
```

394

51 NSRATTAKSA AISYAGIKNE MCKDRSMLCA GRDDVAVTDR DAKINAPPRI  
 101 CIPETLQTM THXKNLINLK PAIEAGYTGR GVEVGIVDTG ESVGSI SFPE  
 151 LYGRKEHGYN ENYXKLYGVY AEGSA\*

m139/a139 97.1% identity in 175 aa overlap

	10	20	30	40	50	60
m139.pep	MRTTPTFPKTKFKPTAMALAVATTL SACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
a139	MRTTPTFPKTKFKPAAMALAVATTL SACLGGGGGTSAPDFNAGGTGIGSNSRATTAKSA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m139.pep	AVSYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETFTQTMTHXKNLINLK					
a139	AISYAGIKNEMCKDRSMLCAGRDDVAVTDRDAKINAPPRICIPETLQTMTHXKNLINLK					
	70	80	90	100	110	120
	130	140	150	160	170	
m139.pep	PAIEAGYTGRGVEVGIVDTGESVGSISFP ELYGRKEHGYNENYKLYGVYAEGSAX					
a139	PAIEAGYTGRGVEVGIVDTGESVGSISFP ELYGRKEHGYNENYXKLYGVYAEGSAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 547>:

g140.seq

1	Atgtcggcac	gCGGCAAGGG	GGCAGgctat	ctcAACAGTA	CCGGACGACa
51	TGTTCCCTTC	CTGAGTGCCG	CCAAAATCGG	GCAGGATTAT	TCTTTCTTCA
101	AAAATATCAA	AACCGACGGC	GGTCTGCTGG	CTTCCCTCGA	CAGCGTCGAA
151	AAAACAGCGG	GCACTGAAGG	CGACACGCCG	TCCTATTATG	TCCGTCGCGG
201	CAATGCGGCA	CGGACTGCTT	CGGCAGCGGC	ACAATTCGCG	CCCGCCGGTC
251	TGAAACACGC	CGTAGAACAG	GGCGGCAGCA	ATCTGGA AAA	CCTGATGGTC
301	GAGCTGGATG	CCTCCGAATC	ATCCGCAACA	CCCGAGACGG	TTGAAACTGC
351	GGTCGCCGAC	CGCACAGATA	TGCCGGGCAT	CCGCCTACGG	CGCACAACTT
401	TCCGCACAGC	GGCAGCCGTA	CAGCATGCGA	ATACCGCCGA	CGGCGTACGc
451	aTCTTcaaCA	GTCTCGCCGC	TAccgTCTAt	GccgACAGTG	CCGCCGCCCA
501	TGccgATATG	CAGGGACGCC	GCCTGAAAGC	CGTATCGGAC	GGGTTGGACC
551	ACAACCGGTAC	GGGTCTGCGC	GTCATCGCGC	AAACCCAACA	GGACGGTGGA
601	ACGTGGGAAC	AGGGCGGTGT	CGAAGGCAAA	ATGCGCGGCA	GTACCCAAAC
651	TATCGGCATT	GCCGCGAAAA	CCGCGAAAAA	TACGACAGCA	GCCGCCACAC
701	TGGGCATAGG	ACGCAGCACA	TGGAGCGAAA	ACAGTGCAAA	TGCAAAAACC
751	GACAGCATTa	GTCTGTTTGC	AGGCATACGG	CACGATGTGG	GCGATATCGG
801	CTATCTCAAA	GGCCTGTTCT	CctaCGGACG	CTACAAAAAC	AGCATCAGCC
851	GCAGCACC GG	TGCGGATGAA	TATGCGGAAG	GCAGCGTCAA	CGGCACGCTG
901	ATGCAGCTGG	GCGCACTGGG	TGGTGTCAAC	GTTCCGTTTG	CCGCAACGGG
951	AGATTTGACG	GTTGAAGGCG	GTCTGCGCCA	CGACCTGCTC	AAACAGGATG
1001	CATTTCGCCGA	AAAAGGCagt	GCTTTGGGCT	GGAGCGGCAA	CAGCCTCACT
1051	GAAGGCACAC	TGGTCGGACT	CGCGGGTCTG	AAACTGTGCG	AACCTTGAG
1101	CGATAAAGCC	GTCCTGTCTG	CGACGGCGGG	CGTGAACGC	GACCTGAACG
1151	GACGCGACTA	CGCGGTAAAC	GGCGGCTTTA	CCGGCGCGGC	TGCAGCAACC
1201	GGCAAGACGG	GTGCACGCAA	TATGCCGCAC	ACCCGCCGGG	TTGCCGGTCT
1251	GGGGGTGGAT	GTCAATTTCG	GCAACGGCTG	GAACGGCTTG	GCACGTTACA
1301	GCTACACCGG	TTCCAACACAG	TACGGCAACC	ACAGCGGACA	AATCGGCGTA
1351	GGCTACCGGT	TCTGA			

This corresponds to the amino acid sequence &lt;SEQ ID 548; ORF 140.ng&gt;:

g140.pep

1	MSARGKGAGY	LNSTGRHVPF	LSAAKIGQDY	SFFKNIKTDG	GLLASLDSVE
51	KTAGEGDTDP	SYVVRGNAA	RTASAAHSA	PAGLKHAVEQ	GGSNLENLMV
101	ELDASESSAT	PETVETAVAD	RTDMPGIRLR	RTTFRATAAV	QHANTADGVR
151	IFNSLAATVY	ADSAAAHADM	QGRRLKAVSD	GLDHNGTGLR	VIAQTQQDGG
201	TWEQGGVEGK	MRGSTQTIGI	AAKTGENTTA	AATLGIGRST	WSENSANAKT

251 DSISLFAGIR HDVGDIGYLK GLFSYGRYKN SISRSTGADE YAEGSVNGTL  
 301 MQLGALGGVN VPFAATGDLT VEGGLRHDLL KQDAFAEKGS ALGWSGNSLT  
 351 EGTIVGLAGL KLSQPLSDKA VLSATAGVER DLNGRDYAVT GGFTGAAAT  
 401 GKTGARNMPH TRRVAGLGVD VEFNGWNGL ARYSYTGSKQ YGNHSGQIGV  
 451 GYRF\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 549>:

m140.seq  
 1 ATGTCGGCAC GCGGCAAGGG GGCAGGCTAT CTCAACAGTA CCGGACGACG  
 51 TGTTCCCTTC CTGAGTGCCG CCAAAATCGG GCAGGATTAT TCTTCTTCA  
 101 CAAACATCGA AACCGACGGC GGCCTGCTGG CTTCCCTCGA CAGCGTCGAA  
 151 AAAACAGCGG GCAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG  
 201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCGGGTC  
 251 TGAAACACGC CGTAGAACAG GGCGGCAGCA ATCTGAAAAA CCTGATGGTC  
 301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC  
 351 GGCAGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCCTAC GGCGCAACTT  
 401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCGA CGGTGTACGC  
 451 ATCTTCAACA GTCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA  
 501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC  
 551 ACAACGGCAC GGGTCTGCGC GTCATCGCGC AAACCCAAAC GGACGGTGGA  
 601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC  
 651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC  
 701 TGGGCATGGG ACGCAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC  
 751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG  
 801 CTATCTCAAA GGCTGTCTCT CCTACGGACG CTACAAAAAC AGCATCAGCC  
 851 GCAGCACCGG TGCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG  
 901 ATGCAGCTGG GCGCACTGGG CGGTGTCAAC GTTCCGTTTG CCGCAACGGG  
 951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG  
 1001 CATTGCGCGA AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCCTCACT  
 1051 GAAGGCACGC TGGTCGGACT CGCGGTCTG AAGCTGTGCG AACCTTGAG  
 1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAACGC GACCTGAACG  
 1151 GACGCGACTA CACGGTAACG GGCGGCTTTA CCGGCGCGAC TGCAGCAACC  
 1201 GGCAAGACGG GGGCACGCAA TATGCCGCAC ACCCGTCTGG TTGCGGCGCT  
 1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA  
 1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA  
 1351 GGCTACCGGT TCTGA

This corresponds to the amino acid sequence <SEQ ID 550; ORF 140>:

m140.pep  
 1 MSARGKGAGY INSTGRRVPF LSAKIGQDY SFFTNIETDG GLLASLDSVE  
 51 KTAGSEGDITL SYVVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV  
 101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAAV QHANAADGVR  
 151 IFNSLAATVY ADSTAAHADM QGRLKAVSD GLDHNGTGLR VIAQTQDGG  
 201 TWEQGVVEGK MRGSTQTVGI AAKTGENTTA AATLGMGRST WSENSANAKT  
 251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL  
 301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSLT  
 351 EGTIVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT  
 401 GKTGARNMPH TRRVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV  
 451 GYRF\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 140 shows 94.5% identity over a 454 aa overlap with a predicted ORF (ORF 140.ng) from *N. gonorrhoeae*:

m140/g140

	10	20	30	40	50	60
m140.pep	MSARGKGAGYLNSTGRRVPFLSAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDITL					
g140	MSARGKGAGYLNSTGRHVPFLSAKIGQDYSFFKNIKTDGGLASLDSVEKTAGSEGDTP					
	10	20	30	40	50	60
	70	80	90	100	110	120

m140 . pep	SYVVRGNAARTASAAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAAAD
g140	SYVVRGNAARTASAAAHSAPAGLKHAVEQGGSNLENLMVELDASESSATPETVETAVAD
	70 80 90 100 110 120
m140 . pep	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNSLAATVYADSTAAHADMQGRRLLKAVSD
g140	RTDMPGIRLRRRTTFRATAAVQHANTADGVRIFNSLAATVYADSAAAHADMQGRRLLKAVSD
	130 140 150 160 170 180
m140 . pep	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST
g140	GLDHNGTGLRVIAQTQQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLIGRST
	190 200 210 220 230 240
m140 . pep	WSENSANAKTDSISLFAIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL
g140	WSENSANAKTDSISLFAIRHDVGDIGYLKGLFSYGRYKNSISRSTGADEYAEGSVNGTL
	250 260 270 280 290 300
m140 . pep	MQLGALGGVNVFPAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSLTGEGTLVGLAGL
g140	MQLGALGGVNVFPAATGDLTVEGGLRHDLLKQDAFAEKGSALGWSGNSLTGEGTLVGLAGL
	310 320 330 340 350 360
m140 . pep	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD
g140	KLSQPLSDKAVLSATAGVERDLNGRDYAVTGGFTGAAAATGKTGARNMPHTRRVAGLGVD
	370 380 390 400 410 420
m140 . pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX
g140	VEFGNGWNLARYSYTGSKQYGNHSGQIGVGYRFX
	430 440 450

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 551>:

```

a140 . seq
1  ATGTCCGGCAG GCGGTAAGGG GGCAGGCTAT CTCAACCGTA CCGGACAACG
51  TGTTCCCTTC CTGAGTGCCG CCAAATCGG GCGGGATTAT TCTTCTTCA
101 CAAACATCGA AACCGACGGC GGTCTGCTGG CTTCCTCGA CAGCGTCGAA
151 AAAACAGCGG GTAGTGAAGG CGACACGCTG TCCTATTATG TCCGTCGCGG
201 CAATGCGGCA CGGACTGCTT CGGCAGCGGC ACATTCCGCG CCCGCCGGTC
251 TGAAACACGC CGTAGAACAG GGCGGCAGCA ATCTGGA AAA CCTGATGGTC
301 GAACTGGATG CCTCCGAATC ATCCGCAACA CCCGAGACGG TTGAAACTGC
351 GGCCGCCGAC CGCACAGATA TGCCGGGCAT CCGCCCTAC GGCGCAACTT
401 TCCGCGCAGC GGCAGCCGTA CAGCATGCGA ATGCCGCCG CCGGTGTACGC
451 ATCTTCAACA ATCTCGCCGC TACCGTCTAT GCCGACAGTA CCGCCGCCCA
501 TGCCGATATG CAGGGACGCC GCCTGAAAGC CGTATCGGAC GGGTTGGACC
551 ACAACGCTAC GGGCTGCGC GTCATCGCGC AAACCCAACA GGACGGTGA
601 ACGTGGGAAC AGGGCGGTGT TGAAGGCAAA ATGCGCGGCA GTACCCAAAC
651 CGTCGGCATT GCCGCGAAAA CCGGCGAAAA TACGACAGCA GCCGCCACAC
701 TGGGCATGGG ACACAGCACA TGGAGCGAAA ACAGTGCAAA TGCAAAAACC
751 GACAGCATTG GTCTGTTTGC AGGCATACGG CACGATGCGG GCGATATCGG
801 CTATCTCAAA GGCCTGTTCT CCTACGGACG CTACAAAAAC AGCATCAGCC
851 GCAGCACC GG TCGGACGAA CATGCGGAAG GCAGCGTCAA CGGCACGCTG
901 ATGCAGCTGG GCGCACTGGG CCGTGTCAAC GTTCCGTTTG CCGCAACGGG

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951 AGATTTGACG GTCGAAGGCG GTCTGCGCTA CGACCTGCTC AAACAGGATG
1001 CATTGCGCCG AAAAGGCAGT GCTTTGGGCT GGAGCGGCAA CAGCATCACT
1051 GAAGGCACAC TGGTCGGACT CGCGGGTCTG AAGCTGTCGC AACCCCTGAG
1101 CGATAAAGCC GTCCTGTTTG CAACGGCGGG CGTGGAACGC GACCTGAACG
1151 GACGCGACTA CACGGTAACG GCGGGCTTTA CCGGCGCGAC TGCAGCAACC
1201 GGCAAGACGG GGGCAGGCAA TATGCCGCAC ACCCGCCTGG TTGCCGGTCT
1251 GGGCGCGGAT GTCGAATTCG GCAACGGCTG GAACGGCTTG GCACGTTACA
1301 GCTACGCCGG TTCAAACAG TACGGCAACC ACAGCGGACG AGTCGGCGTA
1351 GGCTACCGGT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 552; ORF 140.a>:

a140.pep

```

1 MSAGGKGAGY LNRTGQRPVF LSAAKIGRDY SFFTNIETDG GLLASLDSVE
51 KTAGSEGDTL SYVRRGNAA RTASAAHSA PAGLKHAVEQ GGSNLENLMV
101 ELDAESSAT PETVETAAAD RTDMPGIRPY GATFRAAAV QHANAADGVR
151 IFNNLAATVY ADSTAAHADM QGRRLKAVSD GLDHNATGLR VIAQTQDGG
201 TWEQGGVEGK MRGSTQTVGI AAKTGENTTA AATLGMGHST WSENSANAKT
251 DSISLFAGIR HDAGDIGYLK GLFSYGRYKN SISRSTGADE HAEGSVNGTL
301 MQLGALGGVN VPFAATGDLT VEGGLRYDLL KQDAFAEKGS ALGWSGNSIT
351 EGTLVGLAGL KLSQPLSDKA VLFATAGVER DLNGRDYTVT GGFTGATAAT
401 GKTGARNMPH TRLVAGLGAD VEFNGWNGL ARYSYAGSKQ YGNHSGRVGV
451 GYRF*

```

m140/a140 98.2% identity in 454 aa overlap

m140.pep	10	20	30	40	50	60
	MSARGKGAGYLNSTGRRVPFLSAAKIGQDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
a140	MSAGGKGAGYLNRTGQRPVFLSAAKIGRDYSFFTNIETDGGLLASLDSVEKTAGSEGDTL					
	10	20	30	40	50	60
m140.pep	70	80	90	100	110	120
	SYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
a140	SYVRRGNAAARTASAAHSAAPAGLKHAVEQGGSNLENLMVELDAESSATPETVETAAAD					
	70	80	90	100	110	120
m140.pep	130	140	150	160	170	180
	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLSLAATVYADSTAAHADMQGRRLKAVSD					
a140	RTDMPGIRPYGATFRAAAVQHANAADGVRIFNLAATVYADSTAAHADMQGRRLKAVSD					
	130	140	150	160	170	180
m140.pep	190	200	210	220	230	240
	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGRST					
a140	GLDHNATGLRVIAQTQDGGTWEQGGVEGKMRGSTQTVGIAAKTGENTTAAATLGMGHST					
	190	200	210	220	230	240
m140.pep	250	260	270	280	290	300
	WSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
a140	WSENSANAKTDSISLFAGIRHDAGDIGYLKGLFSYGRYKNSISRSTGADEHAEGSVNGTL					
	250	260	270	280	290	300
m140.pep	310	320	330	340	350	360
	MQLGALGGVNVFPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
a140	MQLGALGGVNVFPFAATGDLTVEGGLRYDLLKQDAFAEKGSALGWSGNSITEGTLVGLAGL					
	310	320	330	340	350	360
m140.pep	370	380	390	400	410	420
	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					
a140	KLSQPLSDKAVLFATAGVERDLNGRDYTVTGGFTGATAATGKTGARNMPHTRLVAGLGAD					

398

	370	380	390	400	410	420
	430	440	450			
m140 . pep	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
a140	VEFGNGWNLARYSYAGSKQYGNHSGRVGVGYRFX					
	430	440	450			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 553>:

```

g141.seq
1  atgagcttca aAaccgATGC CGAAACCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAGCTG
151 CCGCAAAAC AAGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GGC GGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGTGTTTCG GCGTGAAGG CGGCGCGGCA GCGCGCGGCT ACGCGCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGCGGAC TTCCACGCCA
401 TCGGTGCGGC GAATAACCTC CTCGCGGCCA TGCTCGACAA CCATATCTAC
451 CAAGGTAACG AGTTGAACAT CGACCCCAAA CGCGTGCTGT GCGGCGCGCT
501 GGTCGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGTATGGGCA
551 AGCCTGTtga cggCGTGATG CGtcccGACG GCTTCGACAT CACCGTCGCC
601 TCCGAAGTga tggcgGTATT CTGCCTTGCC AAAGACATCA GCGATTGAA
651 AGAGCGTttt gGCAATATTC TCGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAG GCACACGGCG CGATGGCGGC ATTGCTAAAA
751 GATGCGATTA AGCCCAATTT GGTGCAAACC ATCGAAGGCA CTCCGGCCTT
801 TGTACACGGC GGCCCGTTCG CCAACATCGC CCACGGCTGC AACTCCGTTA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG TGC GGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCAGT CGTCGTGGCG ACTGTCCGCG
1001 CCCTGAAATA CAACGGCGGC GTGGAACGCG CCAACCTTGG TGAAGAAAC
1051 CTCGAAGCCT TGGCAAAAGG TTTGCCCAAC CTGTTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTTCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GCGGCGCGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA TGCCATCGAC AACCAACCTA
1301 ATAACCTTCG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCCAAAAAGT GTACGGCGCG GAAGATGTCG ATTTAGCGC
1401 GGAAGCGTCT GCCGAAATCG CCTCGCTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATATT CATTGAGCGA CAACGCCAAA
1501 CTCTTGGGCT GCCCCGAAGG CTTCCGCATC GCCGTACGCG GTATCACTGT
1551 TTCCGCGGCG GCGGGCTTCA TCGTTGCGTT GTGCGGCAAT ATGATGAAAA
1601 TGCCGCGGCT GCCGAAAGTT CCGGCTGCCG AGAAAATCGA TGTGACGAA
1651 CACGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 554; ORF 141.ng>:

```

g141.pep
1  MSFKTDAETA QSSTMRPIGE IAAKLGLNVD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGAA GGGYAQVLPD EDINLHFTGD FHAIGAANNL LAAMLDNHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKPDVDM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERF GNILVAYAKD GSPVYAKDLK AHGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAVVVA TVRALKYNGG VERANLGEEN
351 LEALAKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDSDAE LAMIEKACAE
401 HGEVSVLTV WGKGAGGAD LARKVNAID NQPNNFGEFAY DVELGIKDKI
451 RAIQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPGEGFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDE
551 HGVHGLF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 555>:

m141.seq

```

1   ATGAGCTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGCGGAA ATTGCGGCCA AGCTTGGTCT GAATGCCGAC AACATTGAGC
101 CTTACGGTCA TTACAAGGCG AAAATCAATC CTGCCGAAGC GTTCAAAGCT
151 CCGCAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC
201 GCGCGGCGAA GGCAAAACCA CCGTAACCAT CGGTTTGGCG GACGCGTTGC
251 GCCACATCGG CAAAGATGCC GTGATTGCCC TGCGCGAACC TTCTCTGGGG
301 CCGGTGTTCG GCGTGAAAGG CGGCGCGGCA GCGGCGGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACCT CACCGGAGAT TTTCACGCCA
401 TCGGTGCGGC AAATAATCTG CTTGCCGCGA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GGCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGTA
551 AACCCTTGA CCGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCATTGTGAA
651 AGAGCGTTTG GGCAACATCC TTGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAACC ATCGAAGGCA CGCCGCGCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAC ACATTTCCTA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGACGCG CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CGGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACTTCGG TTTCCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGGCGATTG CCCAAAAGT GTACGGCGCG GAAGATGTTG ATTTCAGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCGCCGAAGA CTTCCGCATC GCGGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGTT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 556; ORF 141>:

m141.pep

```

1   MSFKTDAEIA QSSTMRPIGE IAAKLGLNAD NIEPYGHYKA KINPAEAFKL
51  PQKQGRLLIV TAINPTPAGE GKTTVTIGLA DALRHIGKDA VIALREPSLG
101 PVFVKGKGA GGGYAQVLP EDINLHFTGD FHAIGAANL LAAMLNDHIY
151 QGNELNIDPK RVLWRRVVDN NDRQLRNIID GMGKFPDGV RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKCRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NRFVSDADAE LAMIEKACAE
401 HGVEVSLTEV WGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TOYSLSDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVIHGLF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 141 shows 97.5% identity over a 558 aa overlap with a predicted ORF (ORF 141.ng) from *N. gonorrhoeae*:

m141/g141

```

          10      20      30      40      50      60
m141.pep  MSFKTDAEIAQSSTMRPIGEIAAKLGLNADNIEPYGHYKAKINPAEAFKL PQKQGRLLIV
          |||||  |||||  |||||  |||||  |||||  |||||
g141      MSFKTDAETAQSSTMRPIGEIAAKLGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRLLIV
          10      20      30      40      50      60

```



400

	70	80	90	100	110	120
m141.pep	TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYAQVLP					
g141	TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYAQVLP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m141.pep	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
g141	EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID					
	130	140	150	160	170	180
	190	200	210	220	230	240
m141.pep	GMGKPVGDGVMRPGDITVASEVMAVFLAKDISDLKERLGNILVAYAKDGSFVYAKDLK					
g141	GMGKPVGDGVMRPGDITVASEVMAVFLAKDISDLKERFGNILVAYAKDGSFVYAKDLK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m141.pep	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	:					
g141	AHGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m141.pep	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
g141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLEALAKGLPN					
	310	320	330	340	350	360
	370	380	390	400	410	420
m141.pep	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEGHGEVSLTEVWGKGGAGGAD					
g141	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEGHGEVSLTEVWGKGGAGGAD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m141.pep	LARKVVNAIESQTNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	:					
g141	LARKVVNAIDNQNNFGFAYDVELGIKDKIRAIQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
	490	500	510	520	530	540
m141.pep	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
g141	LDKMPICMAKTQYSLSDNAKLLGCPGEGFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
	550	559				
m141.pep	PAAEKIDVDAEGVIHGLFX					
	:					
g141	PAAEKIDVDEHGVHGLFX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 557>:

a141.seq

```

1  ATGAGTTTCA AAACCGATGC CGAAATCGCC CAATCCTCCA CCATGCGCCC
51  GATTGGCGAA ATTGCCGCCA AGCTGGGTTT GAACGTTGAC AACATTGAGC
101 CTTACGGTCA TTACAAAGCC AAAATCAATC CTGCCGAAGC GTTCAAACCTG
151 CCGCAAAAC AGGGCAGGCT GATTTTGGTT ACCGCCATCA ACCCGACTCC

```

```

201 GCGGGGCGAA GGTAACCA CCGTAACCAT CGGTTTGGCG GACGCATTGC
251 GCCATATCGG CAAAGACTCT GTGATTGCTT TGCGCGAGCC TTCTTTGGGT
301 CCGGTGTTCG GCGTGAAAGG CGGCGCGGCA GCGGGCGGCT ATGCCCAAGT
351 TTTGCCGATG GAAGACATCA ACCTGCACTT CACCGGAGAT TTTACGCCCA
401 TCGGTGCGGC AAATAATCTG CTTGCGCGCA TGCTCGACAA CCATATCTAC
451 CAAGGCAACG AGTTGAACAT CGACCCCAA CGCGTGCTGT GCGGCGCGT
501 GGTGATATG AACGACCGCC AGTTGCGCAA CATCATCGAC GGCATGGGCA
551 AGCCTGTGTA CCGCGTGATG CGTCCTGACG GTTTCGATAT TACCGTTGCT
601 TCCGAAGTGA TGGCGGTATT CTGTCTTGCC AAAGACATCA GCGATTTGAA
651 AGAGCGTTTG GGCAACATCC TTGTCGCCTA CGCCAAAGAC GGCAGCCCCG
701 TTTACGCCAA AGATTGAAA GCGAATGGCG CGATGGCGGC ATTGCTTAAA
751 GATGCGATTA AGCCCAACTT GGTGCAAAACC ATCGAAGGCA CGCCCGCCTT
801 CGTACACGGC GGCCCGTTTC CCAACATCGC CCACGGCTGC AACTCCGTAA
851 CCGCAACCCG TCTGGCGAAA CACCTTGCCG ATTACGCCGT AACCGAAGCA
901 GGCTTCGGCG CGGACTTGGG CGCGGAAAAA TTCTGCGACA TCAAATGCCG
951 CCTTGCCGGT TTGAAACCTG ATGCGGCTGT TGTCGTGGCG ACTGTCCGCG
1001 CGTTGAAATA TAACGGCGGC GTGGAACGCG CCAACCTCGG CGAAGAAAAT
1051 TTAGACGCTT TGGAAAAAGG TTTGCCCAAC CTGCTGAAAC ACATTTCCAA
1101 CCTGAAAAAC GTATTGCGAC TGCCCGTCGT CGTTGCGCTC AACCGCTTCG
1151 TGTCGACTC CGATGCCGAG TTGGCGATGA TTGAAAAAGC CTGTGCCGAA
1201 CACGGCGTTG AAGTTTCCCT GACCGAAGTG TGGGGCAAAG GTGGTGCGGG
1251 CCGCGCGGAT TTGGCGCGCA AAGTCGTCAA CGCCATTGAA AGTCAAACCA
1301 ATAACCTCGG TTTGCGCTAC GATGTCGAGT TGGGCATCAA AGACAAAATC
1351 CGTGCGATTG CCAAAAAGT GTACGGCGCG GAAGATGTTG ATTTACGCGC
1401 GGAAGCGTCT GCCGAAATCG CTTCACTGGA AAAACTGGGC TTGGACAAAA
1451 TGCCGATCTG CATGGCGAAA ACCCAATACT CTTTGAGCGA CAACGCCAAA
1501 CTGTTGGGCT GCCCGAAGA CTTCCGCATC GCCGTGCGCG GCATCACCGT
1551 TTCCGCAGGC GCAGGTTTCA TCGTCGCCCT GTGCGGCAAC ATGATGAAAA
1601 TGCCCGGCCT GCCCAAAGT CCGGCTGCCG AGAAAATCGA TGTGGACGCA
1651 GAAGGCGTGA TTCACGGCTT GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 558; ORF 141.a>:

a141.pep

```

1 MSFKTDAEIA QSSTMRPIGE IAAKGLNVD NIEPYGHYKA KINPAEAFKL
51 PQKQGRILIV TAINPTPAGE GKTTVTIGLA DALRHIGKDS VIALREPSLG
101 PVFGVKGGAA GGYAQVLP EDINLHFTGD FHAIGAANNL LAAMLDNHIY
151 QGNELNIDPK RVLWRRVDM NDRQLRNIID GMGKPDVDM RPDGFDITVA
201 SEVMAVFCLA KDISDLKERL GNILVAYAKD GSPVYAKDLK ANGAMAALLK
251 DAIKPNLVQT IEGTPAFVHG GPFANIAHGC NSVTATRLAK HLADYAVTEA
301 GFGADLGAEK FCDIKRLAG LKPDAAVVVA TVRALKYNGG VERANLGEEN
351 LDALEKGLPN LLKHISNLKN VFGLPVVVAL NREVSDDAE LAMIEKACAE
401 HGVEVSLTEV WKGKGAGGAD LARKVVNAIE SQTNNFGFAY DVELGIKDKI
451 RAIAQKVYGA EDVDFSAEAS AEIASLEKLG LDKMPICMAK TQYSLDNAK
501 LLGCPEDFRI AVRGITVSAG AGFIVALCGN MMKMPGLPKV PAAEKIDVDA
551 EGVHGLF*

```

m141/a141 99.5% identity in 558 aa overlap

```

          10      20      30      40      50      60
m141.pep MSFKTDAEIAQSSTMRPIGEIAAKGLNADNIEPYGHYKAKINPAEAFKL PQKQGRILIV
|||||
a141 MSFKTDAEIAQSSTMRPIGEIAAKGLNVDNIEPYGHYKAKINPAEAFKL PQKQGRILIV
          10      20      30      40      50      60

          70      80      90      100     110     120
m141.pep TAINPTPAGEGKTTVTIGLADALRHIGKDAVIALREPSLGPVFGVKGAAGGGYQVLP
|||||
a141 TAINPTPAGEGKTTVTIGLADALRHIGKDSVIALREPSLGPVFGVKGAAGGGYQVLP
          70      80      90      100     110     120

          130     140     150     160     170     180
m141.pep EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID
|||||
a141 EDINLHFTGDFHAIGAANNLLAAMLDNHIYQGNELNIDPKRVLWRRVDMNDRQLRNIID
          130     140     150     160     170     180

```

402

m141.pep	190	200	210	220	230	240
	GMGKPVGDGVMRPDGFDTVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
a141	GMGKPVGDGVMRPDGFDTVASEVMAVFCLAKDISDLKERLGNILVAYAKDGSPVYAKDLK					
	190	200	210	220	230	240
m141.pep	250	260	270	280	290	300
	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
a141	ANGAMAALLKDAIKPNLVQTIEGTPAFVHGGPFANIAHGCNSVTATRLAKHLADYAVTEA					
	250	260	270	280	290	300
m141.pep	310	320	330	340	350	360
	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
a141	GFGADLGAEKFCDIKCRLAGLKPDAVVVATVRALKYNGGVERANLGEENLDALEKGLPN					
	310	320	330	340	350	360
m141.pep	370	380	390	400	410	420
	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEGHVEVSLTEVWKGKGAGGAD					
a141	LLKHISNLKNVFGLPVVVALNRFVSDADAELAMIEKACAEGHVEVSLTEVWKGKGAGGAD					
	370	380	390	400	410	420
m141.pep	430	440	450	460	470	480
	LARKVVNAIESQTNNFGFAYDVELGIKDKIRALAQKVYGAEDVDFSAEASAEIASLEKLG					
a141	LARKVVNAIESQTNNFGFAYDVELGIKDKIRALAQKVYGAEDVDFSAEASAEIASLEKLG					
	430	440	450	460	470	480
m141.pep	490	500	510	520	530	540
	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
a141	LDKMPICMAKTQYSLSDNAKLLGCPEDFRIAVRGITVSAGAGFIVALCGNMMKMPGLPKV					
	490	500	510	520	530	540
m141.pep	550	559				
	PAAEKIDVDAEGVIHGLFX					
a141	PAAEKIDVDAEGVIHGLFX					
	550					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 559>:

```

g142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCCGTGC AGGTGCGCCA
51  ACGCGCCTTC TATTTCAAGT TGTCCCGTTT TGCCGCGATG CCAAATATGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCAT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATcggaATG AttcgCGCAC TCCGGTTTAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCGGT AACCggCGCA ACCGCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC CGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCC ATGTGCAGCA GTTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 560; ORF 142.ng>:

```

g142.pep
1  MRADFMFADN MPVQVRQRAF YFKLSRFAAM PNMVGKPLFG RQAGQPGKMF
51  GNILMFVRQH IDAEAAVFRQ DRNDSRTVPY AQHHGRRLVG NRRNRRHCNA
101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN RPLYKNAAHK
151 ASPHVQQF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 561>:

```
m142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCCGCATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTGCGGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCG ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCGC
351 AAGATGCCAT CGCATCACGG AACGAAGTTT GAAAATTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCATCCCCCc ATGTGCAGCA GTTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 562; ORF 142>:

```
m142.pep
1  MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF
51  GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLVG NRRDRRHCA
101 VTPCRTVCRD DMNACRARCH RITERSLKIF LQIRHFSPLN CPLYKNAAHK
151 ASPHVQQF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 142 shows 93.7% identity over a 158 aa overlap with a predicted ORF (ORF 142.ng) from *N. gonorrhoeae*:

```
m142/g142
10      20      30      40      50      60
m142.pep MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMFNGNILMFVRQR
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
10      20      30      40      50      60
MRADFMFADNMPVQVRQAFYFKLSRFAAMPNMVGKPLFGRQAGQPGKMFNGNILMFVRQH

70      80      90      100     110     120
m142.pep IDAEAAVFRQDRNDSRTPVDAQHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRARCH
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
70      80      90      100     110     120
IDAEAAVFRQDRNDSRTPVYAQHGRRLVGNRRDRRHCAVTPCRTVCRDDMNACRTGCH

130     140     150     159
m142.pep RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX
g142      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
130     140     150
RITERSLKSFLQIRHFSPLNRPLYKNAAHKASPHVQQFX
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 563>:

```
a142.seq
1  ATGCGTGCCG ATTTTCATGTT TGCCGACAAT ATGCCCGTGC AGGTGCGCCA
51  ACGCGCCCTC TATTTCAAGT TGTCCCGTTT TGCCCGCATG CCAGATGTGG
101 TAGGCAAACC GCTCTTCGGG CGACAGGCCG GTCAGCCCGG CAAAATGTTC
151 GGCAACATCC TGATGTTTCGT CCGCCAGCGT ATTGATGCAG AGGCTGCCGT
201 TTTCCGACAG GATCGGAATG ATTGCGGCAC TCCGGTTGAT GCACAGCATC
251 ACGGTCGGCG GCTCGTCCGT AACCGGCGCA ACCGCCGTCA TTGTAATGCC
301 GTAACGCCCT GCCGCACCGT CTGTCGTGAT GACATGAACG CCTGCCGCAC
351 AGGATGCCAT CGCATCACGG AACGAAGTTT GAAAAGTTT CTGCAAATCC
401 GCCATTTTTC CCCTTTAAAC TGTCCCCTAT ATAAGAATGC TGCACACAAG
451 GCACCCCCCA TGTGCAGCAG TTCTGATTCA AAAAGCCGTC GGTCCGACAT
501 TTCCGCGCGT TACGGCGTAT TACGAGTTCA ACGCATCCTC GATTTTGCCA
551 AGTTCTGCCA ACAGGTCTTT AAGCAGCAGC ATTTTCTCGC GGCCAGCAC
601 TTCCTCGATA GCGTCGTAAC GTCGTCCAC TTCTTCGCCG ATTTCTCAT
651 ACAGCTTCTC GCCCTCGGCA GTCAGCTTCA GAAAACACG TCGTTGGTCG
701 TTGGAAAGTT TCAGGCGGAC AACCACCCG GCTTTTCAA GGCGGGTCAG
751 GATACCGGTC AGGCTGGGGC GCAAAATGCA CGCCTGATTC GCCAAATCTT
```

801 GAAAGTCCAG CGTGCCGTTT TCCGCCAAAA GACGGATAAT CCGCCATTGC  
 851 TGATCGGTAA TATTCGCCTG ATTCAGAATA GGCCTGAATT GGGTCATCAG  
 901 GGCTTCCCTT GCCTGTATCA GACCGATATT GATAGACGCA TGTTTTGA

This corresponds to the amino acid sequence <SEQ ID 564; ORF 142.a>:

a142.pep  
 1 MRADFMFADN MPVQVRQAL YFKLSRFAAM PDVVGKPLFG RQAGQPGKMF  
 51 GNILMFVRQR IDAEAAVFRQ DRNDSRTPVD AQHHGRRLLVR NRRNRRHCNA  
 101 VTPCRTVCRD DMNACRTGCH RITERSLKSF LQIRHFSPLN CPLYKNAAHK  
 151 APPMCSSSDS KSRRSDISAR YGVLVRQRI LDFGKFCQQVF KQOHFLAAQH  
 201 FLDSVVTLVH FFADFLIQLL ALGSOLQKNT SLVVGRFQAD NQTRFFKAGO  
 251 DTGOAGAONA RLIRQILKVQ RAVFRQKTDN PPLLIGNIRL IQNRPELGHQ  
 301 GFPCLYQTDI DRRMF\*

m142/a142 96.1% identity in 153 aa overlap

	10	20	30	40	50	60
m142.pep	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF	GNILMFVRQR				
a142	MRADFMFADNMPVQVRQALYFKLSRFAAMPDVVGKPLFGRQAGQPGKMF	GNILMFVRQR				
	70	80	90	100	110	120
m142.pep	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVGNRRDRRHCNAVTPCRTVCRDDMNACRARCH					
a142	IDAEAAVFRQDRNDSRTPVDAQHHGRRLLVGNRRDRRHCNAVTPCRTVCRDDMNACRTGCH					
	130	140	150	159		
m142.pep	RITERSLKIFLQIRHFSPLNCPPLYKNAAHKASPHVQQFX					
a142	RITERSLKSFQIRHFSPLNCPPLYKNAAHKAPPMCSSSDSKSRRSDISARYGVLVRQRI					
	190	200	210	220	230	240
a142	DFGKFCQQVFQOHFLAAQHFLDSVVTLVHFFADFLIQLLALGSOLQKNTSLVVGRFQAD					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 565>:

g143.seq  
 1 ATGTTGAGCT TCGGCTATCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG  
 51 CTCGCAGATG AGCCGCATT TTTCAAACGCT AGGCGCAGAC CCGCACAAAT  
 101 TGGGCTGGTT TTTTCATCTG CCGCCGCTGG CGGGGATGCT GGTTCAGCCG  
 151 ATAGTGgGCT ACTACTCAGA CCGCACTTGG AAGCCGCGCT TGGGCGGCGC  
 201 CCGCCTGCCG TATCTGCTTT ACGGCACGCT GATTGCGGTC ATCGTGATGA  
 251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG  
 301 GCCTTGTCGT TCGGCGCGCT GATGATTGCG CTGTTGGACG TGTCGTCGAA  
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGATATG GTCAACGAGG  
 401 AGCAGAAAAG CTACGCCTAC GGGATTCAAA GTTTCTTAGC GAATACGGAC  
 451 GCGGTTGTGG CAGCGATTCT GCCGTTTGTG TTcgcgata TCGGTTTGGC  
 501 GAACACTGCC GAGAAAGGCG TTGTGCCACA AACCGTGGTC GTAGCATTCT  
 551 ATGTGGGTGC GCGGTTACTG ATTATTACCA GTGCGTTCAC AATCTCCAAA  
 601 GTCAAAGAAT ACGACCCGGA AACCTACGCC CGTTACCACG GCATCGATGT  
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGTT CGAACTCTTA AAAACCGCGC  
 701 CTAAAGTGTT TTGGACGGTT ACTCCGGTAC AGTTTTCTCG CTGTTTCGCC  
 751 TTCCGGTATA TGTGGACTTA CTCGGCAGGC GCGATTGCAG AAAACGTCTG  
 801 GCACACTACC GATGCGTCTT CCGTAGGCCA TCAGGAGGCG GGCAACCGGT  
 851 ACGGCGTTTT GCGGCGGGTG TAGTCGGTTG CGGCGGTGAT TTGTTGCTTT  
 901 ATTCTGGCAA AAGTACCGAA TAAATACCAT AAGCGGGGTT ATTTGCGCTG  
 951 TTTGGCTTTG GCGCGGCTCG GTTTCTTCTC TATCTTCTTC ATCTACAATC  
 1001 AATACGCACT CATCCTGTCT TATATCTTAA TCGGCATCGC TTGGGCGGGC  
 1051 ATTATCACTT ATCCGCTGAC GATTGTGGCC AACGCTTGT CGGGCAAACA  
 1101 CATGGATACT TATTTGGGCC TGTTtaacgg ctctgtCTGT ATGCcgcaaa  
 1151 tcgTcgctTC GctgttagAG TTCGTGCTTT TCCCGATGCT GGGCGGCCAT

1201 CAGGCAACCA TGTTCTTGGT TGCAGGCGCA GTCTTGCTGC TGGGAGCCTT  
 1251 CTCAGTCTGT CTGATTAAAG AGATCCACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 566; ORF 143.ng>:

g143.pep

1 MLSFGYLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP  
 51 IVGYYSDRTW KPRLGRRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA  
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKSYAY GIQSFLANTD  
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL IITSAFTISK  
 201 VKEYDPETYA RYHGIDVAAN QEKANWFELL KTAPKVFMTV TPVQFFCWFA  
 251 FRYMWTSYAG AIAENVWHTT DASSVGHQEA GNRYGVLAAY \*SVAAVICSF  
 301 ILAKVPNKYH KAGYFGCLAL GALGFFSIFV IYNOYALILS YILIGIAWAG  
 351 IITYPLTIVA NALSGKHMMDT YLGLFNGSVC MPQIVASLLS FVLFPMLGGH  
 401 QATMFLVAGA VLLLGAFSVC LIKEIHGGV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 567>:

m143.seq

1 ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG  
 51 CTCGCAAATG AGCCGCATTT TTCAAACGCT AGGCGCAGAC CCGCACAAAT  
 101 TGGGCTGGTT TTTCATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAAGCC  
 151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG  
 201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA  
 251 TTTTGATGCC GAACCTCGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG  
 301 GCTTTGTGCT TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA  
 351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG  
 401 AGCAGAAAGG CTACGCCTAC GGGATTCAAA GTTTCTTAGC AAATACGGGC  
 451 GCGGTCGTGG CGGCGATTCT GCCGTTTGTG TTTGCGTATA TCGGTTTGCG  
 501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGGTC GTGGCGTTTT  
 551 ATGTGGGTGC GGCCTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA  
 601 GTGAAGGAAT ACGATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT  
 651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGCCG  
 701 CTAAGGCGTT TTGGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCCGC  
 751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG  
 801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGGT  
 851 ACGGCGTTTT GCGCGCGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTT  
 901 GTATTGGCGA AAGTCCGAA TAAATACCAT AAGGCGGGTT ATTTCCGCTG  
 951 TTTGGCTTTG GCGCGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC  
 1001 AATACGCGCT GGTGTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC  
 1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CCGGCAAGCA  
 1101 TATGGGCACT TACTTGGGCT TGTTTAACGG CTCTATCTGT ATGCCTCAA  
 1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG  
 1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT  
 1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 568; ORF 143>:

m143.pep

1 MLSFGFLGVO TAFTLQSSQM SRIFQTLGAD PHNLGWFFIL PPLAGMLVQP  
 51 IVGHYSDRTW KPRLGRRRLP YLLYGTLIIV IVMILMPNSG SFGFGYASLA  
 101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDV VNEEQKGYAY GIQSFLANTG  
 151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK  
 201 VKEYDPETYA RYHGIDVAAN QEKANWIELL KTAPKAFMTV TLVQFFCWFA  
 251 FQYMWTSYAG AIAENVWHTT DASSVGYQEA GNWYGVLAAY QSVAAVICSF  
 301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNQYALVLS YTLIGIAWAG  
 351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPQIVASLLS FVLFPMLGGH  
 401 QATMFLVGGV VLLLGAFSVF LIKEIHGGV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m143 / g143 93.9% identity in 429 aa overlap

10 20 30 40 50 60

406

m143.pep	MLSFGFLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW
g143	MLSFGYLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGYSDRTW
	10 20 30 40 50 60
m143.pep	70 80 90 100 110 120
m143.pep	KPRLGGRRLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
g143	KPRLGGRRLPYLLYGTLLIAVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM
	70 80 90 100 110 120
m143.pep	130 140 150 160 170 180
m143.pep	QPFKMMVGDVNEEQKGYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGVVPQTVV
g143	QPFKMMVGDVNEEQKSYAYGIQSFLANTDAVVAAILPFVFAYIGLANTAEGVVPQTVV
	130 140 150 160 170 180
m143.pep	190 200 210 220 230 240
m143.pep	VAFYVGAALLVITSFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV
g143	VAFYVGAALLIITSFTISKVKEYDPETYARYHGIDVAANQEKANWFELLKTAPKVEWTV
	190 200 210 220 230 240
m143.pep	250 260 270 280 290 300
m143.pep	TLVQFFCWFAFYQYMWYTSAGAIENVWHTTDASSVGYQEAGNRYGVLAQVSVAAVICSF
g143	TPVQFFCWFAFRYMWYTSAGAIENVWHTTDASSVGHQEAGNRYGVLAQVXSVAAVICSF
	250 260 270 280 290 300
m143.pep	310 320 330 340 350 360
m143.pep	VLAQVFNKYHKAGYFGCLALGALGFFSVFFIGNQYALVLSYTLIGIAWAGIITYPLTIVT
g143	ILAKVPNKYHKAGYFGCLALGALGFFSIFFIYNOYALILSYILIGIAWAGIITYPLTIVA
	310 320 330 340 350 360
m143.pep	370 380 390 400 410 420
m143.pep	NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLPMLGGLQATMFLVGGVLLLGAFSVC
g143	NALSGKHMDTYLGLFNGSVCMPQIVASLLSFVLPMLGGHQATMFLVAGAVLLLGAFSVC
	370 380 390 400 410 420
m143.pep	430
m143.pep	LIKETHGGVX
g143	LIKEIHGGVX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 569>:

```

a143.seq
1  ATGCTCAGTT TCGGCTTTCT CGGCGTTCAG ACGGCCTTTA CCCTGCAAAG
51  CTCGCAGATG AGCCGCATCT TCCAGACGCT CGGTGCCGAT CCGCACAGCC
101 TCGGCTGGTT CTTTATCCTG CCGCCGCTGG CGGGGATGCT GGTGCAGCCG
151 ATTGTCGGCC ATTACTCCGA CCGCACTTGG AAGCCGCGTT TGGGCGGCCG
201 CCGTCTGCCG TATCTGCTTT ATGGCACGCT GATTGCGGTT ATTGTGATGA
251 TTTTGATGCC GAACTCGGGC AGCTTCGGTT TCGGCTATGC GTCGCTGGCG
301 GCTTTGTCTG TCGGCGCGCT GATGATTGCG CTGTTAGACG TGTCGTCAAA
351 TATGGCGATG CAGCCGTTTA AGATGATGGT CGGCGACATG GTCAACGAGG
401 AGCAGAAAGG CTACGCCCTAC GGGATTCAAA GTTTCTTAGC GAATACGGGC
451 GCGGTCGTGG CCGCGATTCT GCCGTTTGTG TTTGCCGTATA TCGGTTTGGC
501 GAACACCGCC GAGAAAGGCG TTGTGCCGCA GACCGTGCTC GTGGCGTTT
551 ATGTGGGTGC GCGTTTGCTG GTGATTACCA GCGCGTTCAC GATTTTCAAA
601 GTGAAGGAAT ACAATCCGGA AACCTACGCC CGTTACCACG GCATCGATGT
651 CGCCGCGAAT CAGGAAAAAG CCAACTGGAT CGAACTCTTG AAAACCGGCC
701 CTAAGCGGTT TTGACGGTT ACTTTGGTGC AATTCTTCTG CTGGTTCGCC

```

```

751 TTCCAATATA TGTGGACTTA CTCGGCAGGC GCGATTGCGG AAAACGTCTG
801 GCACACCACC GATGCGTCTT CCGTAGGTTA TCAGGAGGCG GGTAACGTGT
851 ACGGCGTTTT GCGGCGGGTG CAGTCGGTTG CCGCGGTGAT TTGTTCTGTT
901 GTATTGGCGA AAGTGCCGAA TAAATACCAT AAGGCGGGTT ATTTCCGCTG
951 TTTGGCTTTG GCGCGGCTCG GCTTTTCTC CGTTTTCTTC ATCGGCAACC
1001 AATACGCGCT GGTGTTGTCT TATACCTTAA TCGGCATCGC TTGGGCGGGC
1051 ATTATCACTT ATCCGCTGAC GATTGTGACC AACGCCTTGT CGGGCAAGCA
1101 TATGGGCACT TACTTGGGCC TGTTAACGG CTCTATCTGT ATGCCGCAAA
1151 TCGTCGCTTC GCTGTTGAGT TTCGTGCTTT TCCCTATGCT GGGCGGCTTG
1201 CAGGCCACTA TGTTCTTGGT AGGGGGCGTC GTCCTGCTGC TGGGCGCGTT
1251 TTCCGTGTTT CTGATTAAAG AAACACACGG CGGGGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 570; ORF 143.a>:

```

a143.pep
1  MLSFGLGVQ TAFTLQSSQM SRIFQTLGAD PHSLGWFFIL PPLAGMLVQP
51  IVGHYSDRTW KPRLGRRRLP YLLYGTIAIV IVMILMPNSG SFGFGYASLA
101 ALSFGALMIA LLDVSSNMAM QPFKMMVGDM VNEEQKYAY GIQSFLANTG
151 AVVAAILPFV FAYIGLANTA EKGVPQTVV VAFYVGAALL VITSAFTIFK
201 VKEYNPETYA RYHGIDVAAN QEKANWIELL KTAPKAFWTV TLVQFFCWFA
251 FOYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAAV QSVAAVICSF
301 VLAKVPNKYH KAGYFGCLAL GALGFFSVFF IGNOYALVLS YTLIGIAWAG
351 IITYPLTIVT NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGL
401 QATMFLVGGV VLLGAFSVF LIKETHGGV*

```

m143/a143 99.5% identity in 429 aa overlap

	10	20	30	40	50	60
m143.pep	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
a143	MLSFGLGVQTAFTLQSSQMSRIFQTLGADPHNLGWFFILPPLAGMLVQPIVGHYSDRTW					
	10	20	30	40	50	60
m143.pep	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
a143	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
a143	KPRLGRRRLPYLLYGTIAIVIVMILMPNSGSFGFGYASLAALSFGALMIALLDVSSNMAM					
	70	80	90	100	110	120
m143.pep	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTVV					
a143	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTVV					
	130	140	150	160	170	180
m143.pep	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTVV					
a143	QPFKMMVGDMVNEEQKYAYGIQSFLANTGAVVAAILPFVFAYIGLANTAEGKVPQTVV					
	130	140	150	160	170	180
m143.pep	VAFYVGAALLVITSAFTIFKVKEYDPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
a143	VAFYVGAALLVITSAFTIFKVKEYNPETYARYHGIDVAANQEKANWIELLKTAPKAFWTV					
	190	200	210	220	230	240
m143.pep	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAAV QSVAAVICSF					
a143	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAAV QSVAAVICSF					
	250	260	270	280	290	300
m143.pep	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAAV QSVAAVICSF					
a143	TLVQFFCWFAFOYMWYSAG AIAENVWHTT DASSVGYQEA GNWYGVLAAV QSVAAVICSF					
	250	260	270	280	290	300
m143.pep	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
a143	VLAKVPNKYHKAGYFGCLALGALGFFSVFFIGNOYALVLSYTLIGIAWAGIITYPLTIVT					
	310	320	330	340	350	360
m143.pep	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGL QATMFLVGGV VLLGAFSVF					
a143	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGL QATMFLVGGV VLLGAFSVF					
	370	380	390	400	410	420
m143.pep	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGL QATMFLVGGV VLLGAFSVF					
a143	NALSGKHMGT YLGLFNGSIC MPOIVASLLS FVLFPMLGGL QATMFLVGGV VLLGAFSVF					



```

a143      |||||
          NALSGKHMGTYLGLFNGSICMPQIVASLLSFVLFPMGLGLQATMFLVGGVVLLLGAFSVF
          370      380      390      400      410      420

          430
m143.pep  LIKETHGGVX
          |||||
a143      LIKETHGGVX
          430

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 571>:

```

g144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGGGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGTGC GTCTCGTG
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC CCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGTAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCggtt
351 CAACGCGGTG GCGGCAGACG GccgacggTt atCCCAACGA TTGGatatT
401 TCctaccgCT TGGACGAGGA CGGCCGGCTT ACCGttaccT ATCGCGCCAC
451 CGCgctCGGC GACACGGTGT TCGACCCGAC GCTGCACATT TACTGGCGGC
501 TGGACGCGGG CCTGCACGAT GCGGTTCTGC ATATTCCGCA GGGCGGACAT
551 ATTCCGGCCG ATGCCGAAAA ACTGCCCGTC TTAACGGTTT CAGACGGCCT
601 CGAAGTATTT GA

```

This corresponds to the amino acid sequence <SEQ ID 572; ORF 144.ng>:

```

g144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTC VFVLDLGGIV QEFSVLADGV
51  RENPVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRRLSQR FGyFLPLGRG RPAYRYLSRH
151 RARRHGVRPD AAHLAAGRG PARCSAYS AGRYSGRCRK TARLNGFRRP
201 RSI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 573>:

```

m144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGTCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGATGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTCGCAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCCTGg
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCCTA
451 CCGCTTGAC GAGGACGACC GGCTTACCGT TAaCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATGCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 574; ORF 144>:

```

m144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFSVLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAAFDIN GRTRYVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLATVGRRL SQRFGyFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAHLL AAGRGPARCG SAYSAGRTYA
201 GRCRK TARLN GFRRPRSI*

```

Computer analysis of this amino acid sequence gave the following results:

# Homology with a predicted ORF from *N. gonorrhoeae*

m144 / g144 91.3% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD
          |||||
g144      MSDTPATRDFGLIDGRAVTGYVLSNRRGTCVFVLDLGGIVQEFVSLADGVRENPVVSFDD
          10      20      30      40      50      60

      70      80      90     100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          |||||
g144      AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
          70      80      90     100     110     120

      130     140     150     160     170     180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFYFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL
          |||
g144      AAD-----GRRLSQRFG--YFLPLGRGRPAYRYLSRHRARRHGVRPDAAHLL
          130     140     150     160

      190     200     210     219
m144.pep  AAGRGPARCGSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
          |||||
g144      AAGRGPARCGSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
          170     180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 575>:

```

a144.seq
1  ATGAGCGATA CCCCCGCTAC CCGCGATTTC GGCCTGATCG ACGGGCGTGC
51  CGTAACCGGC TATGTGCTGT CCAACCGGCG TGGTACGCGT GTCTGCGTGC
101 TGGACTTGGG CGGGATTGTG CAGGAATTTT CCGTTTGGC AGACGGCGTG
151 CGCGAAAACC TCGTGGTGTC GTTCGACGAT GCGGCTTCCT ATGCGGACAA
201 TCCGTTTCAG ATTAACAAGC AGATAGGGCG CGTGGCCGGA CGCATCCGCG
251 GTGCGGCGTT CGACATCAAC GGCAGGACTT ACCGCGTGGA GGCCAACGAA
301 GGCAGGAACG CGCTGCACGG CGGTTTCGAC GGGCTGGCCG TTACCCGTTT
351 CAACGCGGTG GCGGCAGACG GCCGTTCCGT GGTGCTGCGC AGCCGCGCTG.
401 CAACAGTCGG CCGACGGTTA TCCCAACGAT TTGGATTGG ATATTTCTTA
451 CCGCTTGGAC GAGGACGACC GGCTTACCGT TACCTATCGC GCCACCGCGC
501 TCGGCGACAC GGTGTTTCGAC CCGACGCTGC ACATTACTG GCGGCTGGAC
551 GCGGGCCTGC ACGATGCGGT TCTGCATATT CCGCAGGGCG GACATATTCC
601 GGCCGATGCC GAAAACTGC CCGTCTCAAC GGTTCAGAC GACCTCGAAG
651 TATTTGA

```

This corresponds to the amino acid sequence <SEQ ID 576; ORF 144.a>:

```

a144.pep
1  MSDTPATRDF GLIDGRAVTG YVLSNRRGTR VCVLDLGGIV QEFVSLADGV
51  RENLVVSFDD AASYADNPFQ INKQIGRVAG RIRGAADFIN GRTYRVEANE
101 GRNALHGGSH GLAVTRFNAV AADGRSVVLR SRLXTVGRRL SQRFGFGYFL
151 PLGRGRPAYR YLSRHRARRH GVRPDAAHLL AAGRGPARCG SAYSAGRTYS
201 GRCRKRTARLN GFRRPRSI*

```

m144/a144 99.1% identity in 218 aa overlap

```

      10      20      30      40      50      60
m144.pep  MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD
          |||||
a144      MSDTPATRDFGLIDGRAVTGYVLSNRRGTRVCVLDLGGIVQEFVSLADGVRENLVVSFDD
          10      20      30      40      50      60

      70      80      90     100     110     120
m144.pep  AASYADNPFQINKQIGRVAGRIRGAADFINGRTYRVEANEGRNALHGGSHGLAVTRFNAV

```

410

```

|||||
a144      AASYADNPFQINKQIGRVAGRIRGAAFDINGRTYRVEANEGRNALHGGSHGLAVTRFNAV
              70      80      90      100      110      120

              130      140      150      160      170      180
m144.pep  AADGRSVVLRSLATVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
|||||
a144      AADGRSVVLRSLXTVGRRLSQRFGFGYFLPLGRGRPAYRYSRHRARRHGVRPDAHLL
              130      140      150      160      170      180

              190      200      210      219
m144.pep  AAGRGPARGCSAYSAGRTYAGRCRKRTARLNGFRRPRSIX
|||||
a144      AAGRGPARGCSAYSAGRTYSGRCRKRTARLNGFRRPRSIX
              190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 577>:

```

g146.seq
1  ATGAAGCAAA TCCCCCTCCG CCTTCTCCAG GTCGTCATTG ACCACGACAA
51 AGTCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA ctTCCCGACT GTCCGTCCCG CGCcttTGA GCGCGCGGC
151 AAGCACGTCG AAAGAAGGCG GCAGGATAAA GATACCGACA GCTTCCGGCA
201 GCGCGTTGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCAG
251 TCATAGCCTG CCGCCGCCAA CGCATTCACG CCCTCCGTGC TTGTGCCGTA
301 ATAGTTGCCG AATACGTCGT CGTATTCCAA AAAAGCCTCC TGC GCGATAA
351 GCGATTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTATGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAA CCGATTGTAT CACAACGGAC ACCCTATTTT
601 ATATTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 578; ORF 146.ng>:

```

g146.pep
1  MKQIPLRLLO VVIDHDKVEQ YGLDFMPCL RQPPLDNFPT VRPAPFEARG
51 KHVERRRQDK DTDSFRQVA NLRRALNVDF QNHVIACRRQ RIHALRACAV
101 IVAEYVCVFQ KSLLRDKREF LFFGNKVIMY AVCFAFTRRA RRMHRGNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPYF
201 IFADAHILPL LF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 579>:

```

m146.seq
1  ATGGCGCAAA TCCTCCTCCG CTCGCGCCAA GTCGTCATTG ACCACGACAA
51 AGTCAAACAA TACGGACTGC TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTGTA GCGCGCGGC
151 AAGTACGTCG AAAGAAGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCGTCGCG AACCTGCGCC GCGCCCTGAA CGTCGATTTC CAAAATCAG
251 TCATAGCCTG CCGCCGCCAA CGCATTCACA CCCTCCGCGC CTGTGCCGTA
301 ATAGTTGCCA AATACGTCGG CGTATTCCAA AAAAGCCTCC TGC GCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGGCG CGTCGTGTGC GACACGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAATGGAC ACCCAGTTTC
601 CTATTGCCG ATGCCCATAT TTTGCCGCTA TTGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 580; ORF 146>:

```

m146.pep
1  MAQILLRSRQ VVIDHDKVKQ YGLLDFMPCL RQPPLDNFPT VRPASVEARG
51 KYVERRRQDK DADGFGQVA NLRRALNVDF QNHVIACRRQ RIHTLRACAV
101 IVAKYGVVFQ KSFLRDKRLK LFFGNKVIMY AVCFAFTRRA RRVHRGNAQT
151 VMVCQQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQWTPSF
201 LFADAHILPL LF*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m146 / g146 90.1% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
g146	MKQIPLRLQVVVIDHDKVEQYGLFDFMPCLRQPPLDNFPTVRPAPFEARGKHVERRRQDK					
	10	20	30	40	50	60
m146.pep	70	80	90	100	110	120
	DADGFGQVRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK					
g146	DTDSFRQVRVANLRRALNVDFQNHVIACRRQRIHALRACAVIVA EYVCVFQKSLLRDKRFK					
	70	80	90	100	110	120
m146.pep	130	140	150	160	170	180
	LFFGNKVIMYAVCFAFTRRRVRHGNNAQTMVCCQPRHQRFARAGSGRNDKDVAFSIS					
g146	LFFGNKVIMYAVCFAFTRRRVRHGNNAQTMVCCQPRHQRFARAGSGRNDKDVAFSIS					
	130	140	150	160	170	180
m146.pep	190	200	210			
	GHIFYLYIFQPIVSQWTPSFLFADAHILPLLFX					
g146	GHIFYLYIFQPIVSQRTPYFIFADAHILPLLFX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 581>:

```

a146.seq
1  ATGGCGCAAA TCCTCCTCCG CCGCGGCCAA GTCATCATTG ACCACGACAA
51  AATCGAACAA TACGGACTGT TCGATTTCAT GCCTTGCCTT CGACAGCCTC
101 CTTTGGATAA CTTCCCGACT GTCCGTCCCG CGTCCGTTGA GACGCGCAGC
151 AAGCACATCG AAAGACGGCG GCAGGATAAA GATGCCGACG GCTTCGGGCA
201 GCGCATCTCG AACCTGAGCC GCGCCCTGAA CGTCGATTTC CAAAATCAGC
251 TCATAACCTG CCGCCGCCAA CGCATTACCA CCCTCCGCGC TTGTGCCGTA
301 ATAGTTGCCG AACACGTCCG CGTATTCCAA AAAAGCCTCC TGCGCGATAA
351 GCGACTCAAA CTCTTCTTTG GAAACAAAGT GATAATGTAC GCCGTTTGCT
401 TCGCCTTCAC GCGGCGGACG CGTCGTGTGC GACACGGAAA CGCGCAAACC
451 GTTATGGTTT GCCAACAGCC GCGACACCAG CGTGGTTTTC CCCGTGCCGG
501 AAGCGGCCGA AATGATAAAG ATGTTGCCTT TTCGATAAGC GGACATATTT
551 TTTACCTGTA TATTTTCCAG CCGATTGTAT CACAACGGAC ACCCGGTTTC
601 CTATTTGCCG ATGCCCATAT TTGCGCGCTA TTGTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 582; ORF 146.a>:

```

a146.pep
1  MAQILLRPRQ VIIDHDKIEQ YGLDFMPCL RQPPLDNFPT VRPASVETR
51  KHIERRRQDK DADGFGQRIS NLSRALNVDF QNHVITCRRQ RIHTLRACAV
101 IVAEHVRVFQ KSLLRDKRLK LFFGNKVIMY AVCFAFTRRT RVRHGNNAQ
151 VMVCCQPRHQ RGFARAGSGR NDKDVAFSIS GHIFYLYIFQ PIVSQRTPGF
201 LFADAHILPL LF*

```

m146/a146 90.6% identity in 212 aa overlap

m146.pep	10	20	30	40	50	60
	MAQILLRSRQVVVIDHDKVKQYGLLDFMPCLRQPPLDNFPTVRPASVEARGKYVERRRQDK					
a146	MAQILLRPRQVIIDHDKIEQYGLDFMPCLRQPPLDNFPTVRPASVETR SKHIERRRQDK					
	10	20	30	40	50	60
	70	80	90	100	110	120

412

```

m146.pep      DADGFGQRVANLRRALNVDFQNHVIACRRQRIHTLRACAVIVAKYVGVFQKSFLRDKRLK
                |||||:::| | |||||:::| | |||||:::| | |||||:::| | |||||:::|
a146          DADGFGQRI SNLSRALNVDFQNHVITCRRQRIHTLRACAVIVA EHVRFQKSLLRDKRLK
                70          80          90          100         110         120

                130         140         150         160         170         180
m146.pep      LFFGNKVIMYAVCFAFTRRRVRHGN AQTMVCQPRHQRGFARAGSGRNDKDVAFSIS
                |||||:::| | |||||:::| | |||||:::| | |||||:::| | |||||:::|
a146          LFFGNKVIMYAVCFAFTRRRVRHGN AQTMVCQPRHQRGFARAGSGRNDKDVAFSIS
                130         140         150         160         170         180

                190         200         210
m146.pep      GHIFYLYIFQPIVSQWTPSELFADAHILPLLEFX
                |||||:::| | |||||:::| | |||||:::| | |||||:::|
a146          GHIFYLYIFQPIVSQRTPGFLFADAHILPLLEFX
                190         200         210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 583>:

```

g147.seq (partial)
1  ..ATGCGACGAG AAGCCAAAAT GGCACAAATC ACACTCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CGCCCAAGCG CATGAAACTG
101 AGCAATCGGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTCCG
151 CGCGCGACTT CGGGCTGCT GCACACTTCG ACCGCCTCCG ACAAATCAT
201 CTCCGGCGAT ACTTTGCGCC AAAAAGCCGT CAACTTGGGC GACGCTTGG
251 ACGGCGTACC GGGCATCCAC GCTTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATTC GCGGTCAAAC GGGCAGACGG ATTAAAGTAT TGAACCATCA
351 CGGCGAAACG GCGGATATGG CGGACTTTTC TCCGATCAC GCCATTATGG
401 TAGATACCGC CTTGTGCGAA CAGGTTGAAA TCCTGCGCGG GCCGTTACG
451 CTCTTGTA CA GCTCGGgcaa tgtggccgGG GCTGGtcaat gttgccgatg
501 gAAAAAtccc caaaaAAtg cc..

```

This corresponds to the amino acid sequence <SEQ ID 584; ORF 147.ng>:

```

g147.pep (partial)
1  ..MRREAKMAQI TLKPIVLSIL LINTPLLAQA HETEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDTALSQ QVEILRGPVT
151 LLYSSGNVAG AGQCCRWNKP PKNA..

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 585>:

```

m147.seq (partial)
1  ..CCGCATAAAA CTGAGCAATC GGTGGATTG GAAACGGTCA GCGTCGTCGG
51  CAAAAGCCGT CCGCGCGCCA CGTCGGGGCT GTTGCACT TCGACCGCT
101 CCGACAAAT CATCTCCGGC GATACCTTGC GCCAAAAGC CGTCAACTTG
151 GGCGACGCTT TAGACGGCGT ACCGGGCATC CACGCTTCGC AATACGGCGG
201 CGGCGCGTCT GCTCCCGTCA TTCGCGGTCA AACAGGCAGG CGGATTAAAG
251 TGTTGAACCA TCACGGCGAA ACAGGCGATA TGGCGGATT TTCCGCCGAT
301 CACGCCATTA TGGTAGATAC CGCCTTGTCG CAACAGGTCG AAATCCTGCG
351 CGGGCCGGTT ACGCTCTTGT ACAGCTCGGG CAATGTGGCG GGGCTGGTCG
401 ATGTTGCCGA TGGCAAAATC CCCGAAAAA TGCTGAAAA CGGCGTATCG
451 GCGGAACTCG GATTGCGTTT GAGCAGCGGC AATCTGAAA AACTCACGTC
501 CGGCGGCATC AATATCGGTT TGGGCAAAA CTTTGATTG CACACGGAAG
551 GGCTGTACCG CAAATCGGGG GATTACGCCG TACCGGTTA CCGCAATCTG
601 AAACGCCTGC CCGACAGCCA CGCCGATTGC CAAACGGGCA GCATCGGGCT
651 GTCTTGGGTT GGCGAAAAAG GTTTTATCGG CGTAGCGTAC AGCGACCGTC
701 GCGACCAATA TGGTCTGCCT GCCACAGCC ACGAATACGA TGATTGCCAC
751 GCCGACATCA TCTGGCAAAA GAGCTTGATT AACAAACGCT ATTTACAGCT
801 TTATCCGCAC CTGTTGACCG AAGAAGACAT CGATTACGAC AATCCGGGCT
851 TGAGCTGCGG CTTCCACGAC GACGATAATG CACACGCACA CACCCACAGC
901 GGCAGACCGT GGATAGACCT GCGCAACAAA CGTACGAAC TCCGTGCCGA
951 ATGAAGCAA CCGTTCCCGG GTTTTGAAGC CCTGCGCGTA CACCTGAACC
1001 GCAACGACTA CCGCCACGAC GAAAAAGCAG GCGATGCAGT CGAAAACCTT
1051 TTTAACAACC AAACGCAAAA CGCCGCGATC GAGTTGGGCC ACCAACCCAT

```

```

1101 AGGTCGTCTG AAAGGCAGCT GGGGCGTGCA ATATTTACAA CAAAATCCA
1151 GTGCTTTATC TGCCATATCC GAAGCGGTTA AACACCGGAT GCTGCTTGAC
1201 AACAAAGTGC AACATTACAG CTTTTTCGGT GTAGAACAGG CAAACTGGGA
1251 CAACTTCACG CTTGAAGGAG GCGTACGCGT GGAAAAACAA AAAGCCTCCA
1301 TTCAGTACGA CAAAGCATTG ATTGATCGGG AAAACTACTA CAACCACCCC
1351 CTGCCCGACC TCGGCGCGCA CCGCCAAACC GCCCGCTCAT TCGCACTTTC
1401 GGGCAACTGG TATTTACACG CACAACACAA ACTCAGCCTG ACCGCCTCCC
1451 ATCAGGAACG CCTGCCGTCA ACGCAAGAGC TGTACGCACA CGGCAAACAC
1501 GTCGCCACCA ACACCTTTGA AGTCGGCAAC AAACACCTCA ACAAAGAGCG
1551 TTCCAACAAT ATCGAACTCG CGCTGGGCTA CGAAGGCGAC CGCTGGCAAT
1601 ACAATCTGGC ACTCTACCGC AACCGCTTCG GTAACATACAT TTACGCCCAA
1651 ACCTTAAACG ACGGACGCGG CCCCAAATCC ATCGAAGACG ACAGCGAAAT
1701 GAAGCTCGTG CGCTACAACC AATCCGGCGC CGACTTCTAC GCGCGGGAAG
1751 GCGAAATCTA CTTCAAACCG ACACCGCGCT ACCGCATCGG CGTTTCCGGC
1801 GACTATGTAC GAGGCGGTCT GAAAAACCTG CCTTCCCTAC CCGGCAGAGA
1851 AGATGCCTAC GGCAACCGTC CTTTCATCGC ACAGGACGAC CAAAATGCCC
1901 CCCGTGTTCC GGCTGCGCGC CTCGGCTTCC ACCTGAAAGC CTCGCTGACC
1951 GACCGTATCG ATGCCAATTT GGAATACTAC CGCGTGTTCC CCCAAACAA
2001 ACTCGCCCGC TACGAAACGC GCACGCCCGG ACACCATATG CTCACCTCG
2051 GCGCAAACTA CCGCCGCAAT ACGCGCTATG GCGAGTGGAA TTGGTACGTC
2101 AAAGCCGACA ACCTGCTCAA CCAATCCGTT TACGCCACA GCAGCTTTCT
2151 CTCTGATACG CCGCAAATGG GCCGCAGCTT TACCGCGCGC GTGAACGTGA
2201 AGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 586; ORF 147>:

```

m147.pep (partial)
1 ..PHKTEQSVDL ETVSVVGKSR PRATSGLLHT STASDKIISG DTLRQKAVNL
51 GDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGE TGDMAFSPD
101 HAIMVDTALS QQVEILRGPV TLLYSSGNVA GLVDVADGKI PEKMPENGVS
151 GELGLRLSSG NLEKLTSGGI NIGLGKNEVL HTEGLYRKSG DYAVPRYRNL
201 KRLPDSHADS QTSIGLSWV GEKGFIVGAY SDRRDQYGLP AHSHEYDDCH
251 ADIIWQSLI NKRYLQLYPH LLTEEDIDYD NPGLSCGFHD DDNAHAHTHS
301 GRPWIDLRNK RYELRAEWKQ PFPGFALRV HLNRRNDYRD EKAGDAVENF
351 FNNQTQNAI ELRHQPIGRL KGSWGVQYLQ QKSSALS AIS EAVKQPMLLD
401 NKVQHYSEFFG VEQANWDNFT LEGGVRVEKQ KASIQYDKAL IDRENYNHP
451 LPDLGAHRQT ARSFALSGNW YFTPOHKLSL TASHQERLPS TOELYAHGKH
501 VATNTFEVGN KHLNKERSNN IELALGYEGD RWQYNLALYR NRGNYIY AQ
551 TLNDGRGPKS IEDDSEMKLV RYNQSGADFY GAEGEIYFKP TPRYRIGVSG
601 DYVRGRLLNL PSLPGREDAY GNRPFIAQDD QNAPRVPAAR LGFHLKASLT
651 DRIDANLDYY RVFAQNKLAR YETRTPGHHM LNLGANYRRN TRYGEWNWYV
701 KADNLLNQSV YAHSSFLSDT PQMGRSFTGG VNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m147 / g147 92.3% identity in 142 aa overlap

```

m147.pep          10      20      30
                   PHKTEQSVDL ETVSVVGKSR PRATSGLLHTS
g147              10      20      30      40      50      60
MRREAKMAQITLKP IVL SILLINTPLLAQAHETE QSVGLETVSVVGKSR PRATSGLLHTS
                   10      20      30      40      50      60
m147.pep          40      50      60      70      80      90
TASDKIISGDTLRQ KAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
g147              70      80      90      100     110     120
TASDKIISGDTLRQ KAVNLGDALDGVPGI HASQYGGGAS APVIRGQTGR RIKVLNHHGET
                   100     110     120     130     140     150
m147.pep          GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGLVDVADGKIPEKMPENGVS
g147              GDMADFSPDHAIMVDTALSQQVEILRGPV TLLYSSGNVAGAGQCCRWNPKNA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 587>:

a147.seq

```

1  ATGCGACGAG AAGCCAAAAT GGCACAAACT ACAC TCAAAC CCATTGTTTT
51  ATCAATTCTT TTAATCAACA CACCCCTCCT CTCCCAAGCG CATGGAAC TG
101 AGCAATCAGT GGGCTTGGAA ACGGTCAGCG TCGTCGGCAA AAGCCGTC CG
151 CGCGCCACTT CGGGGCTGCT GCACACTTCT ACCGCTCCG ACAAATCAT
201 CAGCGGCGAC ACCTTGCGAC AAAAAGCCGT CAACTTGGGT GATGCTTTAG
251 ACGGCGTACC GGGCATT CAT GCCTCGCAAT ACGGCGGCGG CGCATCCGCT
301 CCCGTTATT CCGGTCAAAC AGGCAGACGG ATTAAAGTGT TGAACCATCA
351 CGCGGAAACG GGCACATGG CGGACTTCTC TCCAGACCAT GCAATCATGG
401 TGGACAGCGC CTTGTGCGAA CAGGTCGAAA TCCTGCGCGG TCCGGTTACG
451 CTCTTGTA CA GCTCGGGCAA TGTGGCGGGG CTGGTCGATG TTGCCGATGG
501 CAAAATCCCC GAAAAATGC CTGAAAACGG CGTATCGGGC GAACTCGGAT
551 TGGCTTTGAG CAGCGCAAT CTGGAAAAAC TCACGTCCGG CGGCATCAAT
601 ATCGGTTTGG GCAAAAAC TTATTGCAC ACGGAAGGGC TGTACCGCAA
651 ATCGGGGGAT TACGCCGTAC CGCGTTACCG CAATCTGAAA CGCCTGCCCG
701 ACAGCCACGC CGATTGCAA ACGGGCAGCA TCGGGCTGTC TTGGGTTGGC
751 GAAAAAGGCT TTATCGGCGC AGCATACAGC GACCGTCGCG ACCAATATGG
801 TCTGCCTGCC CACAGCCACG AATACGATGA TTGCCACGCC GACATCATCT
851 GGC AAAAGAG TTTGATTAA CAAACGCTATT TGCAGCTTTA TCCGCACCTG
901 TTGACCGAAG AAGACATCGA TTACGACAAT CCGGGCTTGA GCTGCGGCTT
951 TCACGACGAC GATGATGCAC ACGCCCATGC CCACAACGGC AAACCTTGGA
1001 TAGACCTGCG CAACAAACGC TACGAACTCC GCGCCGAATG GAAGCAACCG
1051 TTCCCCGGTT TTGAAGCCCT GCGCGTACAC CTGAACCGCA ACGACTACCG
1101 CCACGACGAA AAAGCAGGCG ATGCAGTAGA AAAC TTTTTT AACAACCAA
1151 CGCAAAACGC CCGTATCGAG TTGCGCCACC AACCCATAGG CCGTCTGAAA
1201 GGCAGCTGGG GCGTGCAATA TTTGGGACAA AAATCCAGTG CTTTATCTGC
1251 CACATCCGAA GCGGTCAAAC AACCGATGCT GCTTGACAAT AAAGTGCAAC
1301 ATTACAGCTT TTTGCGTGTG GAACAGGCAA ACTGGGACAA CTCACGCTT
1351 GAAGCGGCGG TACGCGTGA AAAACAAAAA GCCTCCATCC GCTACGACAA
1401 AGCATTGATT GATCGGGAAA ACTACTACAA CCATCCCCTG CCCGACCTCG
1451 GCGCGCACC G CCAAACCGCC CGCTCATTCG CACTTTCGGG CAACTGGTAT
1501 TTCACGCCAC AACACAACT CAGCCTGACC GCCTCCATC AGGAACGCCT
1551 CCCGTCAACG CAAGAGCTGT ACGCACACGG CAACACGTC GCCACCAACA
1601 CCTTTGAAGT CGGCAACAAA CACCTCAACA AAGAGCGTTC CAACAATATC
1651 GAACTCGGCG TGGGCTACGA AGGCGACCGC TGGCAATACA ATCTGGCACT
1701 CTACCGCAAC CGCTTCGGCA ACTACATTTA CGCCCAAACC TTAACGACG
1751 GACGCGGCCC CAAATCCATC GAAGACGACA GCGAAATGAA GCTCGTGCGC
1801 TACAACCAAT CCGGTGCGGA CTTCTACGGC GCGGAAGGCG AAATCTACTT
1851 CAAACCGACA CCGCGCTACC GCATCGGCGT TTCCGCGGAC TATGTACGAG
1901 GCCGTCTGAA AAACCTGCCT TCCCTACCCG GCAGGGAAGA CGCCTACGGC
1951 AACC GCCCAC TCATTGCCCA AGCCGACCAA AACGCCCTC GCCTTCCGGC
2001 TCGCGCGCTC GCGGTCCACC TGAAGCCTC GCTGACCGAC CGCATCGATC
2051 CCAATTGGA CTACTACGCG GTGTTGCGCC AAAACAACT CGCCCGTAC
2101 GAAACGCGCA CGCCCGGACA CCATATGCTC AACCTCGGCG CAACTACCG
2151 CCGCAATACG CGCTATGGCG AGTGAATTG GTACGTCAA GCGGACAACC
2201 TGCTCAACCA ATCCGTTTAC GCCCACAGCA GCTTCCTCTC TGATACGCCG
2251 CAAATGGGCC GCAGCTTTAC CCGCGGCGTG AACGTGAAGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 588; ORF 147.a>:

a147.pep

```

1  MRREAKMAQT TLKPIVLSIL LINTPLLSQA HGTEQSVGLE TVSVVGKSRP
51  RATSGLLHTS TASDKIISGD TLRQKAVNLG DALDGVPGIH ASQYGGGASA
101 PVIRGQTGRR IKVLNHHGET GDMADFSPDH AIMVDSALSQ QVEILRGFVT
151 LLYSSGNVAG LVDVADGKIP EKMPENGVS G ELGLRLSSGN LEKLTSGGIN
201 IGLGKNFVLH TEGLYRKSGD YAVPRYRNK RLPDSHADSQ TSGISLWSVG
251 EKGFIGAAYS DRRDQYGLPA HSHEYDDCHA DIIWQKSLIN KRYLQLYPHL
301 LTEEDIDYDN PGLSCGFHDD DDAHAHAHNG KPWIDLNRKR YELRAEWKQP
351 FPGFEALRVH LNRNDYRHDE KAGDAVENFF NNQTONARIE LRHQPIGRLL
401 GSWGVOYLQ KSSALSATSE AVKQPMLLDN KVQHYSFEGV EQANWDNFTL
451 EGGVRVEKOK ASIRYDKALI DRENYYNHPL PDLGAHQRTA RSFALSGNWY
501 FTPQHKLSLT ASHQERLPST QELYAHGKHV ATNTFEVGNK HLNKERSNNI
551 ELALGYEGDR WQYNLALYRN RFGNYIYAQT LNDGRGPKSI EDDSEMKLVR

```

601 YNQSADFYG AEGEIYFKPT PRYRIGVSGD YVRGLKNLP SLPGREDAYG  
651 NRPLIAQADQ NAPRVFAARL GVHLKASLTD RIDANLDYYR VFAQNKLARY  
701 ETRTPGHML NLGANYRNT RYGEWNWYVK ADNLLNOSVY AHSSFLSDTP  
751 QMGRSFTGGV NVKF\*

m147/a147 98.1% identity in 734 aa overlap

m147.pep				10	20	30
				PHKTEQSV	DLTVSVVGKSR	PRATSGLLHTS
a147	MRREAKMAQTTLKPIVLSILLINTPLLSQA	HGTEQSVG	LETVSVVGKSR	PRATSGLLHTS		
	10	20	30	40	50	60
m147.pep	40	50	60	70	80	90
	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
a147	TASDKIISGDTLRQKAVNLGDALDGVPGI	HASQYGGGASAPVIRGQTGRRIKVLNHHGET				
	70	80	90	100	110	120
m147.pep	100	110	120	130	140	150
	GDMADFS	PDHAIMVDTALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
a147	GDMADFS	PDHAIMVDSALSQQVEILRG	PVTLLYSSGNVAGLVDVADGKIPEKMPENGVS			
	130	140	150	160	170	180
m147.pep	160	170	180	190	200	210
	ELGLRLSSGNLEKLTSGGINIGLGNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ				
a147	ELGLRLSSGNLEKLTSGGINIGLGNFV	LHTEGLYRKSGDYAVPRYRNKRLPDSHADSQ				
	190	200	210	220	230	240
m147.pep	220	230	240	250	260	270
	TGSIGLSWVG	EKGFIGVAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHL			
a147	TGSIGLSWVG	EKGFIGAAYS	DRRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHL			
	250	260	270	280	290	300
m147.pep	280	290	300	310	320	330
	LTEEDIDYDN	PGLSCGFHDDDNAHAH	THSGRPWIDLNRKRYELRAEWKQFPFGFEALRVH			
a147	LTEEDIDYDN	PGLSCGFHDDDAHAH	ANGKRPWIDLNRKRYELRAEWKQFPFGFEALRVH			
	310	320	330	340	350	360
m147.pep	340	350	360	370	380	390
	LNRNDYRHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRLKGSWG	VQYLGQKSSALSATSE			
a147	LNRNDYRHDEKAGDAVENFFNNQ	TQNARIELRHQPIGRLKGSWG	VQYLGQKSSALSATSE			
	370	380	390	400	410	420
m147.pep	400	410	420	430	440	450
	AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGV	RVEKQKASIQYDKALIDRENYNHL			
a147	AVKQPM	LLDNKVQHYSFFGVEQANWDNFTLEGGV	RVEKQKASIRYDKALIDRENYNHL			
	430	440	450	460	470	480
m147.pep	460	470	480	490	500	510
	PDLGAHRQTARSFALSGN	WYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
a147	PDLGAHRQTARSFALSGN	WYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNK				
	490	500	510	520	530	540
m147.pep	520	530	540	550	560	570
	HLNKERSNNIELALGYEGDRWQYNLALYRN	RFGNYIYAQTLNDGRGPKSIEDDSEMKLVR				
a147	HLNKERSNNIELALGYEGDRWQYNLALYRN	RFGNYIYAQTLNDGRGPKSIEDDSEMKLVR				



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	550	560	570	580	590	600
	580	590	600	610	620	630
m147 . pep	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFI AQDDQ					
a147	YNQSGADFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFI AQADQ					
	610	620	630	640	650	660
	640	650	660	670	680	690
m147 . pep	NAPRVPAARLGFHLKASLTDRIDANLDYYRVFAQNK LARYETRTPGHHMLNLGANYRRNT					
a147	NAPRVPAARLGVHLKASLTDRIDANLDYYRVFAQNK LARYETRTPGHHMLNLGANYRRNT					
	670	680	690	700	710	720
	700	710	720	730		
m147 . pep	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
a147	RYGEWNWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					
	730	740	750	760		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 589>:

```

g148 . seq
1  ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGctgg ttcaTCCCGA
51  AgctATgagt gtcggcgCGC TTGccgAcaa AATCCGCAAA AtcgaAAact
101 gGCCGCAAAA AGgcaTCTTA TTCCACGACA TCACGCCCGT CCTGCAAAAGT
151 GCGGAATACT TCCGCCTTTT GGTGCGATTG CTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGCTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGtcg gctTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTAcg cgcTCGAATA
351 CGGGGAAGCT GCGGTGGA AAA TCCACACCGa tgccgTCAAA CCGGTTTCGC
401 GCGTCCTGCT GGTGATGAT TTGGTTGCCA CGGGCGGCAC AATGCTTGCC
451 GGGCTGGAAC TGATCCGCAA ACTCGGCGGG GAAATTGTG AAgccgcgcG
501 CATTTTGGAA TTTACCGACC TTCAAGCGG CAAGAATATC CGCGCAAGTG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGCAT GAAAGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 590; ORF 148.ng>:

```

g148 . pep
1  MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKIL FHDITPVLOS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK
101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK PGRVLLVDD LVATGGTMLA
151 GLELIRKLGG EIVEAAAIL EFTDLQGGKNI RASGAPLFTL LQNEGCMKG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 591>:

```

m148 . seq
1  ATGGCGTTAA AAACATCAAA CTTGGAACAC GCAATGCTGG TTCATCCCGA
51  AGCTATGAGT GTCGGCGCGC TTGCCGACAA AATCCGCAAA ATCGAAAAC
101 GGCCGCAAAA AGGCATCTTA TTCCACGACA TCACGCCCGT CCTTCAAAGC
151 GCGGAATACT TCCGCCTTTT GGTGATTGTTA TTGGTTTACC GCTATATGGA
201 TCAGAAAATC GACATCGTTG CCGGTTTGA CGCGCGCGGC TTCATTATCG
251 GCGCGGCACT CGCCTACCAG CTCaACGTCG GTTTCGTCCC CATCCGCAAA
301 AAAGGCAAGC TGCCTTTTGA AACCGTATCG CAAAGCTACG CGCTCGAATA
351 CGGGGAAGCT GCGGTGGA AAA TCCACACCGA TGCCGTCAAA CTCGGTTTCGC
401 GCGTCCTGCT GGTGATGAT TTGATTGCCA CGGGCGGCAC GATGCTTGCC
451 GGAAGGCAAC TGATCCGCAA ACTCGGCGGA GAAATTGTG AAGCCGCGC
501 CATTTTGGAA TTTACCGACC TTCAAGCGG CAAGAATATC CGTGCAAGCG
551 GCGCGCCCTT ATTTACCCTG CTTCAAAACG AAGGCTGTAT GAAGGGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 592; ORF 148>:

```

m148 . pep
1  MALKTSNLEH AMLVHPEAMS VGALADKIRK IENWPQKIL FHDITPVLOS
51  AEYFRLLVDL LVYRYMDQKI DIVAGLDARG FIIGAALAYQ LNVGFVPIRK

```

101 KGKLPFETVS QSYALEYGEA AVEIHTDAVK LGSRVLLVDD LIATGGTMLA  
 151 GLELIRKLGG EIVEAAAILE FTDLQGGKNI RASGAPLFTL LQNEGCMKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m148 / g148 99.0% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
g148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m148.pep	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
g148	LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m148.pep	AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
g148	AVEIHTDAVKPGSRVLLVDDLVATGGTMLAGLELIRKLGG EIVEAAAILEFTDLQGGKNI					
	130	140	150	160	170	180
	190	200				
m148.pep	RASGAPLFTLLQNEGCMKGX					
g148	RASGAPLFTLLQNEGCMKGX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 593>:

a148.seq

1	ATGGCGTTAA	AAACATCAAA	CTTGGAACAC	GCAATGCTGG	TTCATCCCGA
51	AGCTATGAGT	GTCGGTGCGC	TTGCCGACAA	AATCCGCAAA	ATCGAAAAC
101	GGCCGCAAAA	AGGCATCTTA	TTCCACGACA	TCACGCCCGT	CCTGCAAAGC
151	GCGGAATACT	TCCGACTTTT	GGTTGATTTA	TTGGTTTACC	GCTATATGGA
201	TCAGAAAATC	GACATCGTTG	CCGGTTTGGA	CGCGCGCGGC	TTCATTATCG
251	CGCGGGCACT	CGCCTACCAG	CTCAACGTCG	GTTTCGTCCC	CATCCGCAAA
301	AAAGGCAAGC	TGCCTTTTGA	AACCGTATCG	CAAAGCTACG	CGCTCGAATA
351	CGGGGAAGCT	GCGGTGGAAA	TCCACACCGA	TGCCGTCAAA	CTCGGTTTCG
401	GCGTGCTGCT	GGTCGATGAT	TTGGTTGCCA	CGGGCGGCAC	GATGCTTGCC
451	GGAATGGAGC	TGATCCGCAA	ACTCGGCGGG	GAAATTGTCT	AAGCCGCCGC
501	CATTTTGGAA	TTTACCGACC	TTCAAGGCGG	CAAGAATATC	CGTGCAAGCG
551	GCGCGCCCTT	ATTACCTCTG	CTTCAAAACG	AAGGCTGTAT	GAAGGGCTGA

This corresponds to the amino acid sequence <SEQ ID 594; ORF 148.a>:

a148.pep

1	MALKTSNLEH	AMLVHPEAMS	VGALADKIRK	IENWPQKGIL	FHDITPVLQS
51	AEYFRLLVDL	LVYRYMDQKI	DIVAGLDARG	FIIGAALAYQ	LNVGFPVPIRK
101	KGKLPFETVS	QSYALEYGEA	AVEIHTDAVK	LGSRVLLVDD	LVATGGTMLA
151	GLELIRKLGG	EIVEAAAILE	FTDLQGGKNI	RASGAPLFTL	LQNEGCMKG*

m148/a148 99.5% identity in 199 aa overlap

	10	20	30	40	50	60
m148.pep	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
a148	MALKTSNLEHAMLVHPEAMSVGALADKIRKIENWPQKGILFHDITPVLQSAEYFRLLVDL					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m148.pep  LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
|||||
a148      LVYRYMDQKIDIVAGLDARGFIIGAALAYQLNVGFVPIRKKGKLPFETVSQSYALEYGEA
              70      80      90      100     110     120

              130      140      150      160      170      180
m148.pep  AVEIHTDAVKLGSRVLLVDDLIATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
|||||
a148      AVEIHTDAVKLGSRVLLVDDLVATGGTMLAGLELIRKLGGEIVEAAAILEFTDLQGGKNI
              130      140      150      160      170      180

              190      200
m148.pep  RASGAPLFTLLQNEGCMKGX
|||||
a148      RASGAPLFTLLQNEGCMKGX
              190      200

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 595>:

```

g149.seq
1   ATGTTGATTG ACAACAATGT CCGCCATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAATTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATCCGGTAC GACAAAGCAT TGATTGATCG AGAAAACTAC
151 TACAACCAGC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 GTTCGCACTT TCGGGCAACT GGTATTTTAC GCCACACCAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAa cgCCTGCCGT CAACGCaaga actGtACgca
301 cacggcAAGC ACGtcgccac CAACACCTTT GAagtcgga acaaACACCT
351 CAACAAAGaG CgttccaacA atatcgaACT CGCGCTGGgc tAcaaaggcg
401 accGCTGGCA ATACAATCTG GCAGCTTACC GCAACCGaTt CGGCAACTAC
451 ATTTACGCCC AAACCTTAaa cgacggacgc GGCCCCAAAT CCATCgaaga
501 cgacagcgaa ATGaagcTCG TCGCTACAA CCAATCCGGT GCCGACTTCT
551 ACgcgcgga aggcgaaatc tACTTcaaaC CGAcACCGCG CTACCGCATC
601 GGTGTTTCCG GCGACTatgt acgaggccgt CTGAAAAACC TGCCGTCCCT
651 ACCCGGCAGG gaagatccCT AcggcAAACG TCccttcaTC GCACAAGCCG
701 ACCAAACGC CCCCCGCATT ccggctGCGC GCCTCGGCTT CCACCTGAAA
751 ACCTCGCTAA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCCGGTGTT
801 CGCCCAAAAC AAATCGCCC GCTACGAAAC GCGTACGCCC GGACACCATA
851 TGCTCAACCT CGGTGCAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGctc aACcaatCcg tTTACGCCCa
951 cAGCAGCTTC CTCTCTGATA CGCCGCAAAt gGGCCGAGC TTtgccgGCg
1001 gcgtaACGT GaAGTTttaA

```

This corresponds to the amino acid sequence <SEQ ID 596; ORF 149.ng>:

```

g149.pep
1   MLIDNNVRHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY
51  YNQPLPDLGA HRQTARSFAL SGNWYFTPHH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YKDRWQYNL AAYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDPYGKRPFi AQADQNAPRI PAARLGFLHK
251 TSLTDRIDAN LDYRVFAQN KLARYETRTP GHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FAGGVNVKF*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 597>:

```

m149.seq
1   ATGCTGCTTG ACAACAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA
51  GGCAAACCTG GACAACTTCA CGCTTGAAGG AGGCGTACGC GTGGAAAAAC
101 AAAAAGCCTC CATTCACTAC GACAAAGCAT TGATTGATCG GGAAAACTAC
151 TACAACCACC CCCTGCCCCG CCTCGGCGCG CACCGCCAAA CCGCCCGCTC
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAATCAGCC
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA
301 CACGGCAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGGCG
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGTAACTAC

```

```

451 ATTTACGCCC AAACCTTAA CGACGGACGC GGCCCCAAAT CCATCGAAGA
501 CGACAGCGAA ATGAAGCTCG TGCCTACAA CCAATCCGGC GCCGACTTCT
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC
601 GCGGTTTCCG GCGACTATGT ACGAGGCGGT CTGAAAAACC TGCCTTCCCT
651 ACCCGGCAGA GAAGATGCCT ACGGCAACCG TCCTTTTCATC GCACAGGACG
701 ACCAAAATGC CCCCCGTGTT CCGGCTGCGC GCCTCGGCTT CCACCTGAAA
751 GCCTCGCTGA CCGACCGTAT CGATGCCAAT TTGGACTACT ACCGCGTGTT
801 CGCCCAAAAC AAACCTCGCCC GCTACGAAAC GCGCACGCCC GGACACCATA
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA
951 CAGCAGCTTT CTCTCTGATA CGCCGCAAAT GGGCCGCAGC TTTACCGGCG
1001 GCGTGAACGT GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 598; ORF 149>:

m149.pep

```

1  MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIQY DKALIDRENY
51  YNHPLPDLGA HRQTARFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFGNY
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQS ADFYGAEGEI YFKPTPRYRI
201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPFI AQDDQNAPRV PAARLGFHLK
251 ASLTDRIDAN LDYRVFAQN KLARYETRTP GHHMLNLGAN YRRNTRYGEW
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 149 shows 95.9% identity over a 339 aa overlap with a predicted ORF (ORF 149.ng) from *N. gonorrhoeae*:

m149/g149

m149.pep	10	20	30	40	50	60
	MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIQY DKALIDRENY NHPLPDLGA					
g149	MLIDNNVRHYSFFGVEQANW DNFTLEGGVR VEKQKASIRYDKALIDRENY NQPLPDLGA					
	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
	HRQTARFALSGNWYFTPQH KLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
g149	HRQTARFALSGNWYFTP HHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKE					
	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
	RSNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQS					
g149	RSNNIELALGYKDRWQYNLAAYRNRFGNYIYAQTLNDGRGPKSIEDDSEM KLVRYNQS					
	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGREDAYGNRPFI AQDDQNAPRV					
g149	ADFYGAEGEIYFKPTPRYRIGVSGDYVRGR LKNLPSLPGREDPYGKRPFIAQADQNAPRI					
	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
	PAARLGFHLKASLTDRIDANLDYRVFAQNKLARYETRTPGHHMLNLGAN YRRNTRYGEW					
g149	PAARLGFHLKTSLTDRIDANLDYRVFAQNKLARYETRTPGHHMLNLGAN YRRNTRYGEW					
	250	260	270	280	290	300
m149.pep	310	320	330	340		
	NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX					

g149 NWYVKADNLLNQSVYAHSSFLSDTPQMGRSFAGGVNVKFX  
310 320 330 340

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 599>:

a149.seq  
1 ATGCTGCTTG ACAATAAAGT GCAACATTAC AGCTTTTTCG GTGTAGAACA  
51 GGCAAAGCTGG GACAACTTCA CGCTTGAAGG CGGCGTACGC GTGGAAAAAC  
101 AAAAAGCCTC CATCCGCTAC GACAAAGCAT TGATTGATCG GGAAACTAC  
151 TACAACCATC CCCTGCCCGA CCTCGGCGCG CACCGCCAAA CCGCCCGCTC  
201 ATTCGCACTT TCGGGCAACT GGTATTTTAC GCCACAACAC AAATCAGCC  
251 TGACCGCCTC CCATCAGGAA CGCCTGCCGT CAACGCAAGA GCTGTACGCA  
301 CACGCGAAAC ACGTCGCCAC CAACACCTTT GAAGTCGGCA ACAAACACCT  
351 CAACAAAGAG CGTTCCAACA ATATCGAACT CGCGCTGGGC TACGAAGCGC  
401 ACCGCTGGCA ATACAATCTG GCACTCTACC GCAACCGCTT CGGCAACTAC  
451 ATTTACGCCC AAACCTTAAA CGACGGACGC GGCCCCAAAT CCATCGAAGA  
501 CGACAGCGAA ATGAAGCTCG TGCCTACAA CCAATCCGGT GCGGACTTCT  
551 ACGGCGCGGA AGGCGAAATC TACTTCAAAC CGACACCGCG CTACCGCATC  
601 GCGCTTTCGG GCGACTATGT ACGAGGCCGT CTGAAAAACC TGCCTTCCCT  
651 ACCCGGCAGG GAAGACGCCT ACGGCAACCG CCCACTCATT GCCCAAGCCG  
701 ACCAAAACGC CCCTCGCGTT CCGCTGCGCG GCCTCGGCGT CCACCTGAAA  
751 GCCTCGCTGA CCGACCGCAT CGATGCCAAT TTGGACTACT ACCGCGTGT  
801 CGCCCAAAC AAACCTGCCC GCTACGAAAC GCGCACGCCG GGACACATA  
851 TGCTCAACCT CGGCGCAAAC TACCGCCGCA ATACGCGCTA TGGCGAGTGG  
901 AATTGGTACG TCAAAGCCGA CAACCTGCTC AACCAATCCG TTTACGCCCA  
951 CAGCAGCTTC CTCTCTGATA CGCGCAAAT GGGCCGCAGC TTTACCGCGC  
1001 GCGTGAACGT GAAGTTTAA

This corresponds to the amino acid sequence <SEQ ID 600; ORF 149.a>:

a149.pep  
1 MLLDNKVQHY SFFGVEQANW DNFTLEGGVR VEKQKASIRY DKALIDRENY  
51 YNHPLPDLGA HRQTARFAL SGNWYFTPQH KLSLTASHQE RLPSTQELYA  
101 HGKHVATNTF EVGNKHLNKE RSNNIELALG YEGDRWQYNL ALYRNRFGNY  
151 IYAQTLNDGR GPKSIEDDSE MKLVRYNQSG ADFYGAEGEI YFKPTPRYRI  
201 GVSGDYVRGR LKNLPSLPGR EDAYGNRPLI AQADQNAPRV PAARLGVHLK  
251 ASLTDRIAN LDYYRVFAQN KLARYETRTP GHMMLNLGAN YRRNTRYGEW  
301 NWYVKADNLL NQSVYAHSSF LSDTPQMGRS FTGGVNVKF\*

m149/a149 98.8% identity in 339 aa overlap

m149.pep	10	20	30	40	50	60
a149	10	20	30	40	50	60
m149.pep	70	80	90	100	110	120
a149	70	80	90	100	110	120
m149.pep	130	140	150	160	170	180
a149	130	140	150	160	170	180
m149.pep	190	200	210	220	230	240
a149	190	200	210	220	230	240
m149.pep	250	260	270	280	290	300
a149	250	260	270	280	290	300

g149-1.seq

1	ATGGCACAAA	TCACACTCAA	ACCATTGTGT	TTATCAATTG	TTTTAATCAA
51	CACACCCCTC	CTCGCCCAAG	CGCATGAAAC	TGAGCAATCG	GTGGGCTTGG
101	AAACGGTCA	CTCGCTCGGC	AAAGCGCTC	CGCGCGCGAC	TTCGGGGCTG
151	CTGCACACTT	CGACGCCCTC	CGACAAAATC	ATCTCCGGCG	ATACCTTTGCG
201	CCAAAAAGCC	GTCAACTTGG	GCACGCTTT	GGACCGCGTA	CCGGGCAATCC
251	ACGCTTCCGA	ATACGGCTGG	GGCGCATCCG	CTCCGGTTAT	CGCGCGTCAAT
301	ACGGGCAGAC	GGATTAAAGT	ATTGAACCAT	CACGGCGAAA	CGGGCGATAT
351	GCGGACTTTT	TCTCCCGATC	ACGCCATTAT	GGTAGATACC	GCCTTGTCGC
401	AACAGGTTGA	AATCTCTGCG	GGCGCGGTGT	CGCTCTTGTA	CAGCTCCGGT
451	AATGTGGCGG	GGCTGGTCCG	TGTTGGCGAT	GGAAAAATCC	CGGAAAAAAT
501	GCTTGA AAAC	GGCGTATCGG	GCgaagccgg	ATTGCGTTTG	AGCAGCGGCA
551	ATTTTGA AAA	ACTGACATCC	GCAGGCATCA	ATATCGGACT	GGGCAAAAAC
601	TTCTGTGCTG	ATACCGAAGT	CTTGTACCGC	AAATCGGGCG	ATTACGCCGT
651	ACCGCGTTAC	CGCAATCTGA	AACGCTTGCC	CGACAGCCAT	CGCGATTTCG
701	AAACGGGCGC	CATCGGGCTG	CTCTGGGTGG	GCGAAAAAGG	CTTTATCGGC
751	GACGATACAG	GCGACGGCTG	CGACCGCTAC	GGCCTGCGCT	CCCAACGCCA
801	CGAATACGAT	GATTGCCACG	CGGCATCTAT	CTGGCAAAAG	AGTTTGATCA
851	ACAAACGCTA	TTTGAGCTTT	TATCCGCACT	TGTTGACCGA	AGAAGACATC
901	GATTACGACA	ATCCGGGCTT	GAGCTGCGGC	GTTCACGACG	CGCAGCGGTG
951	ACACGCACAC	ACCCACAACG	GCAAAACGTG	GATAGACCTG	CGCAACAAAC
1001	GCTACGAACT	CCGCGCCGAA	TGGAAGCAGC	CATTCCCCGG	TTTTGAAGCC
1051	CTGCGCGTAC	ATCTGAACCG	CAATGACTAC	CACACACGAC	AAAAAGCAGG
1101	CGATGCAGTA	GAAAATCTCT	TCAACAACAA	ACCAACAACA	CGCGCTATCG
1151	AGTTGCGCCA	CCAACCCATA	GGCCGTCTGA	AAGGCAGCTG	GGGCGTGCAA
1201	TATTTGGGAC	AAAAATCCAG	CGCGCTTTCC	GCCATTCCCG	AAACCGTCCA
1251	ACAACCGATG	TTGATTGACA	ACAAATGTCG	CCATTACAGC	TTTTTCGGTG
1301	TAGAACAGGC	AAATTGGGAC	AACTTCACGC	TTGAAGGCGG	CGTACGGCTG
1351	GAAAAACAAA	AAGCCTCCAT	CCGGTACGAC	AAAGATTGTA	TTGATCGAGA
1401	AAACTACTAC	AACCAGCCCC	TGCCCGCACT	CGGCGCGCAC	CGCCAAACCG
1451	CCCGCTTGTT	CGACTTTTCG	GGCAACTTGT	ATTTCACGCC	ACACCAACAA
1501	CTCAGCTTCA	CCGCTCCCCA	TACGAAACGC	CTGGCGTCAA	CGCAAGAACT
1551	GTACGCACAG	GGCAAGCAGC	TCGCCACCAA	CACCTTTGAA	GTCGGCAACA
1601	AACACCTCAA	CAAGAGCGGT	TTCAACAATA	TCGAATTCCG	CTGTGGGCTAC
1651	GAAGGCGACG	GCTGGCAATT	CAATCTGGCA	GCCTACCGCA	ACCGATTTCG
1701	CAACTACATT	TACGCCAAAA	CTTTAAACGA	CGGACGCGCG	CCCAAAATCCA
1751	TCGAAGACGA	CAGCGAAAATG	AAGCTCTGTG	GTACACAACCA	ATCCGGTGCC
1801	GACTTCTACG	GCGCGGAAGG	CGAAATCTAC	TTCAAACCGA	CACCGCGCTA
1851	CCGCATCGGT	GTTTCCGGCG	ACTATTGACG	AGGCCGTCTG	AAAAACCTGC
1901	CGTCCCTACC	CGGGAGGGAA	GATCCCTACG	GCAAAACGTCC	CTTCATCGCA
1951	CAAGCCGACC	AAAACGCCCC	CCGCATTCCG	GCTGCGCGCC	TCGGGTTCCA
2001	CCTGAAAAAC	TCGCTAACCG	ACCGTATCGA	TGCCAATTTG	GACTACTACC
2051	GCGTGTTCCG	CCAAAACCTA	CTGCCCCGCT	ACGAAACCGG	TACGCCCGGA
2101	CACCATATGC	TCAAACCTCG	TGCAAACTAC	CGCGGCAATA	CGCGCTATGG
2151	CGAGTGGAA	TGGTAGCTCA	AAGCGACCAA	CCTGCTCAAC	CAATCCGTTT
2201	ACGCCCCAG	CAGCTTCTCT	TCGTGATACG	CGCAAAATGG	CCGCAGCTTT
2251	ACCGCGGGCG	TAAACGTGAA	GTTTTAA		

**g149-1.pap**

1	MAQITLKPIV	LSILLINTPL	LAQARETEQS	VGLETVSUVG	KSRPRATSGL
51	LHTSTASDKI	ISGDTLRQA	VNLGDALDGV	PGIHASQYGG	GASAPVIRRG
101	TGRRIKVLNH	HGETGDMADF	SPDHAIMVDT	ALSQQVEILR	GPVTLLYSQQ
151	NVAGLVQVAD	GKIPKMPEN	GVSGEAGLRL	SSNGLEKLTG	AGINIGLGN
201	FVLHTEGLRY	KSGDYAVPRY	RNLKRLPDSH	ADSQTGSIGL	SWVGKGGFIG
251	AAYSDRRDRY	GLPAHSHEYD	DCHADGIWOK	SILINKRYQLG	YQPHLLTEEDI
301	YDYNPLSCG	FHDGGAHAH	THNGKPIWDL	RNKRYELRAE	WKQFPGFEA

```

351 LRVHLNRNDY HHDEKAGDAV ENFFNNKTHN ARIELRHQPI GRLKGSWGVQ
401 YLGQKSSALS AIPETVQQPM LIDNNVRHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NQPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY
551 EGDWRQYNLA AYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DPYGKRPFIA
651 QADQNAPIRI AARLGFHLKT SLTDRIDANL DYYRVFAONK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 603>:

m149-1.seq

```

1 ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51 CACACCCCTC CTCGCCAAG CGCATGAAAC TGAGCAATCG GTGGATTGCG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGGCCAC GTCGGGGCTG
151 TTGCACACTT CGACCGCCTC CGACAAAATC ATCTCCGGCG ATACCTTGCG
201 CCAAAAAGCC GTCAACTTGG GCGACGCTT AGACGGCGTA CCGGGCATCC
251 ACGCTTCGCA ATACGGCGGC GCGCGCTCTG CTCCCGTCAT TCGCGGTCAA
301 ACAGCGAGCG GGATTAAAGT GTTGAACCAT CACGGCGAAA CAGGCGATAT
351 GCGCGATTTT TCGCCCGATC ACGCCATTAT GGTAGATACC GCCTTGTCGC
401 AACAGGTCGA AATCCTGCGC GGGCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCTGA TGTGCGCAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAAAC GCGGTATCGG GCGAACTCGG ATTGCGTTT AGCAGCGGCA
551 ATCTGGAAAA ACTCACGTCC GCGCGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCGCGTCC CGCAATCTGA AACGCTGCC CGACAGCCAC CCGGATTTCG
701 AAACGGGCGC CATCGGGCTG TCTTGGGTG GCGAAAAGG TTTATCGGC
751 GTAGCGTACA GCGACCGTCG CGACCAATAT GGTCTGCCTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGCTTGATTA
851 ACAAACGCTA TTTACAGCTT TATCCGCACC TGTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTCCACGACG ACGATAATGC
951 ACACGCACAC ACCCACAGCG GCAGACCGTG GATAGACCTG CGCAACAAC
1001 GCTACGAACT CCGTGCCGAA TGGAAACAAAC CGTTCCCGG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCAGTC GAAAACCTTT TTAACAACCA AACGCAAAAC GCCCGCATCG
1151 AGTTGCGCCA CCAACCCATA GGTGCTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTACAAC AAAAATCCAG TGCTTTATCT GCCATATCCG AAGCGGTAA
1251 ACAACCGATG CTGCTTGACA ACAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACGAGC AACTGGGAC AACTTCACGC TTGAAGGAGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT TCAGTACGAC AAAGCATTGA TTGATCGGGA
1401 AAATACTACT AACCAACCCC TGCCCGACCT CGCGCGCAC CGCCAAACCG
1451 CCCGCTCAT CGCACTTTCG GGCAACTGGT ATTTCACGCC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCGCTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAAACACG TCGCCACCAA CACCTTTGAA GTCGGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGCTAC
1651 GAAGCGGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 TAACTACATT TACGCCCAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GTTACAACCA ATCCGGCGCC
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGCTG AAAAACCTGC
1901 CTTCCCTACC CGGCAGAGAA GATGCCTACG GCAACGTCC TTTTCATCGCA
1951 CAGGACGACC AAAATGCCCC CCGTGTTCGG GCTGCGCGCC TCGGCTTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGTATCGA TGCCAATTG GACTACTACC
2051 GCGTGTTCGC CCAAAACAAA CTCGCCCGCT ACGAAACGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTTCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCG TGAACGTGAA GTTTTAA

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This corresponds to the amino acid sequence <SEQ ID 604; ORF 149-1>:

m149-1.pop

```

1 MAQTLKPIV LSILLINTPL LAQAHETEQS VDLETVSUVG KSRPRATSG
51 LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGO
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDT ALSQVEILR GPVTLLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSSELGLRL SSGNLEKLT SGINIGLGKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTGSIGL SWVGEKGFIG
251 VAYSDRRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLGSCG FHDDDNAHAH THSGRPWIDL RNKRYELRAE WKQFPFGFEA
351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVQ
401 YLQKSSALS AISEAVQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIQYD KALIDRENY NHPLPDLGAH RQTARSFALS GNWYFTPHHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKER SNNIELALGY

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551 EGDWQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA  
 601 DFYGAEGEII FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPFFIA  
 651 QDDQNAPRVP AARLGFHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG  
 701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSE  
 751 TGGVNVKF\*

m149-1/g149-1 96.2% identity in 758 aa overlap

m149-1.pep	10	20	30	40	50	60
	MAQTTLKPIVLSILLINTPLLAQAHETEQSVLETVSVVGKSRPRATSGLLHTSTASDKI					
g149-1	10	20	30	40	50	60
	MAQITLKPIVLSILLINTPLLAQAHETEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
m149-1.pep	70	80	90	100	110	120
	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
g149-1	70	80	90	100	110	120
	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
m149-1.pep	130	140	150	160	170	180
	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
g149-1	130	140	150	160	170	180
	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSEAGLRL					
m149-1.pep	190	200	210	220	230	240
	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
g149-1	190	200	210	220	230	240
	SSGNLEKLTSGGINIGLGKNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
m149-1.pep	250	260	270	280	290	300
	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
g149-1	250	260	270	280	290	300
	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADIIWQKSLINKRYLQLYPHLLTEEDI					
m149-1.pep	310	320	330	340	350	360
	DYDNFGLSCGFHDDNAHAHSTHSGRPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY					
g149-1	310	320	330	340	350	360
	DYDNFGLSCGFHDDNAHAHSTHSGRPWIDLNRKRYELRAEWKQFPFGFEALRVHLNRNDY					
m149-1.pep	370	380	390	400	410	420
	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGQVQLQKSSALSAISEAVKQPM					
g149-1	370	380	390	400	410	420
	HHDEKAGDAVENFFNNKTHNARIELRHQPIGRLKGSWGQVQLQKSSALSAIPETVQQPM					
m149-1.pep	430	440	450	460	470	480
	LLDNKVQHYSSFFGVEQANWDNFTLEGGVVRVEKQKASIYDKALIDRENYNHPPLDLGAH					
g149-1	430	440	450	460	470	480
	LIDNNVRHYSSFFGVEQANWDNFTLEGGVVRVEKQKASIRYDKALIDRENYNQPLDLGAH					
m149-1.pep	490	500	510	520	530	540
	RQTARSFALSGNWWYFTPHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
g149-1	490	500	510	520	530	540
	RQTARSFALSGNWWYFTPHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
m149-1.pep	550	560	570	580	590	600
	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
g149-1	550	560	570	580	590	600
	SNNIELALGYEGDRWQYNLAAYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
m149-1.pep	610	620	630	640	650	660
	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDAYGNRPFFIAQDDQNAPRVP					
g149-1	610	620	630	640	650	660
	DFYGAEGEIIYFKPTPRYRIGVSGDYVRGRLKNLPSLPGREDPYGKRPFIAQADQNAPRIP					



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        670      680      690      700      710      720
m149-1.pep  AARLGPHLKASLTDRIDANLDYYRVFAQNKLYETRTPGHHMLNLGANYRRNTRYGEWN
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g149-1       AARLGPHLKTSLTDRIDANLDYYRVFAQNKLYETRTPGHHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

        730      740      750      759
m149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 605>:

```

a149-1.seq
1  ATGGCACAAA CTACACTCAA ACCCATTGTT TTATCAATTC TTTTAATCAA
51  CACACCCCTC CTCTCCCAAG CGCATGGAAC TGAGCAATCA GTGGGCTTGG
101 AAACGGTCAG CGTCGTCGGC AAAAGCCGTC CGCGCGCCAC TTCGGGGCTG
151 CTGCACACTT CTACCGCCTC CGACAAAATC ATCAGCGGCG ACACCTTGCG
201 ACAAAAAGCC GTCAACTTGG GTGATGCTTT AGACGCGCTA CCGGGCATTG
251 ATGCTCTCGA ATACGGCGGC GCGCATCCG CTCCCGTTAT TCGCGGTCAA
301 ACAGGCAGAC GGATTAAAGT GTTGAACCAT CACGCGGAAA CGGGCGACAT
351 GCGGCACTTC TCTCCAGACC ATGCAATCAT GGTGGACAGC GCCTTGTCGC
401 AACAGGTGCA AATCCTGCGC GGTCCGGTTA CGCTCTTGTA CAGCTCGGGC
451 AATGTGGCGG GGCTGGTCTG TGTGCCGAT GGCAAAATCC CCGAAAAAAT
501 GCCTGAAATC GCGGTATCGG GCGAACTCGG ATTGCGTTTG AGCAGCGGCA
551 ATCTGGAAAA ACTCACGTCC GCGGCATCA ATATCGGTTT GGGCAAAAAC
601 TTTGTATTGC ACACGGAAGG GCTGTACCGC AAATCGGGGG ATTACGCCGT
651 ACCCGGTTAC CGCAATCTGA AACGCCTGCC CGACAGCCAC GCCGATTTCG
701 AAACGGGCGC CATCGGGCTG TCTGGGTTG GCGAAAAAGG CTTTATCGGC
751 GCAGCATACA GCGACCGTCG CGACCAATAT GGTCTGCGTG CCCACAGCCA
801 CGAATACGAT GATTGCCACG CCGACATCAT CTGGCAAAAG AGTTTGATTA
851 ACAAACGCTA TTTGCAGCTT TATCCGCACC TGTTGACCGA AGAAGACATC
901 GATTACGACA ATCCGGGCTT GAGCTGCGGC TTTCACGACG ACGATGATGC
951 ACACGCCCCA GCCCACAACG GCAAACCTTG GATAGACCTG CGCAACAAAC
1001 GCTACGAAC TCGCGCGGAA TGGAAGCAAC CGTTCGCCCG TTTTGAAGCC
1051 CTGCGCGTAC ACCTGAACCG CAACGACTAC CGCCACGACG AAAAAGCAGG
1101 CGATGCGAGT GAAAACCTTT TTAACAACCA AACGCAAAAC GCCCGTATCG
1151 AGTTGCGCCA CCAACCCATA GGCGGTCTGA AAGGCAGCTG GGGCGTGCAA
1201 TATTTGGGAC AAAAATCCAG TGCTTTATCT GCCACATCCG AAGCGGTCAA
1251 ACAACCGATG CTGCTTGACA ATAAAGTGCA ACATTACAGC TTTTTCGGTG
1301 TAGAACAGGC AAACCTGGAC AACTTCACGC TTGAAGGCGG CGTACGCGTG
1351 GAAAAACAAA AAGCCTCCAT CCGCTACGAC AAAGCATTGA TTGATCGGGA
1401 AAACCTACTA AACCATCCCC TGCCCGACCT CGGCGCGCAC CGCCAAACCG
1451 CCCGCTCATT CGCACTTTCT GGCAACTGGT ATTTACGCGC ACAACACAAA
1501 CTCAGCCTGA CCGCCTCCCA TCAGGAACGC CTGCGCTCAA CGCAAGAGCT
1551 GTACGCACAC GGCAACACAG TCGCCACCAA CACCTTGAA GTCCGCAACA
1601 AACACCTCAA CAAAGAGCGT TCCAACAATA TCGAACTCGC GCTGGGTAC
1651 GAAGCGGACC GCTGGCAATA CAATCTGGCA CTCTACCGCA ACCGCTTCGG
1701 CAACTACATT TACGCCAAA CCTTAAACGA CGGACGCGGC CCCAAATCCA
1751 TCGAAGACGA CAGCGAAATG AAGCTCGTGC GCTACAACCA ATCCGGTGCG
1801 GACTTCTACG GCGCGGAAGG CGAAATCTAC TTCAAACCGA CACCGCGCTA
1851 CCGCATCGGC GTTCCGGCG ACTATGTACG AGGCCGTCTG AAAAACCTGC
1901 CTTCCCTACC CGGAGGGAA GACGCTACG GCAACCGCCC ACTCATTGCC
1951 CAAGCCGACC AAAACGCCCC TCGCGTTCCG GCTGCGCGCC TCGGCGTCCA
2001 CCTGAAAGCC TCGCTGACCG ACCGCATCGA TGCCAAATTG GACTACTACC
2051 GCGTGTTCGC CAAAACAAA CTCGCCGCT ACGAACCGCG CACGCCCGGA
2101 CACCATATGC TCAACCTCGG CGCAAACTAC CGCCGCAATA CGCGCTATGG
2151 CGAGTGGAAT TGGTACGTCA AAGCCGACAA CCTGCTCAAC CAATCCGTTT
2201 ACGCCACAG CAGCTTCCTC TCTGATACGC CGCAATGGG CCGCAGCTTT
2251 ACCGCGGCG TGAACGTGAA GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 606; ORF 149-1.a>:

```

a149-1.pep
1  MAQTLKPIV LSILLINTPL LSQAHGTEQS VGLTVSVVG KSRPRATSGL
51  LHTSTASDKI ISGDTLRQKA VNLGDALDGV PGIHASQYGG GASAPVIRGQ
101 TGRRIKVLNH HGETGDMADF SPDHAIMVDS ALSQQVEILR GPVTTYLYSSG
151 NVAGLVDVAD GKIPEKMPEN GVSGLGLRL SSGNLEKITS GGINIGLKN
201 FVLHTEGLYR KSGDYAVPRY RNLKRLPDSH ADSQTSGISL SWVGERGFIG
251 AAYSDDRDQY GLPAHSHEYD DCHADIIWQK SLINKRYLQL YPHLLTEEDI
301 DYDNPLSCG FHDDDDAHAA AHNGKPWIDL RNKRYELRAE WRQFPFGFEA

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351 LRVHLNRNDY RHDEKAGDAV ENFFNNQTON ARIELRHQPI GRLKGSWGVO
401 YLGQKSSALS ATSEAVKQPM LLDNKVQHYS FFGVEQANWD NFTLEGGVRV
451 EKQKASIRYD KALIDRENY NHPPLDLGAH RQTARSFALS GNWYFTPOHK
501 LSLTASHQER LPSTQELYAH GKHVATNTFE VGNKHLNKR SNNIELALGY
551 EGDWRQYNLA LYRNRFGNYI YAQTLNDGRG PKSIEDDSEM KLVRYNQSGA
601 DFYGAEGEYI FKPTPRYRIG VSGDYVRGRL KNLPSLPGRE DAYGNRPLIA
651 QADQNAAPRV AARLGVHLKA SLTDRIDANL DYYRVFAQNK LARYETRTPG
701 HHMLNLGANY RRNTRYGEWN WYVKADNLLN QSVYAHSSFL SDTPQMGRSF
751 TGGVNVKF*

```

a149-1/ml49-1 98.0% identity in 758 aa overlap

a149-1.pep	10	20	30	40	50	60
	MAQTTLKPIVLSILLINTPLLQAHGTEQSVGLETVSVVGKSRPRATSGLLHTSTASDKI					
ml49-1	MAQTTLKPIVLSILLINTPLLQAHETEQSVDLLETVSVVGKSRPRATSGLLHTSTASDKI					
	10	20	30	40	50	60
a149-1.pep	70	80	90	100	110	120
	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
ml49-1	ISGDTLRQKAVNLGDALDGVPGIHASQYGGGASAPVIRGQTGRRIKVLNHHGETGDMADF					
	70	80	90	100	110	120
a149-1.pep	130	140	150	160	170	180
	SPDHAIMVDSALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
ml49-1	SPDHAIMVDTALSQQVEILRGVPTLLYSSGNVAGLVDVADGKIPEKMPENGVSSELGLRL					
	130	140	150	160	170	180
a149-1.pep	190	200	210	220	230	240
	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
ml49-1	SSGNLEKLTSGGINIGLGNFVLHTEGLYRKSGDYAVPRYRNKRLPDSHADSQTGSIGL					
	190	200	210	220	230	240
a149-1.pep	250	260	270	280	290	300
	SWVGEKGFIGAAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI					
ml49-1	SWVGEKGFIVAYSDDRDQYGLPAHSHEYDDCHADI IWQKSLINKRYLQLYPHLLTEEDI					
	250	260	270	280	290	300
a149-1.pep	310	320	330	340	350	360
	DYDNFGLSCGFHDDDAHAHAHNGKPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
ml49-1	DYDNFGLSCGFHDDNAHAHNGKPWDLRNKRYELRAEWKQFPFGFEALRVHLNRNDY					
	310	320	330	340	350	360
a149-1.pep	370	380	390	400	410	420
	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVOYLGQKSSALSATSEAVKQPM					
ml49-1	RHDEKAGDAVENFFNNQTONARIELRHQPIGRLKGSWGVOYLGQKSSALSATSEAVKQPM					
	370	380	390	400	410	420
a149-1.pep	430	440	450	460	470	480
	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH					
ml49-1	LLDNKVQHYSFFGVEQANWDNFTLEGGVRVEKQKASIRYDKALIDRENYNHPPLDLGAH					
	430	440	450	460	470	480
a149-1.pep	490	500	510	520	530	540
	RQTARSFALSGNWYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
ml49-1	RQTARSFALSGNWYFTPOHKLSLTASHQERLPSTQELYAHGKHVATNTFEVGNKHLNKR					
	490	500	510	520	530	540
a149-1.pep	550	560	570	580	590	600
	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
ml49-1	SNNIELALGYEGDRWQYNLALYRNRFGNYIYAQTLNDGRGPKSIEDDSEMMLVRYNQSGA					
	550	560	570	580	590	600
	610	620	630	640	650	660

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a149-1.pep  DFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPLIAQADQNAPRVP
              |||||
m149-1       DFYGAEGEIYFKPTPRYRIGVSGDYVRGLKNLPSLPGREDAYGNRPFIAQDDQNAPRVP
              610      620      630      640      650      660

              670      680      690      700      710      720
a149-1.pep  AARLGVHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              |||||
m149-1       AARLGFHLKASLTDRIDANLDYYRVFAQNKLARYETRTPGHHMLNLGANYRRNTRYGEWN
              670      680      690      700      710      720

              730      740      750      759
a149-1.pep  WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              |||||
m149-1       WYVKADNLLNQSVYAHSSFLSDTPQMGRSFTGGVNVKFX
              730      740      750

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 607>:

```

g150.seq (partial)
1  ..TACTGCAAGG CAGACCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT
51  CACCGCCCGC CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGA
101 GCGGTTTCGA TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGTTT
151 GACAACGATC CGGCACTGGT CGGGGAAATC CTAGACCTGC TCGGCATCAA
201 TCCGGCAACG GAAATACAGG CGGGCGGAAA AACCTGCCG GTTGCCCTCCG
251 CACTGTTATC CCATTTGAA CTACGCAAA ACACCCCGC CTTTGTCAA
301 GGCTATGCCA CGTTCGCCGA TAATGACGAA CTCGACCGTA TTGCTGCCGA
351 CAACGCCGTT TTGCAAGGCT TTGTGCAAAG CACGCCGATT GCCGGTGTGC
401 TGCACCGCTT CCCGGCAAAA CTGACGGCGG AACAAATCGC CGGCCTGCTG
451 CGCCCGCTTG CGCCGCGCCT GTATTCGATT TCCTCGTCGC AGGCGGAAGC
501 GGGGGACGAA GTGCACCTGA CCGTCGGCGC AGTGCCTTTC GAACACGAAG
551 GGCGCGCCAG GCGGGCGGCG GCATCGGGTT TCTTTGCCGA CCGGCTGGAA
601 GAGGACGGCA CGGTGCGCGT GTTTGCGGAA CGCAACGACG GCTTCAGGCT
651 GCCCGAAGAC AGCCGCAAGC CGATTGTGAT GATCGGCTCC GGTACCGGCG
701 TCGCACCGTT CCGCGCCTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA
751 GGCAGAAACT GGCTGATTTT CGGCAATCCG CATTTTGCCG CCGACTTCCT
801 CTATCAGACC GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT
851 ATGACTTCGC CTGGTCGCGC GATCAGGAAG AAAAAATCTA TGTGCAGGAC
901 AAAATCCGCG AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC
951 GCATATCTAT GTGTGCGGCG ATGCGGCAA AATGGCAAAA GAAGTGAAG
1001 CCGCCTTGCT GGATGTGATT ATCGGGGCG GGCATTCGGA CGAAGACGGC
1051 CCAGAAGGAT ATTTGGATAT GCTGCGCGAA GAAAAACGCT ATCAGCGTGA
1101 TGTATTATGA

```

This corresponds to the amino acid sequence <SEQ ID 608; ORF 150.ng>:

```

g150.pep (partial)
1  ..YCKADFPFAA LLANQKITAR QSDKDVRHIE IDLSGSDLHY LPGDALGVWF
51  DNDPALVGEI LDLLGINPAT EIQAAGKTLF VASALLSHFE LTQNTPAFVK
101 GYATFADNDE LDRIAADNAV LQGFVQSTPI AGVLHRFPK LTAEQFAGLL
151 RPLAPRLYSI SSSQAEAGDE VHLTVGAVRF EHEGRARAGG ASGFFADRLE
201 EDGTVRVFAE RNDGFRLEPED SRKPIVMIGS GTGVAPFRAF VQORAAENAE
251 GRNWLIFGNP HFAADFLYQT EWQQFAKDG F LHRDYFAWSR DQEEKIYVQD
301 KIREQAEGLW OWLQEGAHY VCGDAAKMAK EVEAALLDVI IGAGHSDDEDG
351 AEGYLDMLRE EKRYQRDVY*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 609>:

```

m150.seq
1  ATGCAGAACA CAAATCCGCC ATTACCGCCT CTGCCGCCCG AAATCAACGCA
51  GTCCTGTGTC GGGCTGGACG CGGCACAATG GCGGTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGAAAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGGCGGCGA ACCTTTTTC GTAACCGTCC TTTCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCGG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGCGGAACG CCGCCTGCTG CTGGTTACCT CCACCCAAGG
351 CGAAGGCGAA CCGCCGAAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCGAAATTG GACAACTCC AATTGCGCGT ACTGGGTTTG

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451 GCGACAGTT CCTATCCGAA TTTCTGTCAG GCAGGTAAAG ATTTGACCG
501 GCGTTTTTGAA GAATTGGGCG CAAAACGCT GTCGAACGC GTTGATGCGG
551 ATTTGGACTT TACCGCTCC GCAAACGCT GGACAGATAA TATCGCCGCA
601 CTCTTAAAAG AAGAAGCCGC AAAAAACCG GCAACGCCCG CGCCGAGAC
651 AACGCCCCC GCGGCCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGCCCCCTT TCCCGCCGCC CTGCTGGCCA ATCAGAAAAT CACCGCCGCG
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTGA GCGGTTGCGA
801 TTTGCACTAC CTCCCGGGCG ACGCGCTCGG CGTTTGTTT GACAACGATC
851 CCGCACTGGT CAGGGAAATC CTAGACCTGC TCGGCATCGA TCCGGCAACG
901 GAAATACAGG CGGGCGGAAA GATGATGCCG GTTGGCGCGG CACTTTCATC
951 TCATTTGAA CTCACGCAA AACTCCGGC TTTCGTCAA GGCTATGCCG
1001 CGTTCGCCCA TTATGAAGAA CTCGATAAAA TCATTGCCGA TAACGCCGTT
1051 TTGCAGGATT TCGTGCAAAA CACGCCTATT GTCGATGTGC TGCACCGCTT
1101 CCCGGCAAGC CTGACGGCAG AACAATTCAT CCGTTTACTG CGTCCGCTTG
1151 CACCCCGTTT GTATTGATT TCTTCAGCAC AGGCGGAAGT GGGCGATGAA
1201 GTGCATTAA CTGTCGGCGT GGTTCGTTT GAACACGAAG GCCCGCCAG
1251 AACGGGCGGC GCATCGGGT TCCTTGCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTGTGGAA CGCAACGACG GCTTCAGGCT GCCCGAAGAC
1351 AGCCGCAAGC CGATTGTGAT GATCGGCTCG GGCACCGCG TCGCACCGTT
1401 CCGCGCTTTC GTCCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAACT
1451 GGCTGATTTT CGCAATCCG CATTGTGCC GTGATTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGG ACGATTTCG
1551 CTGGTCCGCG GATCAGGAAG AAAAAATCTA TGTGCAGGAC AAAATCCGCG
1601 AACAGGCGGA AGGACTTTGG CAATGGCTGC AGGAAGGCGC GCATATCTAT
1651 GTGTGCGGCG ATGCGGCAAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT
1701 GGATGTGATT ATCGGGGCG GACATTGGA CGAAGAGGGC GCAGAAGAAT
1751 ATTTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA TGTTTATTGA

```

This corresponds to the amino acid sequence <SEQ ID 610; ORF 150>:

m150.pep

```

1  MQNTNPPLPP LPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ
51  TALPAAEPFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA
101 KNIAGERRLL LVTSTQGEGE PPKEAVVLHK LLNGKKAPKL DKLQFAVLGL
151 GDSSYPNFCQ AGKDFDRRFE ELGAKRLLER VDADLDFTAS ANAWTDNIAA
201 LLKEEAANKR ATPAPQTPP AGLQTAPDGR YCKAAPFPAA LLANQKITAR
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI LDLLGIDPAT
301 EIQAGGKMP VARALSSHFE LTQNTPAFVK GYAFAHYEE LDKIIADNAV
351 LQDFVQNTPI VDLVHRFPAS LTAEQFIRLL RPLAPRLYSI SSAQAEVGDE
401 VHLTVGVVRF EHEGRARTGG ASGFLADRLE EDGTVRVFVE RNDGFRLPED
451 SRKPIVMIGS GTGVAPFRAF VQRAAENAE GKNWLIIGNP HFARDFLYQT
501 EWQQFAKDFG LHRYDPAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHYI
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 150 shows 91.3% identity over a 369 aa overlap with a predicted ORF (ORF 150.ng) from *N. gonorrhoeae*:

m150/g150

```

                210      220      230      240      250      260
m150.pep      LLKEEAANKRAT PAPQTFPAGLQTAPDGRYCKAAPFPAALLANQKITARQSDKDVRHIE
g150                                YCKADPFPAALLANQKITARQSDKDVRHIE
                                10      20      30

                270      280      290      300      310      320
m150.pep      IDLSGSDLHYLPGDALGVWFDNDPALVREILDLLGIDPATEIQAGGKMPVARALSSHFE
g150      IDLSGSDLHYLPGDALGVWFDNDPALVGEILDLLGINPATEIQAGGKTLFVASALLSHEF
                40      50      60      70      80      90

                330      340      350      360      370      380
m150.pep      LTQNTPAFVKGYAFAHYEELDKIIADNAVLDQDFVQNTPIVDVLRFPASLTAEQFIRLL

```

```

a150.seq
1 ATGCAGAACA CAAATCCGCC ATTACCGCCT ATGCCGCCCG AAATCACGCA
51 GCTCCTGTCC GGGCTGGACG CGGCACAATG GCGCTGGCTG TCCGGCTACG
101 CTTGGGCAAA AGCAGGA AAC GGGGCATCTG CAGGACTGCC CGCGCTTCAG
151 ACGGCATTGC CGACGGCAGA ACCTTTTTC GTAACCGTCC TTTCCGCCTC
201 GCAAACCGGC AATGCGAAAT CCGTTGCCGA CAAAGCGGCG GACAGCCTGG
251 AAGCCGCCGG CATCCAAGTC AGTCGCGCCG AACTGAAAGA CTATAAGGCG
301 AAAAACATCG CCGGCGAAGC CCGCCTGTCT CTGGTTACCT CCACCCAAGG
351 CGAAGCGGAA CCGCGGGAAG AAGCCGTCGT GCTGCACAAA CTGCTGAACG
401 GCAAAAAAGC CCCGAAATTG GACAAACTCC AATTTGCCGT ACTGGGTTTG
451 GGCACAGCT CCTATCCGAA TTTCTGCCGG GCGGGCAAAG ATTTGACAA
501 ACGTTTTGAA GAATTGGGCG CAAAACGCCT GCTCGAAGCG GTTGATCGGG
551 ATTTGGACTT TGCCGCCGCC CGACAGCGAT GGACAGATAA TATCGCCGCA
601 CTCTTAAAG AAGAAGCCGC GAACAAACGG GACACGCCCG CGCCGCAGAC
651 AACGCCCCCC GCCGGCCTTC AGACGGCACC GGATGGCAGG TACTGCAAGG
701 CAGACCCCTT TCCCGCGGCC CTGCTGCCCA ATCAGAAAAT CACCGCCCGC
751 CAATCCGATA AAGACGTGCG CCACATCGAA ATCGATTTGA GCGGTTTCGA
801 TTTGCACTAC CTCGCCGGCG ACGCGCTCGG CGTTTGGTTT GACAACGATC
851 CGGCACTGGT CAGGGAATTC CTAGACCTGC TCGGCATCGA TCAGGCAACG
901 GAAATACAGG CGGGCGGAAA AACCCTGCCG GTTGCCCTCCG CACTGTTATC
951 CCATTTTGAA CTCACGCAA ACACCCCGC CTTTGTCAA GGCTATGCCC
1001 CGTTGCGCGA TGATGACGAA CTCGACCCTA TTGCTGCCCA CAACGCCGTT
1051 TTGCAAGGCT TTTGCAAGG CACGCCGATT GCGCATGTGC TGCACCGCTT
1101 CCGGCAAAA CTGACGCGG AACAAATCGC CGCGCTACTG CGCCCGCTTG
1151 CGCCGCGCCT GTATTCGATT TCCTCGTCGC AGGCGGAAGT GGGGGACGAA
1201 GTGCACCTGA CCGTCGGCGC GGTGCGTTTC GAACACGAAG GGCGCCCCAG
1251 GGCGGCGGCG GCATCGGGTT TCCTGCCCGA CCGGCTGGAA GAGGACGGCA
1301 CGGTGCGCGT GTTTGTGGA CGCAACGACG GCTTCAGGCT GCGCGAAGAC
1351 AGCCCGCAAG CATTTGTGAT GATCGGCTCG GGACCCGGCG TCGCACCGTT
1401 CGCGCCTTTC GTTCAACAAC GTGCCGAGA AAATGCGGAA GGCAAAAAC
1451 GGCTGTTTTT CGGCAATCCG CATTTTGCCC GTGATTTTCT CTATCAAACC
1501 GAATGGCAGC AGTTTGCCAA AGACGGCTTC CTGCACAGAT ACGATTTCGC
1551 CTGGTCGCGC GATCAGGAAG AAAAACTA TGTCAGGAC AAAATCCGCG
1601 AACAGCGGGA AGGACTTTGG CAATGGCTGC AGGAAGCGCG GCATATCTAT
1651 GTGTGCGGCG ATCGCGCAA AATGGCAAAA GACGTGGAAG CCGCCTTGCT

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1701 GGATGTGATT ATCGGGGCAG GACATTGGA CGAAGAGGC GCAGAAGAAT  
1751 ATTTGGATAT GCTGCGCGAA GAAAACGCT ATCAGCGTGA TGTTTATTGA

This corresponds to the amino acid sequence <SEQ ID 612; ORF 150.a>:

a150.pep

1 MQNTNPPLPP MPPEITQLLS GLDAAQWAWL SGYAWAKAGN GASAGLPALQ  
51 TALPTAEFFS VTVLSASQTG NAKSVADKAA DSLEAAGIQV SRAELKDYKA  
101 KNIAGERLLL LVTSTQGEGE PPEEAVVLHK LLNGKKAPKL DKLQFAVLGL  
151 GDSSYPNFCR AGKDFDKRFE ELGAKRLLER VDADLDFAAA ADGWTDNIAA  
201 LLKEEAAKNR ATPAPQTTPP AGLQTAPDGR YCKADPFPAF LLANQKITAR  
251 QSDKDVRHIE IDLSGSDLHY LPGDALGVWF DNDPALVREI DLLLGIDQAT  
301 EIQAGGKTLF VASALLSHFE LTQNTPAFVK GYAPFADDDE LDRIAADNAV  
351 LQGFVQSTPI ADVLHRFPK LTAEQFAGLL RPLAPRLYSI SSSQAQEVGDE  
401 VHLTGVAVRF EHEGRARAGG ASGFLADRLE EDGTVRVFVE RNDGFRLEPED  
451 SRKPIVMIGS GTGVAPFRAF VQORAAENAE GKNWLFNGNP HFARDFLYQT  
501 EWQQFAKDGFLHRYDFAWSR DQEEKIYVQD KIREQAEGLW QWLQEGAHY  
551 VCGDAAKMAK DVEAALLDVI IGAGHLDEEG AEEYLDMLRE EKRYQRDVY\*

m150/a150 94.8% identity in 599 aa overlap

m150.pep	10	20	30	40	50	60
a150	10	20	30	40	50	60
m150.pep	70	80	90	100	110	120
a150	70	80	90	100	110	120
m150.pep	130	140	150	160	170	180
a150	130	140	150	160	170	180
m150.pep	190	200	210	220	230	240
a150	190	200	210	220	230	240
m150.pep	250	260	270	280	290	300
a150	250	260	270	280	290	300
m150.pep	310	320	330	340	350	360
a150	310	320	330	340	350	360
m150.pep	370	380	390	400	410	420
a150	370	380	390	400	410	420
m150.pep	430	440	450	460	470	480
a150	430	440	450	460	470	480
m150.pep	490	500	510	520	530	540
a150	490	500	510	520	530	540

```

a150      GKNWLF FGNPHF ARDFLY QT EWQF AKDGF LHR YDFA WSRDQ EEKIY VQDKI REQA EGLW
           490      500      510      520      530      540

m150 . pep      550      560      570      580      590      600
QWLQEGAH IYVCGDAAKMAKDVEAALLDVII GAGHLDEEGAE EYLDMLRE EKRYQRDVYX
|||||
a150      QWLQEGAH IYVCGDAAKMAKDVEAALLDVII GAGHLDEEGAE EYLDMLRE EKRYQRDVYX
           550      560      570      580      590      600

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 613>:

g151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCACACGTCG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTG
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGCGAAG
251 TGGAGCGCGT TTTGGGGATG GTGGATTGCG TCGTCTTGT TGGTGACGCA
301 CAGGAAGGTC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGCG
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAACCGTCCG
401 CCCGTCGAG CTGGGTTATC GACCAGACTT TCGAGTTGTT CGACAACTTG
451 GGTGCGACCG ACGAGCAGTT GGATTTCCTG ATGTTTACG CTTCAGGTTT
501 GAGCGGCTTT GCCAAGCTGG AAGAAaccga CGAGAGCAGC GATATGCGCC
551 CGctgttcga CACCATCCTA AAATACacgc ctgCACCGAG CCGCAGCGCG
601 GACGAGCCGC TGCAACTGCA AATTTCCCAA CTCGACTACG ACAACTACAC
651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGCATC AAACCGCGCC
701 AAACCGTTGC CGTGATGAAC CACGAGCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGCTTGGA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCCGGC GACATTGTGA TTATTTCGGG TATCGAAGAC ATCGGCATCG
851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTAAACA CCAGCCCGCT
951 CGCAGGTACA GAAGGCAAAT TCGTGACCAG CCGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTTGCCG TGCGCGTGGA AGACACCGCC
1051 GatgCCGACG TGTTCCGCGT ATCcgGGCGC GCGGAAGTGC ACCTGACGAT
1101 TTTGCTGGAA AATATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAGC
1151 CGCGCGTCGT GTACCGAGAC ATCGACGGTC AAAAAATGCGA ACCTTATGAA
1201 AACCTGACTG TGGACGTACc cgacgacAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCGTGCGG AACTGACCAA TATGGAAGC GACGCAACG
1301 GacgCACCCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TCATGACCCT GACGCGCGGC GTCGGGCTGA TGAgccacGT
1401 GTTcgacgac tacgcgcccg tcaAACCCGA TATGCCCCGC CGCCACAACG
1451 GCGTactggt GtcccaAGAG CAGGGCGAGG CGTTTGCTTA CGCCTGTGTTG
1501 AATCTTGAAG ACCGCGGCCG TATGTTGCTA TCGCCCAACG ACAAATCTA
1551 CGAAGGTATG ATTATCGGCA TCCACAGCCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTCACCAATA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGGTGC GCCTGACCAC GCCGATCAAA CTGacgcTGG AAGGCGCGGT
1701 CGAGTTTATC GACGATGACG AGCTGGTGGG AATCAGCCG CAatccatcc
1751 gcctgcgcat gcgttacctG AGCGaattgg aacgccgccc tcaTTTTAAA
1801 AagctgGATT AA

```

This corresponds to the amino acid sequence <SEQ ID 614; ORF 151.ng>:

g151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE
51  RGITILAKNT AIDYEGCHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESS DMRPLFDLIL KYTPAPSGSA
201 DEPLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQTVAVMN HEQQIAQGRI
251 NQLLGFKGLE RVPLEAEAG DIVIISGIED IGIGVTITDK DNPKGLEPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLQKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDPDDN QGAVMEELGR RRGETLNMES DGNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHFDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW

```

501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD  
 551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRMYL SELERRRHF  
 601 KLD\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 615>:

m151.seq

```

1  ATGAAACAAA TCCGCAACAT CGCCATCATC GCCCAGTCTG ACCACGGCAA
51  AACCACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA
101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA
151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA
201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GCGCGCGAAG
251 TAGAGCGCGT TTTGGGGATG GTGGACTGCG TCGTCTTGT GGTGGACGCG
301 CAGGAAGGCC CGATGCCGCA AACCCTTTTC GTGACCAAAA AAGCCTTGCG
351 TTTGGGGCTG AAACCGATTG TCGTCATCAA CAAAATCGAC AAGCCGTCCG
401 CTCGTCCGAG CTGGGTTATC GACCAAACTT TCGAGCTGTT CGACAACTTG
451 GCGCGGACCG ACGAGCAGTT GGATTTCCCG ATTGTTTACG CTCAGGGTT
501 GAGCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATGCGTC
551 CGCTGTTCTA TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG
601 GACGAAACGC TGCAACTGCA AATTTCCTAA CTCGACTACG ACAACTACAC
651 CGGCGCGCTC CGTATCGGTC GTATCTTGAA CGGACGCATC AAACCCGGCC
701 AAACCGTTGC CGTCATGAAC CACGATCAGC AAATCGCCCA AGGCCGCATC
751 AACCAGCTTT TGGGTTTCAA AGGTTTGAA CGCGTGCCGC TTGAAGAAGC
801 CGAAGCGGC GACATCGTGA TTATTTCCGG TATCGAAGAC ATCGGTATCG
851 GCGTAACCAT CACCGACAAA GACAATCCCA AAGGCCTACC GATGTTGAGC
901 GTGGACGAAC CGACGCTGAC GATGGACTTT ATGGTCAACA CCAGCCCCTG
951 GCGGGGTACG GAAGGCAAT TCGTAACCAG CGGCCAAATC CGCGACCGCC
1001 TGCAAAAAGA ATTGCTGACC AACGTCGCCC TCGCGTGGA AGATACCGCC
1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGGAGCTGC ACCTGACCAT
1101 TTTGCTGGA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC
1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAATCGCA ACCGTATGAA
1201 AACCTGACCG TGGATGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA
1251 ACTCGGCCGC CGCCGTGGCG AACTGACTAA TATGGAAGC GACGGCAACG
1301 GACGCACCCG CTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGTTTC
1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT
1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCCGGC CGCCACAACG
1451 GCGTGCTGGT GTCCCAAGAG CAGGCGGAGG CAGTCGCTTA CGCCTTGTGG
1501 AATCTGGAAG ACCGCGGCGG TATGTTCTGA TCGCCCAACG ACAAATCTA
1551 CGAAGGCATG ATTATCGGCA TCCACAGTCG CGACAACGAT TTGGTGGTCA
1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC
1651 GAAGCGTTC GCCTGACCAC GCCAATCAAG CTGACGCTGG AAGGTGCGGT
1701 TGAGTTTATC GACGATGACG AACTCGTTGA AATCACGCCG CAATCCATCC
1751 GTCTGCGCAA GCGTTACTTG AGCGAATTGG AACGCCGCCG CCACTTTAA
1801 AAGCTGATT GA

```

This corresponds to the amino acid sequence <SEQ ID 616; ORF 151>:

m151.pep

```

1  MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQVQDER VMDSNDLEKE
51  RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVLLVDA
101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL
151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDLIL KYTPAPSGSA
201 DETLQLQISQ LDYDNYTGRL GIGRIILNGRI KPGQTVAVMN HDQQAQGR
251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IIGVTTITDK DNPKGLPMLS
301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA
351 DADVFRVSGR GELHLTILLE NMRREGYELA VGKPRVVYRD IDGQKCEPYE
401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF
451 QGEFMTLTRG VGLMSHVFD YAPVKPDMFG RHNGVLVSQE QGEAVAYALW
501 NLEDGRGMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGKK LTNIRASGTD
551 EAVRLTTPIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHF
601 KLD*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N.gonorrhoeae*

ORF 151 shows 99.2% identity over a 603 aa overlap with a predicted ORF (ORF 151.ng) from *N. gonorrhoeae*:

m151/g151

m151.pep	10	20	30	40	50	60
	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
g151	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT					
m151.pep	70	80	90	100	110	120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
g151	AIDYEGCHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL					
m151.pep	130	140	150	160	170	180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESN					
g151	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFPIVYASGLSGFAKLEETDESS					
m151.pep	190	200	210	220	230	240
	DMRPLFDITILKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
g151	DMRPLFDITILKYTPAPSGSADEPLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN					
m151.pep	250	260	270	280	290	300
	HDQQIAQGRINQLLGFKGLERVPLEEAEGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
g151	HEQQIAQGRINQLLGFKGLERVPLEEAEGDIVIISGIEDIGIGVTITDKDNPKGLPMLS					
m151.pep	310	320	330	340	350	360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
g151	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDRLQKELLTNVALRVEDTADADVFRVSGR					
m151.pep	370	380	390	400	410	420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDV PDDNQGAVMEELGR					
g151	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDV PDDNQGAVMEELGR					
m151.pep	430	440	450	460	470	480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMFG					
g151	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMFG					
m151.pep	490	500	510	520	530	540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
g151	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGIHSRDNDLVNPLKGKK					
m151.pep	550	560	570	580	590	600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELERRRHFK					
g151	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRMYLSELERRRHFK					

m151.pep      KLDX  
 ||||  
 g151          KLDX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 617>:

a151.seq  
 1 ATGAAACAAA TCCGCAACAT CGCCATCATC GCCACGTCG ACCACGGCAA  
 51 AACACATTG GTCGACCAAC TGCTGCGCCA ATCCGGCACA TTCCGCGCCA  
 101 ACCAGCAGGT TGACGAGCGC GTGATGGACA GCAACGACCT TGAAAAAGAA  
 151 CGCGGCATCA CCATCCTCGC CAAAAACACC GCCATCGATT ACGAAGGCTA  
 201 CCACATCAAT ATCGTCGACA CGCCGGGACA CGCCGACTTC GGCGGCGAAG  
 251 TAGAGCGAGT TTTGGGGATG GTGGACTGCG TCGTCTTGTT GGTGGACGCG  
 301 CAGGAAGGCC CGATGCCGCA AACCCGTTTC GTGACCAAAA AAGCCTTGCC  
 351 TTTGGGGCTG AAACCGATTG TCGTCATCAA TAAAATCGAC AAACCGTCCG  
 401 CCCGTCCGAG CTGGGTATC GACCAAACCT TCGAGCTGTT CGACAACTTG  
 451 GGCGCGACCG ACGAGCAGTT GGATTTCCTG ATTGTTTATG CTTCCGGTCT  
 501 GTCCGGTTTC GCCAAATTGG AAGAAACCGA CGAGAGCAAC GACATCGGTC  
 551 CGCTGTTCTG TACTATCTTA AAATATACGC CTGCACCGAG CGGCAGCGCG  
 601 GACGAAACGC TGCAACTGCA AATTTCCTCA CTCGACTACG ACAACTACAC  
 651 CGGCCGCTC GGTATCGGTC GTATCTTGAA CGGACGTATC AAGCCCGGTC  
 701 AAGTTGTTGC CGTCATGAAC CACGATCAAC AAATCGCCCA AGGCCGCATC  
 751 AACACGCTTT TGGGTTTCAA AGGTTTAGAA CGCGTGCCCG TTGAAGAAGC  
 801 CGAAGCCGGC GACATCGTGA TTATTTCCGG TATTGAAGAC ATCGGCATCG  
 851 GCGTAACCAT CACCGACAAA GACAACCCCA AAGGCCTGCC GATGTTGAGC  
 901 GTGGACGAAC CGACGCTGAC GATGGAATTT ATGGTCAACA CCAGCCCGTT  
 951 GGCAGGTACG GAAGGCAAAT TCGTAACCAG CCGCCAAATC CGCGACCGCC  
 1001 TGCAAAAAGA ATTGCTGACC AACGTCGCC TCGCGTGGA AGATACCGCC  
 1051 GATGCCGACG TGTTCCGCGT ATCCGGGCGC GCGAGCTGC ACCTGACCAT  
 1101 TTTGCTGGA AACATGCGCC GCGAAGGCTA CGAACTCGCC GTCGGCAAAC  
 1151 CGCGCGTCGT GTACCGCGAC ATCGACGGTC AAAAAATGCGA ACCGTATGAA  
 1201 AACCTGACCG TGGACGTACC CGACGACAAC CAAGGCGCGG TAATGGAAGA  
 1251 ATCCGCGCCG CGCCGTGGCG AACTGACTAA TATGGAAAGC GACGGCAACG  
 1301 GACGCAACCG CCTCGAATAC CATATTCCAG CGCGCGGCTT GATCGGCTTC  
 1351 CAAGGCGAAT TTATGACCCT GACGCGCGGG GTCGGGCTGA TGAGCCACGT  
 1401 GTTCGACGAT TACGCGCCCG TCAAACCCGA TATGCCTGGC CGCCACAACG  
 1451 GCGTGCTGGT GTCCCAAGAG CAGGGCGAGG CAGTCGCTTA CGCCTTGTTG  
 1501 AATCTGGAAG ACCGCGGCCG TATGTTCTGA TCGCCCAACG ACAAATCTA  
 1551 CGAAGGTATG ATTATCGCA TCCACAGTCG CGACAACGAT TTGTTGGTCA  
 1601 ACCCGCTCAA AGGCAAAAAA CTTACCAACA TCCGTGCCAG CGGTACCGAC  
 1651 GAAGCCGTTT GCCTGACCAC GCCGATTAAG CTGACGCTGG AAGGTGCGGT  
 1701 CGAGTTTATC GACGATGATG AGCTGGTAGA AATCACGCCG CAATCCATCC  
 1751 GTCTGCGCAA CGCTTACTTG AGCGAATTGG AACGCCGCCG CCATTTCAA  
 1801 AAGCTAGATT GA

This corresponds to the amino acid sequence <SEQ ID 618; ORF 151.a>:

a151.pep  
 1 MKQIRNIAII AHVDHGKTTL VDQLLRQSGT FRANQQVDER VMDSNDLEKE  
 51 RGITILAKNT AIDYEGYHIN IVDTPGHADF GGEVERVLGM VDCVVLVDA  
 101 QEGPMPQTRF VTKKALALGL KPIVVINKID KPSARPSWVI DQTFELFDNL  
 151 GATDEQLDFP IVYASGLSGF AKLEETDESN DMRPLFDITL KYTPAPSGSA  
 201 DETLQLQISQ LDYDNYTGRL GIGRILNGRI KPGQVVAVMN HDQQTAAQGR  
 251 NQLLGFKGLE RVPLEEAEAG DIVIISGIED IGIGVTITDK DNPGLPMLS  
 301 VDEPTLTMDF MVNTSPLAGT EGKFVTSRQI RDRLOKELLT NVALRVEDTA  
 351 DADVFRVSGR GELHLTILE NMRREGYELA VGKPRVYRD IDGQKCEPYE  
 401 NLTVDVPDDN QGAVMEELGR RRGELTNMES DNGRTRLEY HIPARGLIGF  
 451 QGEFMTLTRG VGLMSHVDD YAPVKPDMPG RHNGVLVSQE QGEAVAYALW  
 501 NLEDGRMFV SPNDKIYEGM IIGIHSRDND LVVNPLKGGK LTNIRASGTD  
 551 EAVRLTTFIK LTLEGAVEFI DDELVEITP QSIRLRKRYL SELERRRHFK  
 601 KLD\*

m151/a151 99.8% identity in 603 aa overlap

10 20 30 40 50 60

m151.pep	MKQIRNIAIIAHVDHGKTTLVLDQLLRQSGTFRANQQVDERVMSNDLEKERGITILAKNT
a151	
	10 20 30 40 50 60
m151.pep	70 80 90 100 110 120
	AIDYEGYHINIVDTPGHADFGGEVERVLGMVDCVLLVDAQEGPMPQTRFVTKKALALGL
a151	
	70 80 90 100 110 120
m151.pep	130 140 150 160 170 180
	KPIVVINKIDKPSARPSWVIDQTFELFDNLGATDEQLDFFIVYASGLSGFAKLEETDES
a151	
	130 140 150 160 170 180
m151.pep	190 200 210 220 230 240
	DMRPLFDITLKYTPAPSGSADETLQLQISQLDYDNYTGRLGIGRILNGRIKPGQTVAVMN
a151	
	190 200 210 220 230 240
m151.pep	250 260 270 280 290 300
	HDQQIAQGRINQLLGFKGLERVPLEEAAGDIVIISGIEDIGIGVTITDKDNPKGLPMLS
a151	
	250 260 270 280 290 300
m151.pep	310 320 330 340 350 360
	VDEPTLTMDFMVNTSPLAGTEGKFVTSRQIRDLQKELLTNVALRVEDTADADVFRVSGR
a151	
	310 320 330 340 350 360
m151.pep	370 380 390 400 410 420
	GELHLTILLENMRREGYELAVGKPRVVYRDIDGQKCEPYENLTVDPDDNQGAVMEELGR
a151	
	370 380 390 400 410 420
m151.pep	430 440 450 460 470 480
	RRGELTNMESDGNRTRLEYHIPARGLIGFQGEFMTLTRGVGLMSHVFDYAPVKPDMPG
a151	
	430 440 450 460 470 480
m151.pep	490 500 510 520 530 540
	RHNGVLVSQEQGEAVAYALWNLEDRGRMFVSPNDKIYEGMIIGHSRDNDLVVNPLKGGK
a151	
	490 500 510 520 530 540
m151.pep	550 560 570 580 590 600
	LTNIRASGTDEAVRLTTPIKLTLEGAVEFIDDELVEITPQSIRLRKRYLSELEERRHFK
a151	
	550 560 570 580 590 600
m151.pep	KLDX
a151	KLDX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 619>:

g152.seq

```

1  ATGAAAAaca aaACCaaagt ctgGGacttc cCaccgcc ttTCCactG
51  GctgcttgCC gCATCCctgc CCTTTATGTG gtatagCGCA AAAGCCGGCG
101 GcgataTGCT GcaatgGCAC ACGCGCGTCG GGCTGCTCGT CCTTTTCCTG

```

```

151 CTCGTATTCC GCCTCTGCTG GGGCATTGTTGG GGCAGcgATA CCGCCCCGTTT
201 CTCccgTtTC GTCCGAGGTT GGGCAGGTAT ACGCGGCTAT CTGAAAAAcg
251 gCATTCCCGA ACAtatcCAG CCCGGACACA ACCCCTTGGG CGCACTgatg
301 gtcGTTGCGC TTTTGgccgc cgtcTCATTT CAagtcggca CCGGGCTTTT
351 Tgcccgaat gaaaacacct tcagcaCCAA cggctacctc aaccatttgg
401 ttccgaaca tacgGGCAGC CTTATACGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC CGCAGTCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCATATTC AAAAAGAAAA ACCTCGTCCG CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCCGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGTTGTC CCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 620; ORF 152.ng>:

g152.pep

```

1 MKNKTKVWDF PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLLVLEFL
51 LVFRLCWGIW GSDTARFSRF VRGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAN ENTFTNGYL NHLVSEHTGS LIRKIHLNFF
151 KLLAVFSAVH IAAVAAYRIF KKNLVRPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVAALA AAAILLLS*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 621>:

m152.seq

```

1 ATGAAAAACA AAACCAAAGT CTGGGACCTC CCCACCCGCC TTTTCCACTG
51 GCTGCTTGCC GCGTCCCTGC CCTTTATGTG GTATAGCGCG AAAGCCGGCG
101 GCGATATGCT GCAATGGCAC ACGCGCGTCG GGCTGTTCGT CCTTTTCCTG
151 CTCGTATTTC GCCTCTGCTG GGGCATTGTTGG GGCAGCGATA CCGCCCCGTTT
201 TTCCCGTTTC GTCCAAGGCT GGGCAGGCAT ACGCGGCTAT CTGAAAAACG
251 GTATTCCCGA ACACATCCAG CCCGGACACA ACCCCTTGGG CGCACTGATG
301 GTCGTTGCGC TTTTGCCGCG CGTGTCCTTC CAAGTCGGCA CCGGGCTTTT
351 TGCCGCCGAT GAAAACACCT TCAGCACCAA CGGCTACCTC AACCATTGCG
401 TTCCGAACA TACGGGCGAG CTTATGCGGA AAATCCACCT CAACTTTTTC
451 AAGCTGCTCG CCGTTTTTTC TGCAATCCAC ATCGCCGCCG TCGCCGCATA
501 CCGCGTATTC AAAAAGAAAA ACCTCATCCT CCCGATGATA ACCGGCTTCA
551 AATACATCGA AGGCAAAACC TCAATCCGCT TTGCAGGCAA AGCCGCGCTT
601 GCCGCCGCAT TATCGTTGTC CTCGCTTGCC GCAGCCGCCA TCCTGCTCCT
651 GTCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 622; ORF 152>:

m152.pep

```

1 MKNKTKVWDL PTRLFHWLLA ASLPFMWYSA KAGGDMLOWH TRVGLFVLEFL
51 LVFRLCWGIW GSDTARFSRF VQGWAGIRGY LKNGIPEHIQ PGHNPLGALM
101 VVALLAAVSF QVGTGLFAAD ENTFTNGYL NHLVSEHTGS LMRKIHLNFF
151 KLLAVFSAIH IAAVAAYRVF KKNLILPMI TGFKYIEGKT SIRFAGKAAL
201 AAALSVASLA AAAILLLS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 152 shows 95.4% identity over a 218 aa overlap with a predicted ORF (ORF 152.ng) from *N. gonorrhoeae*:

m152/g152

```

          10      20      30      40      50      60
m152.pep  MKNKTKVWDLPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLFVLFLLVFRLCWGIW
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g152       MKNKTKVWDFPTRLFWLLAASLPFMWYSAKAGGDMLOWHTRVGLLVLEFLLVFRLCWGIW
          10      20      30      40      50      60

          70      80      90     100     110     120
m152.pep  GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g152       GSDTARFSRFVRGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAN
          70      80      90     100     110     120

```

436

	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAHIAAAYAAYRVFKKKNLILPMI					
	:     :     :     :     :     :					
g152	ENTFSTNGYLNHLVSEHTGSLIRKIHLNFFKLLAVFSAVHIAAAYAAYRIFKKKNLVRPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	:     :     :     :					
g152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 623>:

a152.seq

1	ATGAAAAACA	AAACCAAAGT	CTGGGACTTC	CCCACCCGCC	TTTCCACTG
51	GCTGCTTGCC	GCATCCCTAC	CCTTTATGTG	GTATAGCGCG	AAAACCGGCG
101	GCGATATGCT	GCAATGGCAC	ACGCGCGTCG	GGCTGTTTAT	CCTTTTCCTG
151	CTCGTATTCC	GCCTCTGCTG	GGGCATTGGG	GGCAGCGATA	CCGCCCGTTT
201	CTCCCGTTTC	GTCCGCGGAT	GGTCGGGTAT	CAGAGAGTAT	ATGAAAAACG
251	GTATTCCCGA	ACACGTCCAA	CCCGGACACA	ACCCCTTGGG	CGCACTGATG
301	GTCGTTGCCG	TTTTGGCCGC	CGTGTCTGTC	CAAGTCGGCA	CAGGGCTTTT
351	TGCCGCCGAT	GTAAACACCT	TCAGCACCAA	CGGCTACCTC	AACCATTGGG
401	TTTCCGAACA	TACGGGCAGC	CTTATGCGGA	AAATCCATCT	CAACTTTTTC
451	AAACTGCTCG	CCGTTTTC	CGCAGTCCAC	ATCGCCGNCG	TCGCCGCATA
501	CCGCGTGTC	AAAAAGAAAA	ACCTCGTCCT	CCCGATGATA	ACCGGCTTCA
551	AATACATCGA	AGGCAAAACC	TCAATCCGCT	TTGCCGGCAA	AGCCGCGCTT
601	GCCGCCGCAT	TATCGGTTGC	CGCGCTTGCC	GCAGCCGCCA	TCCTGCTCCT
651	GTCCTGA				

This corresponds to the amino acid sequence <SEQ ID 624; ORF 152.a>:

a152.pep

1	MKNKTKVWDF	PTRLFHWLLA	ASLPFMWYSA	KTGGDMLQWH	TRVGLFILFL
51	LVFRLCWGIW	GSDTARFSRF	VRGWSGIREY	MKNGIPEHVQ	PGHNPLGALM
101	VVALLAAVSF	QVGTGLFAAD	VNTFSTNGYL	NHLVSEHTGS	LMRKIHLNFF
151	KLLAVFSAVH	IAXVAAYRVF	KKKNLVLPMI	TGFKYIEGKT	SIRFAGKAAL
201	AAALSVAALA	AAAILLS*			

m152/a152 94.0% identity in 218 aa overlap

	10	20	30	40	50	60
m152.pep	MKNKTKVWDLPTRLFHWLLAASLPFMWYSAKAGDMLQWHTRVGLFVFLLVFRLCWGIW					
	:     :     :     :     :					
a152	MKNKTKVWDFPTRLFHWLLAASLPFMWYSAKTGGDMLQWHTRVGLFILFLLVFRLCWGIW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m152.pep	GSDTARFSRFVQGWAGIRGYLKNGIPEHIQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	:     :     :     :     :					
a152	GSDTARFSRFVRGWSGIREYMKNGIPEHVQPGHNPLGALMVVALLAAVSFQVGTGLFAAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m152.pep	ENTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSIAHIAAAYAAYRVFKKKNLILPMI					
	:     :     :     :     :					
a152	VNTFSTNGYLNHLVSEHTGSLMRKIHLNFFKLLAVFSAVHIAAXVAAYRVFKKKNLVLPMI					
	130	140	150	160	170	180
	190	200	210	219		
m152.pep	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	:     :     :     :					
a152	TGFKYIEGKTSIRFAGKAALAAALSVAALAAAAIILLSX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 625>:

```

g153.seq
1   atgggggtttg cttacAgtat gacgtatatc gaggtCGGga taccggaggc
51  ggcataccgtc ctttCgctGC CCGAGATgat ggcctgatG GTGTTtCagg
101 attATGGTTT TttggcCGAA GTGATGTTTG TgctgaCTTT cGGCGcgcCG
151 GTTCTGTTtC tGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GGCAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTCT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AAAGGTTGCG TTCGGGCGCG CGTTTTATCT
351 GATGTTTCGG CTGTGCGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTCCAA ATCGGGCGGC TGACGGGGAA TAATGCGGTT
451 CAGACGGCAT CGGAAGGCAA AACCTGTTGC AGCCGCTGCC TGTATTTcgg
501 cgacAGTgcc gaatccCCCT GCGGGGTGtg cgCGcgga CTgtacggcg
551 gacggccgaa aagtCTGAGt atttCgtCGG CGTTTCtgac ggcggcggtt
601 GTTTTGtATT TCCctgCcaa TATCctgceg attatGAttt cgtccaATCc
651 tgccggcaeg GAGGcCAACA CCATCTTTAG CGGCATCGCT TATATGTGGG
701 ACgagggcgA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGCTGC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGGCGGCACG
801 GTTCGCTTTG CCGGCGGGCG CAAAGAAATT GTCGCACCTC tacCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTtGT GATTATTATT
901 TTGATGTGTT CGTTCcaca TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTtT GACGATGCTG TCCGCTATT
1001 ATTTCGACCC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAACGAAA CGGAAAAATA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 626; ORF 153.ng>:

```

g153.pep
1   MGFAYSMTYI EVGIPEASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV VRLRQAMMVD VFFVSTLVAY
101 IKLSSVAKVR FGPAPYLMFA LSVMLIRTSV SVPQHVVYFQ IGRLTGNNAV
151 QTASEGKTC SRCLYFRDSA ESPCGVCGAE LYGGRPKSLs ISSAFLTAHV
201 VLYFPANILP IMISSNPAAT EANTIFSGIA YMWDEGDRLI AAVIFSASIL
251 VPVLKIAAMS VLIAAARFAL PAGAKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFHTYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL LWDKRASDGLA
351 FNETEKYD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 627>:

```

m153.seq
1   ATGGCGTTTG CTTACGGTAT GACGTATATC GAGGTGCGGA TACCGGGTGC
51  GGCATCCGTC CTTTCGCTGC CCGAGATGAT GCGCCTGATG GTGTTTCAGG
101 ATTATGGTTT TTTGGCCGAA GTGATGTTTG TGCTGACTTT CGGCGCGCCG
151 GTTCTGTTTC TGCTGCTGTG CCTGTATGTC TATGCCGCGC TGATACGGAA
201 ACAGGCGTAT CCTGCGCTGC GTTTGGCAAC GCGTGTGATG GTGCGCTTGA
251 GACAGGCGAT GATGGTGGAT GTGTTTTTTG TTCCACTTT GGTGGCGTAT
301 ATCAAGCTCT CGTCTGTGGC AGAGGTTGCG TTCGGGCGCG CGTTTTATCT
351 GATGTTTCGG CTGTGAGTTA TGCTGATTG GACTTCGGTA TCGGTTCCCC
401 AGCATTGGGT GTATTTTCAA ATCGGGCGGC TGACGGGGGA TAATGCGGTT
451 CAGACGGCAT CGGAAGGTAA AACCTGTTGC AGCCGCTGCC TGTATTTCCG
501 CGACAGTGCC GAATCCCCCT GCGGCGTGTG CGGTGCGGAA CTGTACCGCC
551 GACGGCCGAA AAGTCTGAGT ATTTGCTCGG CGTTTCTGAC GCGGCGGTT
601 ATTTTGtATT TCCCTGCCAA TATCCTGCCG ATTATGATT CGTCCAATCC
651 TGCCGCCACG GAGGTCAATA CCATCCTTAA CGGCATCGCT TATATGTGGG
701 ACGAGGCGA CAGGCTGATT GCGGCGGTTA TTTTCAGCGC GAGTATTTTG
751 GTGCCGTTAC TGAAGATTGC GGCAATGTCG GTTTTGATTG CGTCCGCGCG
801 CTTGCGTTTG CCAACGGGTG CAAAGAAATT GTCGCACCTC TACCGCATCA
851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTtGT GATTATTATT
901 TTGATGTGTT CGTTCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCTATT
1001 ATTTGACACC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 628; ORF 153>:

```

m153.pep
1   MAFAYGMTYI EVGIPGAASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLLCLYV YAALIRKQAY PALRLATRV VRLRQAMMVD VFFVSTLVAY

```

	10	20	30	40	50	60
m153.pep	MAFAYGMTYIEVGIPGAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLLYV	:	:	:	:	:
g153	MGFAYSMTYIEVGIPLEAASVLSLPEMMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLLYV	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m153.pep	YAALIRKQAYPALRLATRMVRLRQAMMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA	:	:	:	:	:
g153	YAALIRKQAYPALRLATRMVRLRQAMMVDVFFVSTLVAYIKLSSVAKVRFGPAFYLMFA	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m153.pep	LSVMLIRTSVSVPQHWWYPQIGRLTGDNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE	:	:	:	:	:
g153	LSVMLIRTSVSVPQHWWYPQIGRLTGNNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE	:	:	:	:	:
	130	140	150	160	170	180
	190	200	210	220	230	240
m153.pep	LYRRRPKSLSISSAFLTAAVILYPPANILPIMISSNPAATEVNITLNGIAYMWDEGDRLI	:	:	:	:	:
g153	LYGGRPKSLSISSAFLTAAVVLYPPANILPIMISSNPAATEANTIFSGIAYMWDEGDRLI	:	:	:	:	:
	190	200	210	220	230	240
	250	260	270	280	290	300
m153.pep	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHLYRITEAVGRWSMIDIFVII	:	:	:	:	:
g153	AAVIFSASILVPVLKIAAMSVLIAARFALPAGAKKLSHLYRITEAVGRWSMIDIFVII	:	:	:	:	:
	250	260	270	280	290	300
	310	320	330	340	350	359
m153.pep	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLWDKRASDGIAFNETEKHDX	:	:	:	:	:
g153	LMCSFHYYAARVIPGSAAVYFCLVVILTMLSAYYFDPRLLWDKRASDGIAFNETEKYDX	:	:	:	:	:
	310	320	330	340	350	

```

a153.seq
1  ATGGCGTTTG  CTTACGGTAT  GACGTATATC  GAGGTCGGGA  TACCGGGTGC
51  GGCATCCGTC  TTTTCGCTGC  CCGAGATGAT  GCGCCTGATG  GTGTTTCAGG
101 ATTATGGTTT  CTTTGCCGAA  GTGATGTTTG  TTGTGACCTT  CGGCGCGCCG
151 GTTCTGTTTG  TGCTGCTGTG  CTTGTATGTC  TATGCCGCGC  TGATACGGAA
201 ACAGGCGTAT  CCTGCGCTGC  GTTTGGCAAC  GCGTGTGATG  GTGCGCTTGA
251 GACAGCGCAT  GATGCTGGAT  GTGTTTTTTG  TTTTCCACTT  GGTGCGCGAT
301 ATCAAGCTCT  CGTCTGTGGC  AGAGGTTTCG  TTCGGATCGG  CGTTTTATCT
351 GATGTTTCGG  CTGTGCGGTA  TGCTGATTCT  GACTTCGGTA  TCGGTTCCCC
401 AGCATTGGGT  GTATTTTCAA  ATCGGGCGGC  TGACGGGGGA  TAATGCGGTT
451 CAGACGGCAT  CGGAAGGTAA  AACCTGTTGC  AGCCGCTGCC  TGTAATTCCG
501 CGACAGTGCC  GAATCCCCCT  GCGGCGGTGT  CGGTGCGGAA  CTGTACCGCC
551 GACGGCGGAA  AAGTCTGAGT  ATTCGTCGG  GACTTCTGAC  GCGCGCGGTT
601 ATTTTGTATT  TCCCTGCCAA  TATCCTGCCG  ATTATGATT  CGTCCAATCC
651 TGCCGCCACG  GAGGTCAATA  CCATCCTTAA  CGGCATCGCT  TATATGTGGG
701 ACAGAGGGCA  CAGGCTGATT  GCGGCGGTTA  TTTTCAGCGC  GAGTATTTTG
751 GTGCCGGTAC  TGAAGATTGC  GGCATGTGCT  GTTTTGATTG  CGTCCGCCCC
801 CTTGCTTTTG  CCAACGGGTG  CAAAGAAATT  GTGCGACCTC  TACCGCATCA

```

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851 CCGAAGCGGT CGGCCGCTGG TCGATGATTG ATATTTTGT GATTATTATT
901 TTGATGTGTT CGTTCCACAC TTATGCCGCG CGCGTCATTC CGGGCAGTGC
951 GGCAGTCTAT TTCTGCCTGG TCGTGATTCT GACGATGCTG TCCGCCTATT
1001 ATTTGACCCC GCGCTGCTT TGGGACAAAC GCGCTTCAGA CGGCATTGCT
1051 TTCAATGAAA CGGAAAAACA TGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 630; ORF 153.a>:

```

a153.pep
1  MAFAYGMTYI EVGIPGAASV LSLPEMRLM VFQDYGFLAE VMFVLTFGAP
51  VLFLLCLYV YAALIRKQAY PALRLATRV VRLRQAMVD VFFVSTLVAY
101 IKLSSVAEVR FGSAYFLMFA LSVMLIRTSV SVPQHWVYFQ IGRITGDNV
151 QTASEGKTCC SRCLYFRDSA ESPCGVCGAE LYRRRPKSL SISAFLTA
201 ILYFPANILP IMISSNPAAT EVNTILNGIA YMWDEGDR LI AAVIFSASIL
251 VPVLKIAAMS VLIASARFAL PTGAKKLSHL YRITEAVGRW SMIDIFVIII
301 LMCSFH TYAA RVIPGSAAVY FCLVVILTML SAYYFDPRL WDKRASDGI
351 FNETEKHD*

```

m153/a153 99.7% identity in 358 aa overlap

m153.pep	10	20	30	40	50	60
	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
a153	MAFAYGMTYIEVGIPGAASVLSLPEMRLMVFQDYGFLAEVMFVLTFGAPVLFLLCLYV					
	10	20	30	40	50	60
m153.pep	70	80	90	100	110	120
	YAALIRKQAYPALRLATRVVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGPAFYLMFA					
a153	YAALIRKQAYPALRLATRVVRLRQAMVDVFFVSTLVAYIKLSSVAEVRFGSAFYLMFA					
	70	80	90	100	110	120
m153.pep	130	140	150	160	170	180
	LSVMLIRTSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
a153	LSVMLIRTSVSPQHWVYFQIGRLTGDNAVQTASEGKTCCSRCLYFRDSAESPCGVCGAE					
	130	140	150	160	170	180
m153.pep	190	200	210	220	230	240
	LYRRRPKSLSSISAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI					
a153	LYRRRPKSLSSISAFLTA AVILYFPANILPIMISSNPAATEVNTILNGIAYMWDEGDR LI					
	190	200	210	220	230	240
m153.pep	250	260	270	280	290	300
	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
a153	AAVIFSASILVPVLKIAAMSVLIASARFALPTGAKKLSHL YRITEAVGRWSMIDIFVIII					
	250	260	270	280	290	300
m153.pep	310	320	330	340	350	359
	LMCSFH TYAARVIPGSAAVYFCLVVILTML SAYYFDPRL WDKRASDGI AFNETEKHDX					
a153	LMCSFH TYAARVIPGSAAVYFCLVVILTML SAYYFDPRL WDKRASDGI AFNETEKHDX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 631>:

```

g154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CAGCCTCAAG CACGCGTCCG
51  CAAAACAAC accttctct CCGCCGCTCG GCTGGTCCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTAAAG AAATCCGCA CAGGGGCGCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATCGAAG TCAACAATAC
201 GGTCAATTAAG GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TGCGCGACGA CCAAAAAGGC GTGGAAGTTA CTGCCCACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGcgtaa CCGGTTTGGG TACGCTGCTT TCGGGTTCGT

```



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401 ACATCGCTTT TACACCCGGC AAAAGCGGCG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAgcy GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG AccgCATCCT CAACGTcaac AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAAATCG AAAGCGCGCA TTTCGAcccg
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAAT COGCCCCCTCT GCCTGCCCTG
751 CTGTCAGGCG CGATTTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAGGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAATCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT cggTTCGCTT GTCgaATACA AAGGGCtgaa
951 TGTcggCATG GTTTCAGATG TCCCTTATT TGACCGCAAT gacagCCTGC
1001 ACCTgtTTGA aaacggctgg aTTeccGtac gCATCCGCAT cgagccTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAGCAAAGC AAAGAGCATT GGAACAACA
1101 ATTCAGACG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGCGCGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTCATCGC
1251 CACACGGGGC GCGGTTTGG ATGACTTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACaaatT CAACAATCTG CCATTggata aaACCGTTGC CGAATTGAAC
1351 GGCTCGCTCG CCGAACTCAA GTCCGCACTC AAATCCGCCA ATGCCGCCCT
1401 AAGCTCCATT GacaAACTGG TCGgcaatCC GCAGACGCAA AACATCCCGA
1451 ACGAACTGAA CCAAACTCTG AAAGAGTTGC GCATAACCCT GCAAGGCGTA
1501 TCGcctCAAT CGCCTATCTa cgGAgacgta caAAATacgc tgCaaAGTTT
1551 GGACAAAAAC TTAaaagacy TtcaACCCGT CATTAACACT TTGaaAGAAa
1601 aacCCaaCgc actGATTTtc aacaACAGCA GCAAAGAccc tATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 632; ORF 154.ng>:

```

g154.pep
1 MTDNSPPPNNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51 VVTLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTLGLTLL SGSYIAFTPG KSGEAKDVFO
151 VGDIPPVTAI GQSGRLRLNLI GKNDRIILNVN SPVLYENFMV QDIESAHPDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSNAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGM VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQFQT ALNKGLTATI SSNNLLTGKK MIELNDQPSA
401 SPKLRPHTVY AGDTVIAIRG GGLDDLQVKL ADLLDKFNNL PLDKTVAEIN
451 GSLAEKLSAL KSANAALSSI DKLVGNPQTQ NIPNELNQTQ KELRITLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NNSSKDPIPK
551 GSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 633>:

```

m154.seq
1 ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51 CAAAAACAAC ACCTTCCTCT CTGCCGTCGT GCTGGTTCGG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCAATCAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCGGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGAGC AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAAGC GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTCAAC AGCCCTGTTT
551 TGTATGAAAA TTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCATTA CACCATCTTC ATCCAAAGCC CCAACGACAA
651 ACTGATTCAT TCCGCCAGCC GTTTTGGCT GGAAAGCGGC ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCTCAAT COGCCCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTTCATT TGATTGCGCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGACGACCGC TCGCTGTACT ACACCGCGTT TTTCAAACAA
901 TCCGTGCGCG GCCTGACCGT CGGTTCCGCC GTCGAGTACA AAGGGCTGAA
951 TGTGCGCGTG GTTTCGACG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATACCCGTAC GCATCCGCAT TGAACCTTCC
1051 CGTTTGAAAA TCAATGCCGA CGAACAAAGC AAAGAACATT GGAACAACA
1101 ATTTACAGAG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGAAGCAAA ATGATTGAGT TGAACGATCA GCCTTCCGCA

```

```

1201 TACACCTAAGC TGCAGCCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TCGACAAGTT CGACAACTG CTTTAGATA AGACGGTGC CGAATTGAAC
1351 GGTTTCGCTT CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAACCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCGCAAT CGCCTATCTA CGGCGACGTA CAAATACGC TGCAAAGTTT
1551 GGACAAAACT TTAAGAGACG TTCAACCCGT GATTAATACT TTGAAAGAAA
1601 AACCCACGCG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 634 ORF 154.a>:

```

m154.pep
1  MTDNSPPFNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVKPRIDQ SGVTGLGTL SSGYIAFTPG KSDEAKDVPQ
151 VQDIPPVTAI QSGLRNLNI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI KLSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQTAL NKGLTATISS NLLTGSKM IEIENDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDIQVKL ADLLDKFDKL PLDKTVARLN
451 GSIAELKSTL KSANAALSSI DKLVGKPTQ NIPNELNQTL KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

m154 / g154 97.8% identity in 553 aa overlap

	10	20	30	40	50	60
m154.pep	MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
g154	MTDNSPPFNGHAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP VVTLLMDSAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m154.pep	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVKPRIDQ					
g154	GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD VSGLIRSDTQ FWVKPRIDQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m154.pep	SGVTGLGTL SSGYIAFTPG KSDRAKDVPQ VQDIPPVTAI GQSGLRNLNI GKNDRIILNVN					
g154	SGVTGLGTL SSGYIAFTPG KSGRAKDVPQ VQDIPPVTAI GQSGLRNLNI GKNDRIILNVN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m154.pep	SPVLYENFMV GQVESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
g154	SPVLYENFMV GQIESAHFDP SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTSGSI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m154.pep	KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFKQ					
g154	KLSAPLPALLSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEIANLPDDR SLYYTAFKQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m154.pep	SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
g154	SVRGLTVGSP VEYKGLNVGMV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS RLEINADEQS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m154.pep	KEHWKQQTAL NKGLTATISS NLLTGSKM IEIENDQPSA SPKLRPHTVY AGDTVIATQG					
g154	KEHWKQQTAL NKGLTATISS NLLTGSKM IEIENDQPSA SPKLRPHTVY AGDTVIATRG					

442

	370	380	390	400	410	420
	430	440	450	460	470	480
m154.pep	GGLDDLQVKLADLLDKFDKPLDKTVAEIENGSLAELKSTLKSANAALSSIDKLVGKPQTQ					
	:     :     :     :     :					
g154	GGLDDLQVKLADLLDKFNNLPLDKTVAEIENGSLAELKSALKSANAALSSIDKLVGNPQTQ					
	430	440	450	460	470	480
	490	500	510	520	530	540
m154.pep	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVPVINTLKEKPNALIF					
	:     :     :     :     :					
g154	NIPNELNQTLKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVPVINTLKEKPNALIF					
	490	500	510	520	530	540
	550					
m154.pep	NSSSKDPIPKGSRX					
	:					
g154	NNSSSKDPIPKGSRX					
	550					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 635>:

```

a154.seq
1  ATGACTGACA ACAGCCCTCC TCCAAACGGA CACGCCCAAG CACGCGTCCG
51  CAAAAACAAC ACCTTCCTCT CTGCCGTCTG GCTGGTTCCG CTGATCGCGC
101 TGATTGCCGG CGGCTGGCTT TGGGTTAAGG AAATCCGCAA CAGGGGGCCT
151 GTGGTTACGC TCTTGATGGA CAGCGCGGAA GGCATTGAGG TCAACAATAC
201 GGTCATCAAA GTATTGAGCA TCGATGTCGG ACGCGTTACC CGAATCAAAC
251 TCGCGGACGA CCAAAAAGGC GTGGAAGTAA CCGCCCAACT CAATGCGGAC
301 GTATCCGGCC TCATCCGCAG CGATACCCAG TTTTGGGTGG TCAAGCCGCG
351 TATCGACCAA AGCGGCGTAA CCGGTTTGGG TACGCTGCTT TCGGGTTCGT
401 ACATCGCCTT TACACCCGGC AAAAGCGACG AGGCAAAAGA CGTGTTCCAA
451 GTGCAGGACA TTCCGCCCGT TACCGCCATC GGGCAAAGCG GGCTGCGCTT
501 GAATTTGATT GGTAAAAACG ACCGCATCCT CAACGTC AAC AGCCCTGTTT
551 TGTATGAAAA CTTTATGGTC GGGCAAGTCG AAAGCGCGCA TTTCGACCCG
601 TCCGACCAAA GCGTGCAATTA CACCATCTTC ATCCAAAGCC CCAAGGACAA
651 ACTGATTCAT TCCGCCAGCC GTTCTGGCT GGAAGCGGCG ATCAATATCG
701 AAACCACAGG CAGCGGCATC AAACCAATT CCGCCCTCT GCCTGCCCTG
751 CTGTCGGGCG CGATTTTCATT TGATTCGCCG AAAACCAAAA ACAGTAAAAA
801 CGTCAAAAGC GAAGACAGCT TCACGCTTTA CGACAGCCGC AGCGAAGTCG
851 CCAACCTGCC TGATGACCGT TCGCTGTACT ACACGCGGTT TTTCAAACAA
901 TCCGTGCGCG GACTGACCGT CGGTTCGCCT GTCGAGTACA AAGGGCTGAA
951 TGTCGGCGTG GTTTCGATG TTCCTTATTT CGACCGCAAC GACAGCCTGC
1001 ACCTGTTTGA AAACGGCTGG ATTCCCGTAC GCATCCGTAT TGAGCCTTCC
1051 CGTTTGGAAT TCAATGCCGA CGAACAAAGC AAAGAACATT GGAAACAACA
1101 ATTTAGACAG GCCTTAAACA AAGGCCTGAC CGCCACCATC TCCAGCAACA
1151 ACCTGCTGAC CGGCAGCAAA ATGATTGAGT TGAACGATCA GCCTTCGGCC
1201 TCGCCCAAGC TCGGACCGCA TACCGTTTAT GCAGGCGATA CCGTTATCGC
1251 GACCCAGGGC GCGGTTTGG ACGATTGCA GGTCAAATTG GCGGATTGTC
1301 TGGACAAGTT CGACAACTG CCTTTAGATA AGACGGTTGC CGAATTGAAC
1351 GGTTGCTTGG CCGAGCTCAA ATCCACACTC AAATCTGCCA ATGCCGCCCT
1401 AAGCTCCATC GACAACTGG TCGGCAAACC GCAGACACAA AACATTCCGA
1451 ACGAACTGAA CCAAAACCCTG AAAGAGTTGC GCACAACCCT GCAAGGCGTA
1501 TCGCCTCAAT CGCCTATCTA CGGCGACGTA CAAATACGCG TGCAAGTTT
1551 GGACAAAACC TTAAGAGAGC TTCAACCCGT CATTAACTT TGAAGAGAAA
1601 AACCAACGCG GCTGATTTTC AACAGCAGCA GCAAAGACCC TATCCCGAAA
1651 GGAAGCCGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 636; ORF 154.a>:

```

a154.pep
1  MTDNSPPNG HAQARVRKNN TFLSAVWLVP LIALIAGGWL WVKEIRNRGP
51  VVTLLMDSAE GIEVNNTVIK VLSIDVGRVT RIKLRDDQKG VEVTAQLNAD
101 VSGLIRSDTQ FWVVKPRIDQ SGVTGLGTLT SGSYIAFTPG KSDEAKDVEQ

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151 VQDIPPVTAI QOSGLRLNLI GKNDRIILNVN SPVLYENFMV GQVESAHFDP
201 SDQSVHYTIF IQSPNDKLIH SASRFWLESG INIETTGSGI KLNSAPLPAL
251 LSGAISFDSP KTKNSKNVKS EDSFTLYDSR SEVANLPDDR SLYYTAFFKQ
301 SVRGLTVGSP VEYKGLNVGV VSDVPYFDRN DSLHLFENGW IPVRIRIEPS
351 RLEINADEQS KEHWKQQFQT ALNKGLTATI SSNNLLTGSK MIELNDQPSA
401 SPKLRPHTVY AGDTVIATQG GGLDDLQVKL ADLLDKFDKL PLDKTVAELN
451 GSLAELKSTL KSANAALSSI DKLVGKPKTQ NIPNELNQTl KELRTTLQGV
501 SPQSPIYGDV QNTLQSLDKT LKDVQPVINT LKEKPNALIF NSSSKDPIPK
551 GSR*

```

## m154/a154 100.0% identity in 553 aa overlap

m154.pep	10	20	30	40	50	60
	MTDNSPPPNNGHAQARVRKNNTFLSAVWLVPILIALIAGGWLWVKEIRNRGPVVTTLLMDSAE					
a154	10	20	30	40	50	60
	MTDNSPPPNNGHAQARVRKNNTFLSAVWLVPILIALIAGGWLWVKEIRNRGPVVTTLLMDSAE					
m154.pep	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
a154	70	80	90	100	110	120
	GIEVNNTVIKVLSDVGRVTRIKLRDDQKGVEVTAQLNADVSGLIRSDTQFWVVKPRIDQ					
m154.pep	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGOSGLRLNLIGKNDRIILNVN					
a154	130	140	150	160	170	180
	SGVTGLGTLTLLSGSYIAFTPGKSDEAKDVQVQDIPPVTAIGOSGLRLNLIGKNDRIILNVN					
m154.pep	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPSPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSGI					
a154	190	200	210	220	230	240
	SPVLYENFMVGQVESAHFDPSPDQSVHYTIFIQSPNDKLIHSASRFWLESGINIETTGSGI					
m154.pep	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ					
a154	250	260	270	280	290	300
	KLNSAPLPALLSGAISFDSPKTKNSKNVKS EDSFTLYDSRSEVANLPDDRSLYYTAFFKQ					
m154.pep	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
a154	310	320	330	340	350	360
	SVRGLTVGSPVEYKGLNVGVVSDVPYFDRNDSLHLFENGWIPVRIRIEPSRLEINADEQS					
m154.pep	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
a154	370	380	390	400	410	420
	KEHWKQQFQTALNKGLTATISSNNLLTGSKMIELNDQPSASPKLRPHTVYAGDTVIATQG					
m154.pep	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPKTQ					
a154	430	440	450	460	470	480
	GGLDDLQVKLADLLDKFDKLPLDKTVAELNGSLAELKSTLKSANAALSSIDKLVGKPKTQ					
m154.pep	490	500	510	520	530	540
	NIPNELNQTlKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					
a154	490	500	510	520	530	540
	NIPNELNQTlKELRTTLQGVSPQSPIYGDVQNTLQSLDKTLKDVQPVINTLKEKPNALIF					

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```

                    550
m154.pep      NSSSKDPIPKGSRX
              |||||
a154          NSSSKDPIPKGSRX
                    550

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 637>:

```

g155.seq
1   atGAAaatcg GtateCCACG CGAGTCatta tcCGGCGAAA cccgcgtage
51  ctgcAcgccc gCCACCGTTG CCctgctggg caAactAGGC TTTGAAACCG
101 TTGtcgaAAG CGGTGCAggt TTGGCGGCAA GTTTggaCGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGCCTGCCC
201 TTTAATTTAT AAGGTCAACG CGCCGTCCGA AGGCGAGCTG CCGCTGCTCA
251 AAGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAGG CCTTGC GCGC CAAGAAAGTC AACGCGCTGG CGATGGACAT
351 GGTTCCTCCG ATTTCCCGCG CTCAGGCCTT GGACGCTTTG TCTTCAATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT CACTGCCGCC GGCAAAGTGC CGCCTGCGCA
501 GGTTTTGGTG ATTGGCGCCG GTGTGGCGGG TTTGGCGGCA ATCGGTACGG
551 CAAATTCGCT CGGCGCAGTG GTGCGCGCGT TCGATACCCG CTGGAAGTG
601 GCGGAACAAA TCGAATCGAT GGGCGGTAAG TTcctGAAAC TCGACTTCCT
651 GCAAGAATCG GGCGGCAGCG GAGACGgctA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC CGCCGAAATG AAGCTCTTTG CCGAACAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CTCCCAAGCT
801 GATTACAAA GAAATGGTGG AAAGCATGAA ATCCGGATCC GTCATCGTCG
851 ATTTGGCGGC GACGGGCGGC AACTGCGAAC TCACCCGACC GGGCGAATTG
901 TCCGTAAACG GCAACGGCGT GAAATCATC GGCTACACCG ACATGGCAAA
951 CCGCCTTGCC GGACAGTCTT CCCAGCTTTA CGCCACCAAC TTGGTGAACC
1001 TGACCAAGCT GTTAAGCCCG AACAAAGAcg gcaAATCAC GCTGGACTTC
1051 GAAGacgtGA TTATCCGCAA TATGACCGTT ACCCGcgacg gcgaaATCAC
1101 CTTCCCGCCT CCGcgaTTc aggtTTCgc cggcgCAG CAAAcgccgt
1151 ctgaAAAagc cgcGCCTGCC GCCAagcccg AgccGaaacc tgmtCCcctg
1201 tggAAAAaac tcgCGCCCGC CGCcatcgCC GCCGTATTGG tgctgtgGgt
1251 cggCgcggtc gcaccgcag CATTCTTGAA CCACTTTATC GTCTTCGTCC
1301 TCGCCTGCGT CATCGGCTAC CATGTCGTTT GgaacgTCAG CCACTCGCTG
1351 CACACACCGC TGatgtcgtt aaccaaCgcc atctccGGCA tcatggtcgt
1401 cggCGCGCTG CTGCAATCG GTCAGGGcaa cggttcgtT TCgtGCTGT
1451 CGTTTGTTC CATCCTGATT GCCGGCATCA ATATCTTCGG CGGCTTTGCG
1501 GTTACACGGC GTATGCTGAA TATGTTAAG AAAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 638; ORF 155.ng>:

```

g155.pep
1   MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51  QTAGATVADK AAVWACPLIY KVNAPSEGEL PLLKEGQTIV SFLWPRONEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSMANISGYR AVIEAANAFA
151 RFFTQGITAA GKVPQAQVLV IGAGVAGLAA IGTANSLGAV VRAFDTRLEV
201 AEQIESMGGK FLKDLFLQES GSGDGYAKV MSDEFIAAEM KLF AEQAKEV
251 DIIITTAaip GKPAKLITK EMVESMKSGS VIVDLAATGG NCELTRPGEL
301 SVTGNVVKII GYTDMANRLA GSSQLYATN LVNLTKLLSP NKDGEITLDF
351 EDVIIRNMTV TRDGEITFPF PPIQVSARPO QTPSEKAAPA AKPEPKPVPL
401 WKKLAPAAIA AVLVLWVGAV APAAFLNHFI VFVLACVIGY HVVWNVSHSL
451 HTPLMSVTNA ISGIMVVGAL LQIGQNGFV SLLSFVAILI AGINIFGGFA
501 VTRRMLNMEK KG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 639>:

```

m155.seq
1   ATGAAAATCG GTATCCACG CGAGTCATTA TCCGGCGAAA CCCGCTCGC
51  CTGTACGCCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTTGAAACCG
101 TTGTCGAAAG CGGTGCAGGT TTGGCGGCAA GTTTGACGA TGCCGCTTAC
151 CAAACAGCAG GCGCAACCGT TGCCGACAAA GCGGCGGTTT GGGTCTGCCC
201 TTTGATTTAT AAGGTCAACG CGCCGTCCGA ACAGGAAGTG CCGCTTTTGA
251 ACGAAGGTCA AACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT

```

```

301 TTGGTCTGAAG CCTTGCGCGC CAAGAAAGTG AACGCGCTGG CGATGGATAT
351 GGTGCCCCGC ATTTTCGCGCG CGCAGGCTTT GGACGCTTTG TCTTCGATGG
401 CAAACATCAG CGGCTACCGC GCCGTAATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTCTTCA CCGGTCAAAT TACCGCCGCC GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGCGT TCGATACCCG CTTGGAAGTG
601 CGGAACAAA TCGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 ACAAGAATCG GCGCGCAGCG GAGACGGCTA CGCCAAAGTG ATGAGCGACG
701 AATTTATCGC AGCCGAGATG AAGCTCTTTG CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCG CGCCCAAGCT
801 GATTACAAA GAAATGGTGG AAAGCATGAA ATCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGCAGGGC GGCAACTGCG AACTCACCCG CCCGGGCGAA
901 TTGTCCGTAA CCGGCAACGG CGTGAAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGGACAGT CTTCCAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGCGGAAAT CACGTTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCACG ACGGCGAAAT
1101 CACCTTCCCG CCTCCGCCGA TTCAAGTTTC CGCCAGCCG CAGCAAACGC
1151 CGTCTGAAA AGCCGTGCCT GCCGCCAAGC CCGAGCCAAA ACCCGTTCCC
1201 CTGTGGAAAA AACTCGCGCC CGCCGTCATC GCCCGCTCT TGGTACTGTG
1251 GGTGCGCGCG GTCGCACCCG CAGCATTCCT GAACCACTTT ATCGTGTTCG
1301 TTCTCGCCTG CGTCATCGGC TACTACGTCG TCTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGTGATGTC GGTAAACCAAC GCCATCTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAAGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCGGCA TCAACATCTT CGGCGGCTTT
1501 GCGGTAACAC GCGGTATGCT GAATATGTTT AAGAAAGGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 640; ORF 155>:

```

m155.pep
1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
51 QTAGATVADK AAVWVCPLIY KVNAPSEQEL PLLNEGQTIV SFLWPRQNEA
101 LVEALRAKKV NALAMDVPR ISRAQALDAL SSMANISGYR AVIEAANAFG
151 RFFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRAFDRLEV
201 AEQIESMGSK FLKLDFFQES GSGDGYAKV MSDEFIAAEM KLFAEQAQEV
251 DIIITTAIIP GKPAKLITK EMVESMKSGS VIVDLAAATG GNCELTRPGE
301 LSVTGNVGI IGYTDMANRL AGQSSQIYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTHDGEITFP PPPIQVSAQP QQTPEKAVP AAKPEPKVPV
401 LWKKLAPAVI AAVLVLVWGA VAPAAFLNHF IVEVLACVIG YYVVWNVSHS
451 LHTPLMSVTN AISGIIVVGA LLOIGQNGF VSLLSFVAIL IAGINIFGGF
501 AVTRRMLNMF KKG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 155 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 155.ng) from *N. gonorrhoeae*:

```

m155 / g155 97.9% identity in 513 aa overlap
              10      20      30      40      50      60
m155.pep     MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              |||
g155          MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK
              10      20      30      40      50      60

              70      80      90      100     110     120
m155.pep     AAVWVCPLIYKVNAPSEQELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDVPR
              |||
g155          AAVWVCPLIYKVNAPSEGELPLLNEGQTIVSFLWPRQNEALVEALRAKKVNALAMDVPR
              70      80      90      100     110     120

              130     140     150     160     170     180
m155.pep     ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA
              |||
g155          ISRAQALDALSSMANISGYRAVIEAANAFGRFFTGQITAAGKVPPAQVLVIGAGVAGLAA

```

	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
g155	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDLPQESGGSGDGYAKVMSDEFIAAEM					
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
g155	250	260	270	280	290	
	KLFAEQAKEVDIIITTAAPGKPAPKLITKEMVESMKSGSVIVDLAA-TGGNCELTRPGE					
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
g155	300	310	320	330	340	350
	LSVTGNGVKIIGYTDMANRLAQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
m155.pep	370	380	390	400	410	420
	VTHDGEITFPFPPPIQVSAQPQPTPSEKAVPAKPEPKPVPLWKKLAPAVIAAVLVLWVGA					
g155	360	370	380	390	400	410
	VTRDGEITFPFPPPIQVSARPPQPTPSEKAAPAKPEPKPVPLWKKLAPAAIAAVLVLWVGA					
m155.pep	430	440	450	460	470	480
	VAPAAFLNHFIIVFLACVIGYVWVNVSHSLHTPLMSVTNAISGIIIVGALLQIQGNGF					
g155	420	430	440	450	460	470
	VAPAAFLNHFIIVFLACVIGYHVWVNVSHSLHTPLMSVTNAISGIMVVGALLQIQGNGF					
m155.pep	490	500	510			
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
g155	480	490	500	510		
	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 641>:

```

a155.seq
1  ATGAAATCG GTATCCACG TGAGTCATTA TCCGGCGAAA CCCGCGTCGC
51  CTGTACGCC GCCACCGTCG CCCTGCTGGG CAAACTGGGC TTGAAACCG
101 TTGTCGAAAG CGGCGCAGGT TTGGCGGCAA GTTTGGACGA TGCCGCTTAC
151 CAAGCAGCAG GCGCAACCGT TGCCGACAAA GCAGCGGTTT GGGCATACCC
201 TTTAATTAT AAGGTTAACG CGCCGTCCGA AGACGAGCTG CCGCTGCTCA
251 AAGAAGGACA GACCATCGTC AGCTTCCTGT GGCCGCGCCA AAACGAGGCT
301 TTGGTCGAAG CCTTGC GCGC CAAGAAAGTG AACGCGCTGG CAATGGACAT
351 GGTGCCCGCG ATTTGCGCGC GCGAGGCTTT GGACGNTTGT TCTTNGATGG
401 CAAACATCAG CGGCTACCGC GCCGTGATTG AAGCCGCCAA CGCCTTCGGC
451 CGTTTNTTCA CCGGCCAAAT TACTGCCGCA GGCAAAGTGC CGCCCGCGCA
501 GGTTTTGGTG ATTGGTGCAG GTGTGGCAGG TTTGGCGGCG ATCGGTACGG
551 CAAACTCGCT CGGCGCAGTG GTACGCGTGT TCGATACCGC CCTG.AAGTG
601 GCGGAACAAT TAGAATCGAT GGGCGGCAAG TTCCTGAAAC TCGACTTCCC
651 GCAAGAATCG GCGGCGAGCG GCGACGGCTA CGCCAAAGTG ATGAGCGAGC
701 AATTTATCGC CGCCGAGATG AAGCTTTTGT CCGAGCAGGC GAAAGAAGTG
751 GACATCATCA TCACCACCGC CGCCATTCCG GGCAAACCCG CGCCCAAGCN
801 NNTNANCAA GAAATGGTCG AAAGCATGAA ACCCGGCTCC GTCATCGTCG
851 ATTTGGCGGC GCGGACGGGC GGCAACTGCG AACTACCAA ACAGGGCGAA
901 TTGTTCTGTA CCGGCAACGG CGTGAAATC ATCGGCTACA CCGACATGGC
951 AAACCGCCTT GCCGACAGT CTTGCGAGCT TTACGCCACC AACTTGGTCA
1001 ACCTGACCAA GCTGTTAAGC CCGAACAAAG ACGGCGAAAT CACGCTGGAC
1051 TTCGAAGACG TGATTATCCG CAACATGACC GTTACCCGCG ACGGCGAAAT
1101 CACCTTCCCG CTTCCGCCGA TTCAAGTTC CGCCCAACCG CAGCAAACGC
1151 CGTCTGAAAA AGCCGCGCCT GCCGCCAAGC CCGAACCGAA ACCCGTTCCC

```

```

1201 CTGTGGAAAA AACTCGCGCC CGCCNTNATC GCCGCCGTGT TGGTACTGTG
1251 GGTCGGCGCG GTGCGACCCG CAGCATTCTT GAACCACTTT ATCGTCTTCG
1301 TCCTCGCCTG CGTCATCGGC TACTATGTCG TTTGGAACGT CAGCCACTCG
1351 CTGCACACAC CGCTGATGTC GGTGACCAAC GCCATTTCCG GCATCATCGT
1401 CGTCGGCGCG CTGCTGCAAA TCGGTCAGGG CAACGGCTTC GTTTCGCTGC
1451 TGTCGTTTGT TGCCATCCTG ATTGCCAGCA TCAACATCTT CGGCGGCTTC
1501 TTTGTAACGC GGCGGATGCT GAATATGTTT AGGAAAGGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 642; ORF 155.a>:

```

a155.pep
  1 MKIGIPRESL SGETRVACTP ATVALLGKLG FETVVESGAG LAASLDDAAY
 51 QAAGATVADK AAVWAYPLIY KVNAPSEDEL PLLKEGQITV SFLWPRONEA
101 LVEALRAKKV NALAMDMPV ISRAQALDXL SXMANISGYR AVIEAANAFA
151 RXFTGQITAA GKVPPAQVLV IGAGVAGLAA IGTANSLGAV VRVFDTRLXV
201 AEQLESMGGK FLKLDFFQES GSGGDGYAKV MSDEFIAAEM KLFAEQAKEV
251 DIIITTAAP GKPAKPKXXX EMVESMKPGS VIVDLAAATG GNCELTKQGE
301 LEVFTGNGVKI IGYTDMANRL AGQSSQLYAT NLVNLTKLLS PNKDGEITLD
351 FEDVIIRNMT VTRDGEITFP PPPIQVSAQP QQTPEKAAP AAKPEPKPVP
401 LWKKLAPAXI AAVLVLVWGA VAPAAFLNHF IVFVLACVIG YVVVWNVSHS
451 LHTPLMSVTN AISGIIIVGA LLQIGQNGF VSLLSFVAIL IASINIFGGF
501 FVTRRLNMF RKG*

```

m155/a155 95.3% identity in 513 aa overlap

m155.pep	10	20	30	40	50	60
	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQTAGATVADK					
a155	MKIGIPRESLSGETRVACTPATVALLGKLG FETVVESGAGLAASLDDAAYQAAGATVADK					
	10	20	30	40	50	60
m155.pep	70	80	90	100	110	120
	AAVWVCPLIYKVNAPSEQELPLLNEGQITIVSFLWPRONEALVEALRAKKVNALAMDMPV					
a155	AAVWAYPLIYKVNAPSEDELPLLKEGQITIVSFLWPRONEALVEALRAKKVNALAMDMPV					
	70	80	90	100	110	120
m155.pep	130	140	150	160	170	180
	ISRAQALDALSSMANISGYRAVIEAANAFAFRFTGQITAAGKVPPAQVLVIGAGVAGLAA					
a155	ISRAQALDXLSXMANISGYRAVIEAANAFAFRXFTGQITAAGKVPPAQVLVIGAGVAGLAA					
	130	140	150	160	170	180
m155.pep	190	200	210	220	230	240
	IGTANSLGAVVRAFDTRLEVAEQIESMGGKFLKLDFFQESGGSGDGYAKVMSDEFIAAEM					
a155	IGTANSLGAVVRVFDTRLXVAEQLESMGGKFLKLDFFQESGGSGDGYAKVMSDEFIAAEM					
	190	200	210	220	230	240
m155.pep	250	260	270	280	290	300
	KLFAEQAKEVDIIITTAAPGKPAKPKLITKEMVESMKSGSVIVDLAAATGGNCELTRPGE					
a155	KLFAEQAKEVDIIITTAAPGKPAKPKXXXKEMVESMKPGSVIVDLAAATGGNCELTKQGE					
	250	260	270	280	290	300
m155.pep	310	320	330	340	350	360
	LSVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
a155	LFVTGNGVKIIGYTDMANRLAGQSSQLYATNLVNLTKLLSPNKDGEITLDFEDVIIRNMT					
	310	320	330	340	350	360
m155.pep	370	380	390	400	410	420
	VTHDGEITFPPPIQVSAQPQQTPEKAVPAAPKPEPKVPLWKKLAPAVIAAVLVLVWGA					
a155	VTRDGEITFPPPIQVSAQPQQTPEKAAPAAKPEPKVPLWKKLAPAXIAAVLVLVWGA					
	370	380	390	400	410	420



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	430	440	450	460	470	480
m155.pep	VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF					
a155	VAPAAFLNHFIVFVLACVIGYYVWNVSHSLHTPLMSVTNAISGIIIVVGALLQIGQGNGF					
	430	440	450	460	470	480
	490	500	510			
m155.pep	VSLLSFVAILIAGINIFGGFAVTRMLNMFKKGX					
a155	VSLLSFVAILIASINIFGGFFVTRMLNMFKKGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 643>:

```

g156.seq
1  ATGACTTTCG CCTATTGGTG CATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCTCG CGGTTTTCTG GCACATACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG ATTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT GCGCTCGCTG ATGTGGGCGG GCGGATTTGC
351 CTGCACCGTC GGACTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 644; ORF 156.ng>:

```

g156.pep
1  MTFAYWCILI ACLKPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLEI LFRLAFIWCY
101 IADKAALRSL MWAGGFACTV GLFVAAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 645>:

```

m156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTGCCTAT TGCCGCTTTT
51  TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGGTTTTCTA GCGCACACGC AAGGCGCAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTTGAAGCC TTGCAACCGT TTGCCGCCGC
201 CGTTTTGACG GCACACGCAA CCGGCAATGC GCGCAATCG ACCATCAACA
251 CGCTTGCCCTG CCTGTTTCATC CTGTTCCGCC TCGCCTTTAT CTGGTGCTAT
301 ATCGCCGACA AAGCCGCTAT GCGCTCACTG ATGTGGGCAG GCGGATTTGC
351 CTGCACCGTC GGGCTGTTTG TCGCGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 646; ORF 156>:

```

m156.pep
1  MTFAYWCILI ACLKPLFCAA YAKKAGGFRF KDNHNPRGFL AHTQGAAARA
51  HAAQONGFEA FAPFAAAVLT AHATGNAAQS TINTLACLEI LFRLAFIWCY
101 IADKAAMRSL MWAGGFACTV GLFVAAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m156 / g156 96.1% identity in 127 aa overlap

	10	20	30	40	50	60
m156.pep	MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA					
g156	MTFAYWCILIACLKPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m156.pep	FAPFAAAVLTAAHATGNAAQSTINTLACLEIFLFRLAFIWCYIADKAAMRSLMWAGGFACTV					

```

g156      FAPFAAAVLTAAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWAGGFACTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
            |||||
g156      GLFVAAAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 647>:

```

a156.seq
1  ATGACTTTCG CCTATTGGTG TATTCTGATT GCCTACCTAT TGCCGCTTTT
51 TTGTGCGGCG TATGCCAAAA AAGCGGGCGG ATTCCGGTTT AAAGACAACC
101 ACAATCCGCG CGATTTTCTG GCGCGCACGC AAGGCACAGC CGCCCGTGCC
151 CACGCCGCGC AGCAAAACGG TTTGAAGCC TTTGCACCGT TTGCAGCCGC
201 CGTTTGGACG GCACACGCAA CCGGCAATGC CGGACAAGCA ACCGTCAACA
251 CGCTTGCCGG CCTGTTTCATC CTGTCCGCC TCGCCTTAT CTGGTGCTAC
301 ATCGCAGACA AAGCAGCATT ACGCTCGCTG ATGTGGGTGG GCGGATTTGT
351 CTGCACCGTC GGGCTGTTG TCGTGGCTGC TTGA

```

This corresponds to the amino acid sequence <SEQ ID 648; ORF 156.a>:

```

a156.pep
1  MTFAYWCILI AYLLPLFCAA YAKKAGGFRF KDNHNPRDFL ARTQGTAAARA
51 HAAQONGFEA FAPFAAAVLT AHATGNAGQA TVNTLAGLFI LRLAFIWCY
101 IADKAALRSL MWVGGFVCTV GLFVVAAX*

```

m156/a156 90.6% identity in 127 aa overlap

```

              10          20          30          40          50          60
m156.pep  MTFAYWCILIACLLPLFCAAYAKKAGGFRFKDNHNPRGFLAHTQGAAARAHAAQONGFEA
            |||||
a156      MTFAYWCILIAYLLPLFCAAYAKKAGGFRFKDNHNPRDFLARTQGTAAARAHAAQONGFEA
              10          20          30          40          50          60

              70          80          90          100          110          120
m156.pep  FAPFAAAVLTAAHATGNAAQSTINTLACLFI LRLAFIWCYIADKAAMRSLMWAGGFACTV
            |||||
a156      FAPFAAAVLTAAHATGNAGQATVNTLAGLFI LRLAFIWCYIADKAALRSLMWVGGFVCTV
              70          80          90          100          110          120

m156.pep  GLFVAAAX
            |||||
a156      GLFVVAAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 649>:

```

g157.seq
1  atgaggaacg aggAAAAACg cgcctgcgc cgcgaattgC gCgGgcggcg
51 ttcgcAAATg GGgagagacg tGCGgCGGC GGCGgCgata Aaaatcaacc
101 gcctgctcaa aCGTtatatc AAGCGCggtc gGaAaatcgG CGTGTATTgg
151 cCGATGGGCA AGGAATTGcg TTTGGGCGgc tTgtcCGCG CGGCGCAAAA
201 ACGCgCGGCA AAactctatc tgccttATAT CGAACCGCAC ACGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAACGCGGAA TGGAACGGGA ACGCAAGCGC
301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGTTTG TCGGTATTGC TCGTCCCGCT TGTCGGCATA GACCGGAAG
401 GCTACCGTTT GGGGAGGCA GCGGCTATT ACGATGCGAC GCTTTCGGCG
451 ATGAAATACC GTTGCAGGC GAAAACCGTG GCGGTGGGCT TTGCCTGCCA
501 GTTGGTGGAC AGGCTCCAC GCGAGGCGCA CGACCTGCCG CTGGACGGTT
551 TTGTATCGGA AGCGGGGATA TTGTGTTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 650; ORF 157.ng>:

```
g157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAAAI KINRLLKRYI KRGRKIGVYW
  51 PMGKELRLGG FVRAAQKRG A KLYLPYIEPH TRRMWFTYP ERGMERERKR
 101 GRAKLHVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPREAHDL LDGFVSEAGI LCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 651>:

```
m157.seq
  1 ATGAGGAACG AGGAAAAACG CGCCTGCGC CGCGAATTGC GCGGGCGGCG
  51 TTCGCAATG GGGCGGGACG TCGGGGCGGC GGCAACGGTA AAAATCAACG
 101 ACCTGCTCAA ACGTTATATT AAAAAAGGCG GGAAATCGG CGTGTATTGG
 151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
 201 ACGCGGTGCG GAACTCTACC TGCCTTATAT CGAACC CGT TCGCGGCGGA
 251 TGTGGTTTAC GCCGTATCCT GCCGATGGAG TAAACAAGA ACGCAAGCGC
 301 GGTAGGGCGA AGCTGCATGT CCCTCAGTTT GCAGGTCGGA AAAAGCGTGT
 351 GCATGATTG AACCTCCTGC TTGTGCCAGT GGTGCGTATG GACAGGCTGG
 401 GCTACCGCTT GGGACAGGCA GCGGCTATT ACGATGCGAC GCTTTCAGCG
 451 ATGAAATACC GTTGCAGGC AAAAACCGTG GCGTGGGCT TTGCCTGCCA
 501 GTTGGTGGAC AGGCTGCCG TCGAGGCGCA CGACCGGTCT TTGACGGTT
 551 TTGTGTCGGA GCGGGGATA TTGTGTTTTT AG
```

This corresponds to the amino acid sequence <SEQ ID 652; ORF 157>:

```
m157.pep
  1 MRNEEKRALR RELRGRRSQM GRDVRAAATV KINHLLKRYI KKGRKIGVYW
  51 PMGKELRLDG FVRAAQKRG A ELYLPYIEPR SRRMWFTYP ADGVKQERKR
 101 GRAKLHVPQF AGRKKRVHDL NLLVPVVG M DRLGYRLGQA GGYDATLSA
 151 MKYRLQAKTV GVGAFACQLVD RLPVEAHDRS LDGFVSEAGI LCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m157 / g157 88.1% identity in 193 aa overlap

	10	20	30	40	50	60
m157.pep	MRNEEKRALRRELGRRSQMG RDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG					
g157	MRNEEKRALRRELGRRSQMG RDVRAAAAIKINRLLKRYIKRGRKIGVYWPMGKELRLGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m157.pep	FVRAAQKRGAEYLPYIEPRSRMWFTYPADGVKQERKRGRAKLHVPQFAGRKRVHDL					
g157	FVRAAQKRGAKLYLPYIEPHTRRMWFTYP ERGMERERKRGRAKLHVPQFAGRKIRVHGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m157.pep	NLLVPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS					
	::					
g157	SVLLVPLVGIDREGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPREAHDLP					
	130	140	150	160	170	180
	190					
m157.pep	LDGFVSEAGILCFX					
g157	LDGFVSEAGILCFX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 653>:

```
a157.seq
  1 ATGAGGAACG AGGAAAAACA CGCCTTGC GCAGAGTTGC GCCGCGCCCG
  51 CGCGCAGATG GGGCATCAAG GCGGTTGC GCGGGGCAA ACGATTAAC
```

```

101 GCCTGCTCAA ACGTTATATC AAGCGTGGTC GGAAATCGG CGTGTATTGG
151 CCGATGGGCA AGGAATTGCG TTTGGACGGC TTTGTCCGCG CGGCGCAAAA
201 ACGCGGTGCA AAACCTTATC TGCCTTATAT CGAACCGCGT TCGCGGCGGA
251 TGTGGTTTAC GCCGTATCCT GAAAGCGGAA TGGAACGGGA GCGCATACGG
301 GGCAGGGCGA AGTTGAACGT GCCGCAGTTT GCAGGGCGCA AAATCCGCGT
351 GCACGGTTTG TCGGTATTGC TCGTCCCGCT TGTCCGCATA GACCGCGAGG
401 GCTACCGCTT AGGACAGGCA GCGGCTATT ACGATGCGAC GCTTGCGGCG
451 ATGAAATACC GTTTCAGGC AAAAACCCTG GCGGTGGGCT TTGCCTGCCA
501 GTTTGTGGAC AGGCTGCCGC GCGAACCGCA CGATCTGCTG CTGGACGGTT
551 TTGTGTCGGA GCGGGGATA TTGTGCTTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 654; ORF 157.a>:

```

a157.pep
1 MRNEEKHALR RELRRARAQM GHQRLAAGQ TINRLKRYI KRGRKIGVY
51 PMGKELRLDG FVRAAQKRGK KLYLPYIEPR SRRMWFTYPY ESGMERERIR
101 GRAKLNVPQF AGRKIRVHGL SVLLVPLVGI DREGYRLGQA GGYDATLAA
151 MKYRLQAKTV GVGFAQCFVD RLPREPHDLL LDGFVSEAGI LCF*

```

m157/a157 82.4% identity in 193 aa overlap

```

              10      20      30      40      50      60
m157.pep MRNEEKRALRRELGRRSQMGRDVRAAATVKINHLLKRYIKKGRKIGVYWPMGKELRLDG
          |||||:||||| |:|::| || ||:|||||:|||||:|||||
a157 MRNEEKHALRRELRRARAQMGHQRLAAGQTINRLKRYIKRGRKIGVYWPMGKELRLDG
              10      20      30      40      50      60

              70      80      90      100     110     120
m157.pep FVRAAQKRGAEYLYPYIEPRSRMWFTYPADGVKQERKGRAKLHVPOFAGRKKRVHDL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a157 FVRAAQKRGAKLYLPYIEPRSRMWFTYPESGMERERIRGRAKLNVPQFAGRKIRVHGL
              70      80      90      100     110     120

              130     140     150     160     170     180
m157.pep NLLVVPVVGMDRLGYRLGQAGGYDATLSAMKYRLQAKTVGVGFACQLVDRLPVEAHDRS
          ::|||:|:|:| |||||:|||||:|||||:|||||:|||||:|||||
a157 SVLLVPLVGIDREGYRLGQAGGYDATLAAMKYRLQAKTVGVGFACQFVDRLPREPHDLL
              130     140     150     160     170     180

              190
m157.pep LDGFVSEAGILCFX
          |||||:|||||
a157 LDGFVSEAGILCFX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 655>:

```

g158.seq
1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTTCAAG TGGTGGAAG
51 CGGCAGCTTC AGCCGTGCGG CGgagcAGTT GGAGAtggCA AATTCTGCCG
101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGCGT GAacCTGctc
151 aACCGCACCA CGCGGCAACT CAATCTGACG GAAGAAGGCG CGCAATATTT
201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCGG GAAACCGAAA
251 TGCTGGCAGT GCACGAAGTA CCGCAAGGCG TGTTCGCGGT GGATTCCGCG
301 ATGCcgatgg TGCTGCATCT GCTGGCGCCG CTGGCAGCAA AATTCAACGA
351 ACGCTATCCG CATATCcgac TTTCGCTCGT TTCTTCCGAa ggctatatca
401 atctGattGA Acgcaaagtc gAtatTGCCT TACGGGCCGG AGAATTGGAC
451 GATTCCGGGC TCGTGCACG CCATCTGTTT GACAGCCACT TCCGCGtagt
501 cgCCAGTCCT GAATATTTAG CAAAACACGG CACGCCACAA TCTGCAGAAG
551 atcTTGCCAA CCATCAATGT TTAGGCTTCA CAGAACCCGG TTCTCTAAAT
601 ACATGGGCGG TTTTAGAtgC GCAGGGAAT CCCTATAAAA TTTCACCGCA
651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAAGtt
701 gCGGTATTGC TTGCTTATCA GATTTTTTGG TTGACAACGA CATCACTGAA
751 GGAAAGTTAA TTCCcctatt cgCCGAACAA ACCTCCAATA AAACACACCC

```

801 CTTAATGCT GTTATTACA GCGATAAAGC CGTCAACCTC CGCTTACGCG  
 851 TATTTTGGG TTTTATTAGT AAGGAACTGG GAAAAAATAT GAATAGAACG  
 901 AATACCAAT AA

This corresponds to the amino acid sequence <SEQ ID 656; ORF 158.ng>:

g158.pep  
 1 MKTNSEELTV FVQVVEGSGF SRAAEQLEMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTTRQLNLT EEGAQYFRRR QRILQEMAAA ETEMLAVHEV PQGVLRVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSS EYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSHFRVVASP EYLAKHGTPQ SAEDLANHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSSCGIACLS DFLVDNDITE  
 251 GKLIPLFAEQ TSNKTHPFNA VYYSKAVNL RLRVFLDFLV KELGKNNMRT  
 301 NTK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 657>:

m158.seq  
 1 ATGAAAACCA ATTCAGAAGA ACTGACCGTA TTTGTCAAG TGGTGGAAG  
 51 CGGCAGCTTC AGCCGTGCGG CGGAGCAGTT GGCATGGCA AATTCTGCCG  
 101 TAAGCCGCAT CGTCAAACGG CTGGAGGAAA AGTTGGGTGT GAACCTGCTC  
 151 AACCACCA CGCGGCAACT CAGTCTGACG GAAGAAGGCG CGCAATATT  
 201 CCGCCGCGCG CAGAGAATCC TGCAAGAAAT GGCAGCGCG GAAACCGAAA  
 251 TGCTGGCAGT GCACGAAATA CCGCAAGGCG TGTGAGCGT GGATCCGCG  
 301 ATGCCGATGG TGCTGCATCT GCTGCGCGG CTGGCAGCAA AATTCAACGA  
 351 ACGCTATCCG CATATCCGAC TTTCGCTCGT TTCTCCGAA GGCTATATCA  
 401 ATCTGATTGA ACGCAAAGTC GATATTGCCT TACGGGCGCG AGAATTGGAC  
 451 GATTCCGGGC TCGGTGCACG CCATCTGTTT GACAGCCGCT TCCGCGTAAT  
 501 CGCCAGTCCT GAATACCTGG CAAAACACGG CACGCCGCAA TCTACAGAAG  
 551 AGCTTGCCGG CCACCAATGT TTAGGCTTCA CCGAACC CGG TTCTCTAAAT  
 601 ACATGGGCGG TTTTAGATGC GCAGGAAAT CCCTATAAGA TTTCACCGCA  
 651 CTTTACCGCC AGCAGCGGTG AAATCTTACG CTCGTTGTGC CTTTCAGGT  
 701 GCGGTATTGT TTGCTTATCA GATTTTTTGG TTGACAACGA CATCGCTGAA  
 751 GGAAAGTTAA TTCCCCTGCT CGCCGAACAA ACCTCCGATA AAACACACCC  
 801 CTTAATGCT GTTATTACA GCGATAAAGC CGTCAATCTC CGCTTACGCG  
 851 TATTTTGGG TTTTATTAGT GAGGAACTGG GAAACAATCT CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 658; ORF 158>:

m158.pep  
 1 MKTNSEELTV FVQVVEGSGF SRAAEQLAMA NSAVSRIVKR LEEKLGVNLL  
 51 NRTTRQLSLT EEGAQYFRRR QRILQEMAAA ETEMLAVHEI PQGVLSVDSA  
 101 MPMVLHLLAP LAAKFNERYP HIRLSLVSS EYINLIERKV DIALRAGELD  
 151 DSGLRARHLF DSRFRVIASP EYLAKHGTPQ STEELAGHQC LGFTEPGSLN  
 201 TWAVLDAQGN PYKISPHFTA SSGEILRSLC LSGCGIVCLS DFLVDNDIAE  
 251 GKLIPLLAEQ TSKTHPFNA VYYSKAVNL RLRVFLDFLV EELGNNLCG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m158 / g158 94.3% identity in 297 aa overlap

	10	20	30	40	50	60
m158.pep	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSAVSRIVKRLEEKLGVNLLNRTTRQLSLT					
g158	MKTNSEELTVFVQVVEGSGFSRAAEQLAMANSAVSRIVKRLEEKLGVNLLNRTTRQLNLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158.pep	EEGAQYFRRRQRILQEMAAAEETEMLAHVHEIPQGVLSVDSAMPMVLHLLAPLAAKFNERYP					
g158	EEGAQYFRRRQRILQEMAAAEETEMLAHVHEVPQGVLRVDSAMPMVLHLLAPLAAKFNERYP					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158 . pep	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
g158	HIRLSLVSSSEGYINLIERKVDIALRAGELDDSGLRARHLFDSHFRVVASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158 . pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIVCLS					
g158	SAEDLANHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSSCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158 . pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNNLCGX					
g158	DFLVDNDITEGKLIPLFAEQTSNKTHPFNAVYYSKAVNLRRLRVFLDFLVKELGKNMNRT					
	250	260	270	280	290	300
g158	NTKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 659>:

a158 . seq

1	ATGAAAACCA	ATTCAGAAGA	ACTGACCGTA	TTGTGTTCAAG	TGGTGGAAAG
51	CGGCAGCTTC	AGCCGTGCGG	CGGAGCAGTT	GGCGATGGCA	AATTCTGCCG
101	TAAGCCGCAT	CGTCAAACGG	CTGGAGGAAA	AGTTGGGTGT	GAACCTGCTC
151	AACCGCACCA	CGCGGCAACT	CAGTCTGACG	GAAGAAGGCG	CGCAATATTT
201	CCGCCGCGCG	CAGAGAATCC	TGCAAGAAAT	GGCAGCGGCG	GAAACCGAAA
251	TGCTGGCAGT	GCACGAAATA	CCGAAGGCG	TGTTGCGCGT	GGATTCCGCG
301	ATGCCGATGG	TGCTGCATCT	GCTGGCGCGG	CTGGCAGCAA	AATTCAACGA
351	ACGCTATCCG	CATATCCGAC	TTTCGCTCGT	TTCTTCCGAA	GGCTATATCA
401	ATCTGATTGA	ACGCAAAGTC	GATATTGCCT	TACGGGCCGG	AGAATTGGAC
451	GATTCCGGGC	TGCGTGACG	CCATCTGTTT	GACAGCCGCT	TCCGCGTAAT
501	CGCCAGTCCT	GAATACCTGG	CAAAACACGG	CACGCCGCAA	TCTACAGAAG
551	AGCTTGCCGG	CCACCAATGT	TAGGCTTCA	CCGAACCCGG	TTCTCTAAAT
601	ACATGGGCGG	TTTGTAGATG	GCAGGGAAT	CCCTATAAGA	TTTACCCGCA
651	CTTTACCGCC	AGCAGCGGTG	AAATCTTACG	CTCGTTGTGC	CTTTACAGTT
701	GCGGTATTGC	TTGCTTATCA	GATTTTTTGG	TTGACAACGA	CATCGCTGAA
751	GGAAAGTTAA	TTCCCCTGCT	CGCCGAACAA	ACCTCCAATA	AAACGCACCC
801	CTTTAATGCT	GTTTATTACA	GCGATAAAGC	CGTCAACCTC	CGCTTACGCG
851	TATTTTTTGA	TTTTTTAGTG	GAGGAAC TGG	GAAACAATCT	CTGTGGATAA

This corresponds to the amino acid sequence <SEQ ID 660; ORF 158.a>:

a158 . pep

1	MKTNSEELTV	FVQVVEGSF	SRAAEQLAMA	NSAVSRIVKR	LEEKLGVNLL
51	NRTTRQLSLT	EEGAQYFRR	QRIQEMAAA	ETEMLA VHEI	PQGVLRVDSA
101	MPMVLHLLAP	LAAKFENERY	HIRLSLVSS	GYINLIERKV	DIALRAGELD
151	DSGLRARHLF	DSRFRVIASP	EYLAKHGTPQ	STEELAGHQ	LGFTPEPSLN
201	TWAVLDAQGN	PYKISPHFTA	SSGEILRSLC	LSGCGIACLS	DFLVDNDIAE
251	GKLIPLLAEQ	TSNKTHPFNA	VYYSKAVNLR	RLRVFLDFLV	EELGNNLCG*

m158/a158 99.0% identity in 299 aa overlap

	10	20	30	40	50	60
m158 . pep	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
a158	MKTNSEELTVFVQVVEGSFSRAAEQLAMANSVSRIVKRLEEKLGVNLLNRTTRQLSLT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m158 . pep	EEGAQYFRRQRIQEMAAEETEMLA VHEIPQGVLSVDSAMPVVLHLLAPLA AKFENERY					
a158	EEGAQYFRRQRIQEMAAEETEMLA VHEIPQGVLRVDSAMPVVLHLLAPLA AKFENERY					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m158.pep	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
a158	HIRLSLVSEGYINLIERKVDIALRAGELDDSGLRARHLFDSRFRVIASPEYLAKHGTPQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m158.pep	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIVCLS					
a158	STEELAGHQCLGFTEPGSLNTWAVLDAQGNPYKISPHFTASSGEILRSLCLSGCGIACLS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m158.pep	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNLNCGX					
a158	DFLVDNDIAEGKLIPLLAEQTSKTHPFNAVYYSKAVNLRRLRVFLDFLVEELGNLNCGX					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 661>:

```

g160.seq
1  ATGGAcattc  tgGACAAact  ggtcgatCTC  GCccaATTGA  CGGGCAGTGC
51  GGATGTGCAG  TgcctTTTGG  GCGGACAATG  gcATGaaacc  TTGCAACGCG
101 AAGGGCTGGT  ACACATTGTT  ACGGCGGGCA  GCGGTTATCT  CTGCATCGAC
151 GCGGAAACTT  CCCCgcGTCC  GGTcGGCAGC  GCGGATATTG  TATTTTCCCC
201 GCGCGGCTTG  GGTcATGTGT  TGAGCCACGA  CGGAAAATAC  GGAGAAAGTT
251 TACAACCGGA  CATACGACAA  AACGGCACAT  TTATGGTCAA  ACAGTGCGGC
301 AACGGGCTGG  ATATGAGCCT  GTTTTGCGCC  CGTTCCGCT  ACGACACCCA
351 CGCCGATTG  ATGAACGGGC  TGCCGGAAC  CGTTTTCTG  AACATTGCCC
401 ATCCAAGTTT  GCAGTATGTG  GTTCAATGC  TGCAACTGGA  AAGCGAAAAA
451 CCTTTGACGG  GGACGGTTTC  CGTGGTCAAC  GCATTACCGT  CCGTCCTGCT
501 GGTGCTTATC  CTGCGCGCCT  ATCTCGAACA  GGATAAGGAT  GTCGAATCT
551 CGGGCGTATT  GAAAGGTTGG  CAGGACAAAC  GTTTGGGACA  TTTGATCCAA
601 AAGGTGATAG  ACAAACCGGA  AGACGAATGG  AATATTGACA  AAATGTTGTC
651 CGCCGCCAAT  ATGTCGCGCG  CGCAACTGAT  GCGCGCTTC  AAAAGCCAAG
701 TCGGACTCAG  CCCGCACGCC  TTTGTGAACC  ATATCCGCCT  GCAAAAAGGC
751 GCATTGCTGC  TGAAGAAAAC  CCGGATTTCG  GTTTGGAGG  TCGCGCTGTC
801 GGTGGGCTTT  CAGTCGGAAA  CGCATTTCGG  CAAGGCGTTC  AAACGGCAAT
851 ATCACGTTTC  GCCGGGCAA  TACCGGAAAG  AAGGCGGGCA  AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 662; ORF 160.ng>:

```

g160.pep
1  MDILDKLVDL  AQLTGSADVQ  CLLGGQWHET  LQREGLVHIV  TAGSGYLCID
51  GETSPRPVGT  GDIVFFPRGL  GHVLSHDGKY  GESLQPDIRQ  NGTFMVKQCG
101 NGLDMSLFCA  RFRYDTHADL  MNGLPETVFL  NIAHPSLQYV  VSMLQLESEK
151 PLTGTVSVDN  ALPSVLLVLI  LRAYLEQDKD  VELSGVLKGW  QDKRLGHLIQ
201 KVIDKPEDEW  NIDKMVAAN  MSRAQLMRRF  KSQVGLSPHA  FVNHIRLQKG
251 ALLLKPTPDS  VLEALSVGF  QSETHFGKAF  KRQYHVSPGQ  YRKEGGQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 663>:

```

m160.seq
1  ATGGACATTC  TGGACAAACT  GGTGATTTC  GCCCAATTGA  CGGGCAGTGT
51  GGATGTGCAG  TGCCTTTTGG  GCGGACAATG  GTCGGTACGG  CATGAAACCT
101 TGCAACGCGA  AGGATTGGTA  CACATTGTTA  CATCGGGCAG  CGGCTATCTC
151 TGCATCGACG  GCGAACTTC  CCCGCGTCCG  GTCAGTACAG  GGGATATTGT
201 ATTTTCCCG  CGCGGCTTGG  GTCATGTGTT  GAGCCACGAC  GGAAATGCG
251 GAGAAAGTTT  ACAACCGGAT  ATGCGGCAGC  ACGGTGCGTT  TACGGTCAAG
301 CAGTGCGGCA  ACGGACAGGA  TATGAGCCTG  TTTTGCGCCC  GTTCCGCTA
351 CGACACCCAC  GCCGATTGTA  TGAACGGGCT  GCCTGAAACC  GTTTTCTGA
401 ACATTGCCCA  TCCGAGTTTA  CAGTATGTGG  TTTCAATGCT  GCAACTGGAA
451 AGCAAAAAAC  CTTTGACGGG  GACGGTTTCC  ATGGTCAACG  CATTGTCGTC

```

```

501 CGTCCTGCTG GTGCTTATCC TGC GCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTCGCGCGC GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAAC CCGGATTCCG TTTGTGCGGT
801 CGCACTGTCT GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGGTCAAT ACCGGAAGA AggCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 664; ORF 160>:

```

m160.pep
1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 KQGALLKKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m160 / g160 93.4% identity in 301 aa overlap

```

          10      20      30      40      50      60
m160.pep MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      MDILDKLVDL AQLTGSADVQ CLLGGQW--- HETLQREGLV HIVTAGSGYL CIDGETSPRP
          10      20      30      40      50

          70      80      90      100     110     120
m160.pep VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD IRQNGTFMVK QCGNGLDMSL FCARFRYDTH
          60      70      80      90      100     110

          130     140     150     160     170     180
m160.pep ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SKKPLTGTV SMVNALSSVLL VLILRAYLEQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      ADLMNGLPET VFLNIAHPSL QYVVSMLQLE SEKPLTGTV SVVNALPSVLL VLILRAYLEQ
          120     130     140     150     160     170

          190     200     210     220     230     240
m160.pep DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSRVGLS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMVA AANMSRAQLM RRFKSQVGLS
          180     190     200     210     220     230

          250     260     270     280     290     300
m160.pep PHAFVNHIRL QKGALLKKNPDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g160      PHAFVNHIRL QKGALLKKT PDSVLEVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
          240     250     260     270     280     290

m160.pep KX
          ||
g160      KX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 665>:

```

a160.seq
1 ATGGACATTC TGGACAAACT GGTCGATTTC GCCCAATTGA CGGGCAGTGT
51 GGATGTGCAG TGCCTTTTGG GCGGACAATG GTCGGTACGG CATGAAACCT

```



456

```

101 TGCAACGCGA AGGATTGGTA CACATTGTGA CATCGGCAG CGGCTATCTC
151 TGCAATCGACG GCGAAACTTC CCCGCGTCCG GTCAGTACAG GGGATATTGT
201 ATTTTTCCTG CGCGGCTTGG GTCATGTGTT GAGCCACGAC GGAAATGCG
251 GAGAAAGTTT ACAACCGGAT ATGCGGCAGC ACGGTGCGTT TACGGTCAAG
301 CAGTGCGGCA ACGGACAGGA TATGAGCCTG TTTTGC GCCC GTTTCGGCTA
351 CGACACCCAC GCCGATTGTA TGAACGGGCT GCCTGAAACC GTTTTCTGA
401 ACATTGCCCA TCCGAGTTTA CAGTATGTGG TTTCAATGCT GCAACTGGAA
451 AGCAAAAAAC CTTTGACGGG GACGGTTTCC ATGGTCAACG CATTGTCGTC
501 CGTCCTGCTG GTGCTTATCC TGCGCGCCTA TCTCGAACAG GATAAGGATG
551 TCGAACTCTC GGGCGTATTG AAAGGTTGGC AGGACAAACG TTTGGGACAT
601 TTAATCCAAA AGGTGATAGA CAAACCGGAA GACGAATGGA ATGTCGACAA
651 AATGGTGGCG GCTGCCAATA TGTGCGCGCG GCAACTGATG CGCCGTTTCA
701 AAAGCCGGGT CGGACTCAGC CCGCACGCCT TTGTGAACCA TATCCGCTG
751 CAAAAAGGCG CGTTGCTGCT GAAAAAAAC CCGGATTCGG TTTGTGCGGT
801 CGCACTGTGCG GTAGGCTTTC AGTCGGAAAC GCACTTCGGC AAGGCGTTCA
851 AACGGCAATA TCACGTTTCG CCGGTCAAT ACCGGAAGA AGGCGGGCAA
901 AAATAA

```

This corresponds to the amino acid sequence <SEQ ID 666; ORF 160.a>:

```

a160.pep
  1 MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL
 51 CIDGETSPRP VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK
101 QCGNGQDMSL FCARFRYDTH ADLMNGLPET VFLNIAHPSL QYVVSMLQLE
151 SKKPLTGTVS MVNALSSVLL VLILRAYLEQ DKDVELSGVL KGWQDKRLGH
201 LIQKVIDKFE DEWNVDKMA AANMSRAQLM RRFKSRVGLS PHAFVNHIRL
251 QKGALLLKN PDSVLSVALS VGFQSETHFG KAFKRQYHVS PGQYRKEGGQ
301 K*

```

m160/a160 100.0% identity in 301 aa overlap

```

              10      20      30      40      50      60
m160.pep      MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
              |||||
a160           MDILDKLVDF AQLTGSVDVQ CLLGGQWSVR HETLQREGLV HIVTSGSGYL CIDGETSPRP
              10      20      30      40      50      60

              70      80      90     100     110     120
m160.pep      VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
              |||||
a160           VSTGDIVFFP RGLGHVLSHD GKCGESLQPD MRQHGAFTVK QCGNGQDMSL FCARFRYDTH
              70      80      90     100     110     120

              130     140     150     160     170     180
m160.pep      ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGTVSMVNALSSVLLVLILRAYLEQ
              |||||
a160           ADLMNGLPET VFLNIAHPSL QYVVSMLQLESKKPLTGTVSMVNALSSVLLVLILRAYLEQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m160.pep      DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMAAANMSRAQLMRRFKSRVGLS
              |||||
a160           DKDVELSGVL KGWQDKRLGHLI QKVIDKPE DEWNVDKMAAANMSRAQLMRRFKSRVGLS
              190     200     210     220     230     240

              250     260     270     280     290     300
m160.pep      PHAFVNHIRL QKGALLLKNPDSVLSVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ
              |||||
a160           PHAFVNHIRL QKGALLLKNPDSVLSVALSVGFQSETHFGKAFKRQYHVSPGQYRKEGGQ
              250     260     270     280     290     300

m160.pep      KX
              ||
a160           KX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 667>:

```

g161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTCACCGTTA TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGTCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTACGC TCGGTGCTGC CGCCGTATTG CGGCGCGACA CCTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGAC AACCGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTttg GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCG TTTACACGCA GGCGGTGCTG CTCCTTGATT
401 TTGCCGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTGAGGAA
451 CCGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGCAACC GGCGTGGCGA TGTCGTCggt ttgggagacg
601 Ctgaccggct ggCACAcccT GTCCTTTcca tcggcagttt ATCtgtCGGG
651 CATCGGCGTG tccgcgCtgA TTGCCCAaCT GtcgatgAcg cGCGcctaca
701 aaGTCGCGCA CAAATTCACG GTTGCCCTCGC tttcctaTat gaccgtcGTC
751 TTTTCCGCCC TGTCTGCCGC ATTTTCTCTg ggcgaagagc ttttctggCA
801 GGAAATACTC GGTATGTGCA TCATTATcct CAGCGGCATT TTGAGCAGCA
851 TCGCCCCAT TGCCTTCAA CAGCGGCTGC AAGCCCTCTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 668; ORF 161.ng>:

```

g161.pep
1  MDTAKKDILG SGWMLVAAAC FTVMNVLIKE ASAKFALGSG ELVFWRLMFS
51  TVTLGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLTTGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVLL LNPFSRSGQE
151 PAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSAT GVAMSSVWAT
201 LTGWHTLSFP SAVYLSGIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV
251 FSALSAFFL GEELFWQEIL GMCIIILSGI LSSIRPIAFK QRLQALFRQR
301 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 669>:

```

m161.seq
1  ATGGATACCG CAAAAAAGA CATTTTAGGA TCGGGCTGGA TGCTGGTGGC
51  GGCGGCCTGC TTTACCATTG TGAACGTATT GATTAAAGAG GCATCGGCAA
101 AATTGTCCT CGGCAGCGGC GAATTGGTCT TTTGGCGCAT GCTGTTTTCA
151 ACCGTTGCGC TCGGGGCTGC CGCCGTATTG CGTCGGGACA mCTTCCGCAC
201 GCCCCATTGG AAAAACCCT TAAACCGCAG TATGGTCGGG ACGGGGGCGA
251 TGCTGCTGCT GTTTTACGCG GTAACGCATC TGCCTTTGGC CACTGGCGTT
301 ACCCTGAGTT ACACCTCGTC GATTTTTTTG GCGGTATTTT CCTTCCTGAT
351 TTTGAAAGAA CGGATTTCG TTTACACGCA GGCGGTGCTG CTCCTTGATT
401 TTGCCGCGT GGTATTGCTG CTTAATCCCT CGTCCGCAG CGGTGAGGAA
451 ACGGCGGCAC TCGCCGGGCT GGCGGGCGGC GCGATGTCCG GCTGGGCGTA
501 TTTGAAAGTG CGCGAACTGT CTTTGGCGGG CGAACCCGGC TGGCGCGTCG
551 TGTTTTACCT TTCCGTGACA GGTGTGGCGA TGTCGTGCGT TTGGGCGACG
601 CTGACCGGCT GGCACACCCT GTCCTTTCCA TCGGCAGTTT ATCTGTCTGT
651 CATCGGCGTG TCCGCGCTGA TTGCCCAACT GTCGATGACG CGCGCCTACA
701 AAGTCGCGCA CAAATTCACG GTTGCCCTCGC TTTCTATAT GACCGTCGTT
751 TTTTCCGCTC TGTCTGCCGC ATTTTCTCTG GCGGAAGAGC TTTTCTGGCA
801 GGAAATACTC GGTATGTGCA TCATCATCCT CAGCGGTATT TTGAGCAGCA
851 TCGCCCCAC TGCCTTCAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA
901 TAA

```

This corresponds to the amino acid sequence <SEQ ID 670; ORF 161>:

```

m161.pep
1  MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRLMFS
51  TVALGAAAVL RRDXTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV
101 TLSYTSSIFL AVFSFLILKE RISVYTOAVL LLGFAGVLL LNPFSRSGQE

```

151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT  
 201 LTGWHTLSFP SAVYLSCIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
 251 FSALSAAFFL GEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
 301 \*

Computer analysis of this amino acid sequence gave the following results:  
 Homology with a predicted ORF from *N. gonorrhoeae*

m161 / g161 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m161.pep	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMFLSTVALGAAAVL					
	:     :     :     :     :					
g161	MDTAKKDILGSGWMLVAAACFTVMNVLIKEASAKFALGSGELVFWRMFLSTVTILGAAAVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m161.pep	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSTSSIFLAVFSFLILKE					
	:     :     :     :     :					
g161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLTTGVTLSTSSIFLAVFSFLILKE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m161.pep	RISVYTQAVLLLGFAGVLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	:     :     :     :     :					
g161	RISVYTQAVLLLGFAGVLLNPSFRSGQEPALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m161.pep	WRVVFYLSVTGVAMSSVWATLTGWHTLSFSAVYLSCIGVSALIAQLSMTRAYKVGDKFT					
	:     :     :     :     :					
g161	WRVVFYLSATGVAMSSVWATLTGWHTLSFSAVYLSGIGVSALIAQLSMTRAYKVGDKFT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m161.pep	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	:     :     :     :     :					
g161	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPIAFKQRLQALFRQR					
	250	260	270	280	290	300
m161.pep	x					
g161	x					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 671>:

a161.seq

1	ATGGATACCG	CAAAAAAGA	CATTTTAGGA	TCGGGCTGGA	TGCTGGTGCC
51	GGCGGCCTGC	TTTACCATTA	TGAACGTATT	GATTAAAGAG	GCATCGGCAG
101	AATTGCCCCT	CGGCAGCGGC	GAATTGGTCT	TTTGGCGCAT	GCTGTTTTC
151	ACCGTTGCGC	TCGGGGCTGC	CGCCGTATTG	CGTCGGGACA	CCTTCCGCAC
201	GCCCCATTGG	AAAAACCACT	TAAACCGCAG	TATGGTCGGG	ACGGGGGCGA
251	TGCTGCTGCT	GTTTACGCG	GTAACGCATC	TGCCTTTGGC	CACCGGCGTT
301	ACCCTGAGTT	ACACCTCGTC	GATTTTTTTG	GCGGTATTTT	CCTTCCTGAT
351	TTTGAAAGAA	CGGATTTCGG	TTTACACGCA	GGCGGTGCTG	CTCCTTGGTT
401	TTGCCGGCGT	GGTATTGCTG	CTTAATCCCT	CGTCCGCAG	CGGTCAGGAA
451	ACGGCGGCAC	TCGCCGGGCT	GGCGGGCGGC	GCGATGTCGG	GCTGGGCGTA
501	TTTGAAAGTG	CGCGAACTGT	CTTTGGCGGG	CGAACCCGGC	TGGCGCGTCG
551	TGTTTTACCT	TTCCGTGACA	GGTGTGCGCA	TGTCATCGGT	TTGGGCGACG
601	CTGACCGGCT	GGCACACCCT	GTCCTTTCCA	TCGGCAGTTT	ATCTGTCGTG
651	CATCGGCGTG	TCCGCGCTGA	TTGCCCAACT	GTCGATGACG	CGCGCCTACA
701	AAGTCGGCGA	CAAATTCACG	GTTGCCTCGC	TTTCTATAT	GACCGTCGTT
751	TTTTCCGCTC	TGTCTGCCGC	ATTTTTTCTG	GCCGAAGAGC	TTTTCTGGCA
801	GGAAATACTC	GGTATGTGCA	TCATCATCCT	CAGCGGTATT	TTGAGCAGCA

851 TCCGCCCCAC TGCCTTCAAA CAGCGGCTGC AATCCCTGTT CCGCCAAAGA  
901 TAA

This corresponds to the amino acid sequence <SEQ ID 672; ORF 161.a>:

a161.pep  
1 MDTAKKDILG SGWMLVAAAC FTIMNVLIKE ASAKFALGSG ELVFWRMLES  
51 TVALGAAAVL RRDTFRTPHW KNHLNRSVMG TGAMLLLFYA VTHLPLATGV  
101 TLSYTSSIFL AVFSFLIKE RISVYTQAVL LLGFAGVLL LNPSFRSGQE  
151 TAALAGLAGG AMSGWAYLKV RELSLAGEPG WRVVFYLSVT GVAMSSVWAT  
201 LTGWHTLSFP SAVYLSICIGV SALIAQLSMT RAYKVGDKFT VASLSYMTVV  
251 FSALSAAFFL AEELFWQEIL GMCIIILSGI LSSIRPTAFK QRLQSLFRQR  
301 \*

m161/a161 99.3% identity in 300 aa overlap

m161.pep	10	20	30	40	50	60
	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLESSTVALGAAAVL					
a161	MDTAKKDILGSGWMLVAAACFTIMNVLIKEASAKFALGSGELVFWRMLESSTVALGAAAVL					
	10	20	30	40	50	60
m161.pep	70	80	90	100	110	120
	RRDXFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLIKE					
a161	RRDTFRTPHWKNHLNRSVMGTGAMLLLFYAVTHLPLATGVTLSYTSSIFLAVFSFLIKE					
	70	80	90	100	110	120
m161.pep	130	140	150	160	170	180
	RISVYTQAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
a161	RISVYTQAVLLLGAGVLLLNPSFRSGQETAALAGLAGGAMSGWAYLKVRELSLAGEPG					
	130	140	150	160	170	180
m161.pep	190	200	210	220	230	240
	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
a161	WRVVFYLSVTGVAMSSVWATLTGWHTLSFPSAVYLSICIGVSALIAQLSMTTRAYKVGDKFT					
	190	200	210	220	230	240
m161.pep	250	260	270	280	290	300
	VASLSYMTVVFSALSAAFFLGEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
a161	VASLSYMTVVFSALSAAFFLAEEELFWQEILGMCIIILSGILSSIRPTAFKQRLQSLFRQR					
	250	260	270	280	290	300
m161.pep	X					
a161	X					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 673>:

g163.seq  
1 ATGTTTATT TGACGACTTT GTTTTTTGTG TGTGTTTTGG TGGTATTGGT  
51 TTTAACCCTG CCGGATCAGG TGCAGATGTG gctCGACCGG GCAAAAGAAG  
101 TCATTTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTTt  
151 ctgGGTTTt tgcTGATACT CTCGGTCAGC GGTGTTGGGAA ACATcagGCT  
201 AGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTGCG TGGCTGGCGA  
251 TGCTGTTTGC GGCCGGGATG GCGTGGGCC TGATGTTTTT CGGCGTGGCA  
301 GAGCCGTTGA TGCAATTATT TTCGGACATT ACGGTCGGCG CGCCGGAACA  
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTACG  
401 CCTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCGGTTTC

```

451 CGCTACAAAC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCGG
651 CGTGCAGGTC TTGATTATCG CCGCCGTAAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGAAG GCGGTGAAGG TGTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGCTGCT GTTTTTTGTT TTGGCGGCGG ACCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACATC CTCGAAATC
851 TGGTGCGCCT CAGTTTGAAG ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGgc
951 gcCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGg cgcaccatCc
1001 gcgagtttgt CTTCCGGGTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCGAAC TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATT CCCTGTTTTT TGTAACCTCT GCCGACTCCG GGATTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGCGGTG CTGatgtcTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTCAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTCAACCC TACCAGTGTA
1501 TTTTGACCG GCGGCAAGTG GAAAGAACGG CTGGTGCGGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAGTTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CACCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAAC TG
1951 ATGGCGCAG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 674; ORF 163.ng>:

g163.pep

```

1 MVILTLFFV CVLVVLVLTV PDQVQMWLDR AKEVIFTEFS WFYVLTFESIF
51 LGFLILSVS GLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TVGAPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKLPALRS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEMGW IAENSFGVOV LIIAAVMSLA VVSAISGVGK GVKVLSELNL
251 GLAFLLLFFV LAADPTVYLL SAFGDNIGNY LGNLVRLSLK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFGLV
351 WFTVFGNTAI WLNDGVAGGM LEKMTSSPET LLFKFENYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVRIMSTQOE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDEMYGIK SVQDVSQDL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 675>:

m163.seq

```

1 ATGGTTATTT TGACGACTTT GTTTTTTG TGTTGTTTGG TGGTATTGGT
51 TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAAAGAG
101 TCATTTTAC CGAGTTCAGC TGGTTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT
201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTCCTGTCTG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GCGGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCAATATT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GCGGTTACG
401 CTTGGTTCGG GTACGGTACG ATTGCATTGG CTTTGGCTTA TTTCCGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCCGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATGGGCTGG ATTGCCGAAA ACAGCTTCAG

```

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651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GCGGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGCCTTGCGT TTTTGTGCT GTTTTTTGT TTGGCGGCGG GACCCACTGT
801 TTACCTGTTG TCGGCATTCT GCGACAACAT AGGGAACCTAC CTCGGAAATC
851 TGGTGCGCCT CAGTTTTTAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGGTT TGCTCATCC CCGGCCTGTT CGGCGTTTGT
1051 TGGTTTACCG TCTTCGGCAA TACGGCGATT TGGCTGAATG ACGGGGTGTC
1101 GGGGGGAATG CTCGAAAAGA TGACCTCCTC TCCGGAAACG CTGCTTTTTA
1151 AATTCTTTAA TTACCTCCCC CTGCCCAGAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCCG GGATTTATGT
1251 CCTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGTCTG CCGTGGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CTTGCACTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGCT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACC TACCAGTGTA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAATTCCT CAAACAGACT GCATCGCCCG
1601 CTATGCACGA GTTGCAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AAATGTTTCA TCGGGACGAG CCCGCAATCG AGTTCGTATC
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTCGGGC
1751 AGGATGTATC CGACCAAGTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACCTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 676; ORF 163>:

m163.pep

```

1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFYVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFWH GVHAWSVYGT IALALAYFGF
151 RYKLPLALRS CFYPLLEKI SGRFGDAIDI MALLATFFGI ITTLGFASQ
201 LGAGLQEMGW IAENSFSVQV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSFK TYAYEREHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISK RTIREFVFGV LLIPGLFVL
351 WFTVFGNTAI WLNDGVAGM LEKMTSSPET LLFKEFNLYP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLIM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKQT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHRDE PAIEFVIRKE TMRDFMYGIK SVGQDVSDQL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m163 / g163 98.6% identity in 660 aa overlap

	10	20	30	40	50	60
m163.pep	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
g163	MVILTTLFFVCVLVVLVLTVPDQVQMWLDRAKEVIFTEFSWFYVLTFSIFLGFLILSVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m163.pep	SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ					
	:					
g163	GLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITVGAPEHRQQ					
	70	80	90	100	110	120
	130	140	150	160	170	180

462

m163.pep	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
g163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI
	130 140 150 160 170 180
m163.pep	190 200 210 220 230 240
	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
g163	MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLIIAAVMSLAVVSAISGVGK
	190 200 210 220 230 240
m163.pep	250 260 270 280 290 300
	GVKVLSEINLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP
g163	GVKVLSEINLGLAFLLLFFVLAADPTVYLLSAFGDNIGNYLGNLVRLSLKTYAYEREHKP
	250 260 270 280 290 300
m163.pep	310 320 330 340 350 360
	WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
g163	WFESWTVLYWAWWCWAPFVGLFIARISKGRTIREFVFGVLLIPGLFGVLWFTVFGNTAI
	310 320 330 340 350 360
m163.pep	370 380 390 400 410 420
	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
g163	WLNDGVAGGMLEKMTSSPETLLFKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN
	370 380 390 400 410 420
m163.pep	430 440 450 460 470 480
	ITSRDKGLSAPRWQAVMWGVLSAVAVLLMRSGGLGNLQSM TLIVSLPFALLMLIMCFSL
g163	ITSRDKGLSAPRWQAVMWGVLSAVAVLLMRSGGLGNLQSM TLIVSLPFALLMLIMCFSL
	430 440 450 460 470 480
m163.pep	490 500 510 520 530 540
	WKGLSADKKYFETRVNPTS FVFTGGKWKERLVQIMSQTQE QDILKFLKQTAS PAMHELQR
g163	WKGLSADKKYFETRVNPTS FVFTGGKWKERLVRIMSQTQE QDILKFLKHTAS PAMHELQR
	490 500 510 520 530 540
m163.pep	550 560 570 580 590 600
	ELSEEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
g163	ELSEEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR
	550 560 570 580 590 600
m163.pep	610 620 630 640 650 660
	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
g163	HQTTYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVGQELMAHEQVELAE
	610 620 630 640 650 660
m163.pep	X
g163	X

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 677>:

```

a163.seq
1  ATGGTTATTT TGACGACTTT GTTTTTGTG TGTGTTTGG TGGTATTGGT
51  TTTAACCGTG CCGGATCAGG TGCAGATGTG GCTCGATCGG GCAAAGAAG
101 TCATTTTAC CGAGTTCAGC TGTTTATG TTTAACGTT TTCCATTTT
151 CTGGGTTTCC TGCTGATACT CTCGGTCAGC AGTTTGGGAA ACATCAGGCT

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201 CGGACGGGAT GAAGATGTGC CGGAATTCGG CTTCTGTGCG TGGCTGGCGA
251 TGCTGTTTGC GGCCGGGATG GGCGTGGGTC TGATGTTTTT CGGCGTGGCA
301 GAGCCGTTGA TGCATTATTT TTCGGACATT ACGGCCGGCA CGCCGGAACA
351 CAGGCAGCAG CAGGCATTGC TGCACACGGT GTTCCATTGG GGCCTTCACG
401 CTTGGTCGGT GTACGGTACG ATTGCATTGG CTTTGCTTA TTTCGGTTTC
451 CGCTACAAGC TGCCGCTTGC CCTGCGTTCT TGTTTTTACC CCCTGTTGAA
501 AGAAAAAATT TCCGGAAGGT TCGGCGATGC CATTGATATT ATGGCGTTGC
551 TTGCTACTTT TTTCGGCATC ATCACCACAT TGGGGTTCGG GGCTTCGCAA
601 CTGGGCGCCG GATTGCAGGA AATAGGCTGG ATTGCCGAAA ACAGCTTCAG
651 CGTGCAGGTT TTGATTATCG CCGCCGTCAT GTCCCTCGCC GTCGTTTCGG
701 CAATATCCGG CGTGGGGAAG GGTGTGAAGG TGTTGAGCGA GTTGAACCTG
751 GGTCTTGCCT TTTTGTGCT GTTTTTGT TTGGCGGCGG GTCCACTGT
801 TTACCTGTTG TCGGCATTTC GCGACAACAT AGGGAACAC CTCGGAATC
851 TGGTGCCTC CAGTTTTAAA ACTTATGCGT ACGAACGGGA ACACAAGCCG
901 TGGTTTGAAT CTTGGACGGT GCTTTATTGG GCGTGGTGGT GTTCTTGGGC
951 GCCGTTTGTG GGTTTGTTTA TCGCGCGCAT TTCAAAGGGG CGCACCATCC
1001 GCGAGTTTGT CTTGCGGTTT TTGCTCATCC CCGGCCTGTT CGGCGTTTTG
1051 TGGTTTACCG TCTTCGCAA TACGGCGATT TGGCTGAATG ACGGGGTTGC
1101 GGGGGGAGTG CTCGAAAAGA TGACCTCCTC TCCGGAACG CTGCTTTTAA
1151 AATTTCTTAA TTACCTCCCC CTGCCGAAT TGACGAGCAT CGTCAGCCTG
1201 CTGGTCATTT CTCTGTTTTT TGTAACCTCT GCCGATTCGG GGATTTATGT
1251 CTTGAACAAT ATTACCTCTC GGGACAAAGG CTTGAGCGCG CCACGGTGGC
1301 AGGCGGTTAT GTGGGGCGTG CTGATGCTG CCGTTGCCGT TTTGCTGATG
1351 CGCTCGGGCG GACTCGGCAA CCTGCAGTCT ATGACCCTGA TTGTTTCCCT
1401 GCCGTTTGCC CTGCTGATGC TGATAATGTG TTTGAGCCTG TGGAAAGGAT
1451 TGAGTGCGGA TAAGAAATAT TTTGAGACCC GGGTTAACCC TACCAGTGA
1501 TTTTGGACGG GCGGCAAGTG GAAAGAACGG CTGGTGCAGA TAATGAGCCA
1551 GACGCAGGAG CAGGATATTT TAAAATTCCT CAAACATACC GCATCGCCCG
1601 CTATGCACGA GTTACAACGG GAGCTTTCGG AAGAATACGG CTTGAGCGTC
1651 CGGGTCGATA AGATGTTTCA TCAGGACGAG CCCGCAATCG AGTTCGTCAT
1701 TCGGAAAGAG ACGATGCGCG ATTTTATGTA CGGGATTAAG TCTGTGCGGC
1751 AGGATGTATC CGACCACTG ATTAACGACG GCAAGCTGCC GCATATCCGG
1801 CATCAGACAA CTTACAAACC CTACGCTTAT TTTTTCGACG GGCGCGTCGG
1851 GTACGATGTG CAGTATATGA ACAAGGACGA GCTGATTGCC GACATTTTGA
1901 AAAACTACGA ACGTTATTTG ATGTTGTTGG ATGATGTCGG TCAGGAACTG
1951 ATGGCGCACG AGCAGGTGGA ATTGGCAGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 678; ORF 163.a>:

```

a163.pep
1  MVILTTLFFV CVLVVLVLTVPDQVQMWLDR AKEVIFTEFS WFFVLTFSIF
51  LGFLLILSVS SLGNIRLGRD EDVPEFGFLS WLAMLFAAGM GVGLMFFGVA
101 EPLMHYFSDI TAGTPEHRQQ QALLHTVFHW GVHAWSVYGT IALALAYFGF
151 RYKPLPLARS CFYPLLKEKI SGRFGDAIDI MALLATFFGI ITTLGFGASQ
201 LGAGLQEIOW IAENSFSVOV LIIAAVMSLA VVSAISGVGK GVKVLSLNL
251 GLAFLLLFFV LAAGPTVYLL SAFGDNIGNY LGNLVRLSEK TYAYERHKP
301 WFESWTVLYW AWWCSWAPFV GLFIARISKG RTIREFVFGV LLIPGLEFVL
351 WETVFGNTAI WLNDGVAGGV LEKMTSSPET LLEKFFNYLP LPELTSIVSL
401 LVISLFFVTS ADSGIYVLNN ITS RDKGLSA PRWQAVMWGV LMSAVAVLLM
451 RSGGLGNLQS MTLIVSLPFA LLMLIMCFSL WKGLSADKKY FETRVNPTSV
501 FWTGGKWKER LVQIMSQTQE QDILKFLKHT ASPAMHELQR ELSEEYGLSV
551 RVDKMFHQDE PAIEFVIRKE TMRDFMYGIK SVQDVSQDL INDGKLPHIR
601 HQTTYKPYAY FFDGRVGYDV QYMNKDELIA DILKNYERYL MLLDDVGQEL
651 MAHEQVELAE *

```

m163/a163 99.4% identity in 660 aa overlap

```

              10      20      30      40      50      60
m163.pep  MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFSWFFVLTFSIFLGFLILSVS
          |||||
a163      MVILTTLFFVCVLVVLVLTVPDQVQMWLDR AKEVIFTEFSWFFVLTFSIFLGFLILSVS
              10      20      30      40      50      60

              70      80      90     100     110     120
m163.pep  SLGNIRLGRDEDEVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ

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a163	 SLGNIRLGRDEDVPEFGFLSWLAMLFAAGMGVGLMFFGVAEPLMHYFSDITAGTPEHRQQ 70 80 90 100 110 120
m163.pep	130 140 150 160 170 180 QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI 
a163	QALLHTVFHWGVHAWSVYGTIALALAYFGFRYKLPALRSCFYPLLKEKISGRFGDAIDI 130 140 150 160 170 180
m163.pep	190 200 210 220 230 240 MALLATFFGIITTLGFGASQLGAGLQEMGWIAENSFSVQVLLIAAVMSLAVVSAISGVGK 
a163	MALLATFFGIITTLGFGASQLGAGLQEIWIAENSFSVQVLLIAAVMSLAVVSAISGVGK 190 200 210 220 230 240
m163.pep	250 260 270 280 290 300 GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP 
a163	GVKVLSELNLGLAFLLLFFVLAAGPTVYLLSAFGDNIGNYLGNLVRLSFKTYAYEREHKP 250 260 270 280 290 300
m163.pep	310 320 330 340 350 360 WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI 
a163	WFESWTVLYWAWWCSWAPFVGLFIARISKGRITREFVFGVLLIPGLFGVLWFTVFGNTAI 310 320 330 340 350 360
m163.pep	370 380 390 400 410 420 WLNDGVAGGMLEKMTSSPETLLKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN 
a163	WLNDGVAGGVLEKMTSSPETLLKFFNYLPLPELTSIVSLLVISLFFVTSADSGIYVLNN 370 380 390 400 410 420
m163.pep	430 440 450 460 470 480 ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL 
a163	ITSRDKGLSAPRWQAVMWGLMSAVAVLLMRSGGLGNLQSMTLIVSLPFPALLMLIMCFSL 430 440 450 460 470 480
m163.pep	490 500 510 520 530 540 WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQEQDILKFLKQTASPAHMLQR 
a163	WKGLSADKKYFETRVNPTSVFWTGGKWKERLVQIMSQEQDILKFLKHTASPAHMLQR 490 500 510 520 530 540
m163.pep	550 560 570 580 590 600 ELSEYGLSVRVDKMFHRDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR 
a163	ELSEYGLSVRVDKMFHQDEPAIEFVIRKETMRDFMYGIKSVGQDVSDQLINDGKLPHIR 550 560 570 580 590 600
m163.pep	610 620 630 640 650 660 HQTTPYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVQGELMAHEQVELAE 
a163	HQTTPYKPYAYFFDGRVGYDVQYMNKDELIADILKNYERYLMLLDDVQGELMAHEQVELAE 610 620 630 640 650 660
m163.pep	X 
a163	X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 679>:

```

g164.seq (partial)
1  ..ATGAACACAT TTTTGAAAAA CAGCGAATAC GCGTATATCC TGAACGACTG
51  CAAGGCGCGC TTCCTGTTCG CCTCGGCCGG CCTGTCAAAA GAATTGGCGG
101 GCCTGAAGGC GCAAACGCCC GTCGAAAAAA TCATTGGGAC GGACAAAAGC
151 CGGCCGGCGG GCGAAACGGC GGAAGGCGAT GCCTTTTTTG AAAACGTGCG
201 CCGCTTCCCC GAAAAACCCG ACTTGGGCGG CCAACCCCGG ATAAATGATT
251 TGGCACACAT CATCTACACC TCCGGCACGA CGGGGCATCC CAAAGGCGCG
301 CTAATCAGTT ACGCCAACCT GTTCGCCAAC CTGAACGGCA TCGAACGCAT
351 CTTtaaAATT TCCAAACGCG ACCGCTTTAT CGTTTTCTg ccgatgTTCC
401 ACAGCTTCAC GCTGACGGCT ATGGTGCTGC TGCCGATTTA TATGGCGTGT
451 TCGATTATTT TGGTCAAAtc cgttttCCcC ttttccaacG TTTTGAAACA
501 GGCCCTGCTC AAACGCGCAA CCGTGTTTTT GGGCGTACCC GCGATTTACA
551 CCGCGATGAG CAAGGCAAAA ATCCCTTGGT ATTTAGATG GTTCAACCGC
601 ATCCGCCTGT TTATCAGCGG CGGCGCGCCT TTGGCGGAAC AAACCATCCT
651 CGATTTTAAA GCCAAGTTCC CCGCGGCCAA ATTGCTGGAA GGCTACGGAC
701 TGAGCGAAGC CTCGCCCGTC GTGCCCGTCA ATACGCCCGA ACGGCCAAAA
751 GCCCGCAGCG TCGGCATCCC CCTGCCCGGT TTGGAAGCCA AAGCCGTCGA
801 TGAAGAATTG GTCGAAGTGC CGCGCGCGCA AGTGGGCGAA CTGATCGTCA
851 GGGGCGGTTT GGTGATGCGG GGCTACCTCA ATATGCCTGC CGCCACCGAT
901 GAAACCATCG TCAACGGCTG GTTGAAACG GCGGATTTG TTACCATAGA
951 CGAGGACGGC TTTATCTTTA TCGTCGACCG CAAAAAGAT TTGATTATTT
1001 CCAAAGGTCA AAACGTCTAT CCGCGCGAGA TCGAAGAAGA AATCCACAAA
1051 CTCGATGCCG TCGAAGCCGC CGCCGTCATC GGCGTGAAG ACCGTTATGC
1101 CGACGAGGAA ATCGTCGCCT TCGTCCAATT GAAGGAAGGT ATGGATTGGA
1151 GCGAGGACGA aatccgcgc caccTGCgTA CCGTGTGGC AAATTTCAA
1201 ATCCCCAAC AGATCCACTT TAAAGACGGG CTGCCGCGCA ACGTACGGG
1251 CAAAGTATTG AAACGGGTGC TGAAGGAGCA GTTTGAAGGA AACAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 680; ORF 164.ng>:

```

g164.pep (partial)
1  ..MNTFLKNSEY AYILNDCKAR FLFASAGLSK ELAGLKAQTP VEKIIWTDKS
51  RPAGETAEGD AFFENVRRFP EKPDILGRQPR INDLAHIIYT SGTTHGHPKGA
101 LISYANLFAN LNGIERIFKI SKRDRFIVFL PMFHSFTLTA MVLLPIYMAC
151 SILLVKSVPF FSNVLKQALL KRATVFLGVP AIYTAMSKAK IPWYFRWFNR
201 IRLFISGGAP LAEQTILDFK AKFPRAKLE GYGLSEASPV VAVNTPERQK
251 ARSVGIPLPG LEAKAVDEEL VEVPRGEVGE LIVRGGSVMR GYLNMPAATD
301 ETIVNGWLKT GDFVTIDEDG FIFIVDRKDD LIISKQONVY PREIEEIHK
351 LDAVEAAAVI GVKDRYADEE IVAFVQLKEG MDLGEDEIRR HLRTVLANFK
401 IPKQIHFKDG LPRNATGKVL KRVLKEQFEG NK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 681>:

```

m164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTCGCCG CCGCCTGCCG
51  CAAAAACGGA AACGGCACGG CAGTGTTCTGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAG GCCGAAGCCG TCGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCCGGCA CACGGTCGCG CTGGCGGTTT CCAATTCAC
201 AGAATTTATT ACCGCCTATT TCGCCATCTC CGCCATCGGC GCGGTCGCCG
251 TACCGATGAA CACATTTTGG AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCCT GTTCGCCTCG GCCGCGCTGT CAAAAGAATT
351 GGCGGGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGACA
401 AAAGCCGTCC GACCGCGGAA ACGGCGGAAG GCGATGCCTT TTTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCCGATAAAA
501 TGATTTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GCGCGCTAAT CAGTTACGCC AACCTGTTCT CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATTTCCAA GCGCGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTTCGAT TATTTTGGTC AAATCCGTTT TTCCGTTTTT CAACGTTTTG
751 AAACAGACAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TACCCGCGAT
801 TTACACCGCG ATGAGCAAGG CGAAAAATCC TTGGTATTTT AGATGGTTCA
851 ACCGCATTCT CCTGTTTATC AGCGGCGGCG CGCCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA

```

```

951  CGGACTGAGC GAAGCCTCTC CCGTCGTCGC CGTCAATACG CCCGAGAGGC
1001 AAAAAGCCCG CAGCGTCGGC ATCCCCCTGC CCGGTTTGA AGCCAAAGCC
1051  GTCGATGAAG AATTGGTGA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101  CGTCAGGGGC GGTTCGGTGA TGCGGGGCTA CCTCAATATG CCTGCCGCCA
1151  CCGATGAAAC CATCGTCAAC GGCTGGTTGA AAACGGGCGA TTTCGTTACC
1201  ATAGACGAAG ACGGCTTTAT CTTTATCGTC GACCGCAAAA AAGATTTGAT
1251  TATTTCCAAA GGTCAAAATG TCTATCCGCG CGAGATTGAA GAAGAAATCT
1301  ACAAACCTGA TGCCGTCGAA GCCGCCGCCG TCATCGGCGT GAAAGACCGT
1351  TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401  TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451  TCAAAATCCC CAAACAAATC CACTTTAAAG ACGGGCTGCC GCGCAACGCT
1501  ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551  ATGA

```

This corresponds to the amino acid sequence <SEQ ID 682; ORF 164>:

```

m164.pep
1  MNRTYANFYE MLAAACRKNG NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEEI TAYFAISAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTDKSRPTGE TAEGDAFFED
151 VRRFPEKPD LGRQPRINDLA HIIYTS GTTG HPKGALISYA NLFANLNGIE
201 RIFKISKDR FIVFLPMFHS FTLTAMVLLP IYMACSIILV KSVFPFSNVL
251 KQTLKRA TVFLGVP AIYTA MSKAKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFP RAKLLEGY GLS EASPVVAVNT PERQKARSVG IPLPGLEAKA
351 VDEELVEVP RGEVGE LIVRG GSVMRGY LNM PAATDEIVN GWLKTGFVFT
401 IDEGFI FIV DRKKDLI ISK QNVYPREIE EEIYKLDAVE AAIVIGVKDR
451 YADEEIVAFV QLKEGMDL GE NEIRRHLRTV LANFKIPKQI HFKDGLPRNA
501 TGKVLKRV LK EQFDGNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* m164 / g164 98.6% identity in 432 aa overlap

```

          60      70      80      90      100      110
m164.pep  GDTVALAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSK
          |||||||
g164      MNTFLKNSEYAYILNDCKARFLFASAGLSK
          10      20      30

          120      130      140      150      160      170
m164.pep  ELAGLKAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPD LGRQPRINDLAHIIYT
          |||||||
g164      ELAGLKAQTPVEKIIWTDKSRPAGETAEGDAFFENVRRFPEKPD LGRQPRINDLAHIIYT
          40      50      60      70      80      90

          180      190      200      210      220      230
m164.pep  SGTTHGHPKGALISYANLFANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
          |||||||
g164      SGTTHGHPKGALISYANLFANLNGIERIFKISKRD RFIVFLPMFHSFTLTAMVLLPIYMAC
          100      110      120      130      140      150

          240      250      260      270      280      290
m164.pep  SIILVKSVPFSNVLKQTLKRA TVFLGVP AIYTA MSKAKIPWYFRWFNRIRLFISGGAP
          |||||||
g164      SIILVKSVPFSNVLKQALLKRA TVFLGVP AIYTA MSKAKIPWYFRWFNRIRLFISGGAP
          160      170      180      190      200      210

          300      310      320      330      340      350
m164.pep  LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVG IPLPGLEAKAVDEEL
          |||||||
g164      LAEQTILDFKAKFPRAKLLEGYGLSEASPVVAVNTPERQKARSVG IPLPGLEAKAVDEEL
          220      230      240      250      260      270

          360      370      380      390      400      410

```

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m164.pep  VEVPRGEVGEIVRGGSSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
g164      VEVPRGEVGEIVRGGSSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKD
          280      290      300      310      320      330

          420      430      440      450      460      470
m164.pep  LIISKQNVYPREIEEEIYKLDVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRR
          ||||||||||||||||:||||||||||||||||||||||||||||||||||
g164      LIISKQNVYPREIEEEIHKLDVEAAVIGVKDRYADEEIVAFVQLKEGMDLGEDEIRR
          340      350      360      370      380      390

          480      490      500      510
m164.pep  HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX
          ||||||||||||||||||||||||||||||||||||:||||
g164      HLRTVLANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFEGNKX
          400      410      420      430

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 683>:

```

a164.seq
1  ATGAACCGGA CTTATGCCAA TTTCTACGAA ATGCTGACCG CCGCCTGCCG
51  CAAAAACGGC AACGGCACGG CAGTGTTCGA CGGCAAGGAA AAAACCGCCT
101 ACCGCGCGCT CAAGCAGGAA GCCGAAGCCG TTGCGGCGTA TCTGCAAAAT
151 ATCGGCGTGA AGTTCGGCGA CACGGTCGCG CTGGCGGTTT CCAATTCCAC
201 GGAATTTATT ACCGCCTATT TCGCCGTATC CGCCATCGGC GCGGTTGCGG
251 TACCGATGAA CACATTTTGT AAAAACAGCG AATACGCGTA TATCCTGAAC
301 GACTGCAAGG CGCGCTTCTT GTTCGCCTCG GCCGGCCTGT CAAAAGAATT
351 GGC GGCGCTTG AAGGCGCAAA CGCCCGTCGA AAAAATCATT TGGACGGGCC
401 AAAGCCGTCC GGACGGCGAA ATGGCGGAAG GCGATGCCTT TTTGAAGAC
451 GTGCGCCGCT TCCCCGAAAA ACCCGACTTG GGCCGCCAAC CCGGATAAAA
501 TGATTGGCA CACATCATCT ACACCTCCGG CACGACGGGG CATCCCAAAG
551 GTGCGCTAAT CAGCTACGCC AACCTGTTCG CCAACCTGAA CGGCATCGAA
601 CGCATCTTTA AAATCTCCAA GCGGACCGC TTTATCGTTT TCCTGCCGAT
651 GTTCCACAGC TTCACGCTGA CGGCTATGGT GCTGCTGCCG ATTTATATGG
701 CGTGTTCGAT TATTTTGGTC AAATCCGTTT TCCCTTTTTC CAACGTTTTG
751 AAACAGGCAC TGCTCAAACG CGCGACCGTG TTTTGGGCG TGCCCGCGAT
801 TTACACCGCG ATGAGCAAGA CGAAAATCCC TTGGTATTTT AGATGGTTCA
851 ACCGCATCCG CCTGTTTATC AGCGGCGGAG CACCTTTGGC GGAACAAACC
901 ATCCTCGATT TCAAAGCCAA GTTCCCCCGC GCCAAATTGC TGGAAGGCTA
951 CGGACTGAGC GAAGCCTCGC CCGTCGTCGC CGTCAATACG CCGAGAGGC
1001 AAAAAAGCCC CAGCGTCGGC ATCCCCCTGC CCGGTTTGGA AGTCAAAGCC
1051 GTCGATGAAG AATTGGTCTA AGTGCCGCGC GGCGAAGTGG GCGAACTGAT
1101 CGTCAGGGGC GGTTCGGTGA TCGGGGGCTA CCTCAATATG CCTGCCGCCA
1151 CCGATGA AAC CATCGTCAAC GGCTGTTGA AAACGGGCGA TTTCGTTACC
1201 ATAGACGAAG ACGGCTTTAT CTTATCGTTC GACCGCAAAA AAGATTTGAT
1251 TATTTCCAAA GGTCAAATG TCTATCCGCG CGAAATCGAA GAAGAAATCT
1301 ACAAACTCGA TGCCGTCGAA GCCGCCGCGC TCATCGGCGT GAAAGACCGT
1351 TATGCCGACG AGGAAATCGT CGCCTTCGTC CAATTGAAGG AAGGTATGGA
1401 TTTGGGCGAG AACGAAATCC GCCGCCACCT GCGTACCGTG CTGGCAAATT
1451 TCAAAATCCC CAAACAAATC CACTTTAAG ACGGGCTGCC GCGCAACGCT
1501 ACGGGCAAGG TATTGAAACG GGTGTTGAAG GAGCAGTTTG ACGGAAACAA
1551 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 684; ORF 164.a>:

```

a164.pep
1  MNRTYANFYE MLTAACRKNQ NGTAVFDGKE KTAYRALKQE AEAVAAYLQN
51  IGVKFGDTVA LAVSNSTEFI TAYFAVSAIG AVAVPMNTFL KNSEYAYILN
101 DCKARFLFAS AGLSKELAGL KAQTPVEKII WTGQSRPDGE MAEGDAFFED
151 VRRFPEKPD L GRQPRINDLA HIIYTS GTTG HPGKALISYA NLFANLNGIE
201 RIFKISKRDR FIVFLPMFHS FTLTAMVLLP IYMACSIIIV KSVFPFSNVL
251 KQALLKRATV FLGVPAIYTA MSKTKIPWYF RWFNRIRLFI SGGAPLAEQT
301 ILDFKAKFPR AKLLEGYGLS EASPVVAVNT PERQKARSVG IPLPGLEVKA
351 VDEELVEVPR GEVGEIVRGG GSVMRGYLNM PAATDETIVN GWLKTGDFVT
401 IDEDGFIFIV DRKKDLISK QONVYPREIE EEIYKLDVE AAVIGVKDR
451 YADEEIVAFV QLKEGMDLGE NEIRRHRTV LANFKIPKQI HFKDGLPRNA

```

501 TGKVLKRVLK EQFDGNK\*

m164/a164 98.3% identity in 517 aa overlap

m164.pep	10	20	30	40	50	60
	MNRTYANFYEMLAACRKNGTAVFDGKEKTAYRALKQEAEEAAYLQNIQVKGFDGDTVA					
a164	MNRTYANFYEMLTAAACRKNGTAVFDGKEKTAYRALKQEAEEAAYLQNIQVKGFDGDTVA					
	10	20	30	40	50	60
m164.pep	70	80	90	100	110	120
	LAVSNSTEFITAYFAISAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
a164	LAVSNSTEFITAYFAVSAIGAVAVPMNTFLKNSEYAYILNDCKARFLFASAGLSKELAGL					
	70	80	90	100	110	120
m164.pep	130	140	150	160	170	180
	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDLAGRQPRINDLAHIIYTSGETTG					
a164	KAQTPVEKIIWTDKSRPTGETAEGDAFFEDVRRFPEKPDLAGRQPRINDLAHIIYTSGETTG					
	130	140	150	160	170	180
m164.pep	190	200	210	220	230	240
	HPKGALISYANLFANLNGIERIFKISKRDGFIVFLPMFHSFTLTAMVLLPIYMACSIIIV					
a164	HPKGALISYANLFANLNGIERIFKISKRDGFIVFLPMFHSFTLTAMVLLPIYMACSIIIV					
	190	200	210	220	230	240
m164.pep	250	260	270	280	290	300
	KSVFPFSNVLKQTLKTRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
a164	KSVFPFSNVLKQTLKTRATVFLGVPAIYTAMSKAKIPWYFRWFNRIRLFISGGAPLAEQT					
	250	260	270	280	290	300
m164.pep	310	320	330	340	350	360
	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLKAVDEELVEVPR					
a164	ILDFKAKFPRAKLLEGYGLSEASPVAVNTPERQKARSVGIPLPGLKAVDEELVEVPR					
	310	320	330	340	350	360
m164.pep	370	380	390	400	410	420
	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
a164	GEVGELIVRGGSVMRGYLNMPAATDETIVNGWLKTGDFVTIDEDGFIFIVDRKKDLISK					
	370	380	390	400	410	420
m164.pep	430	440	450	460	470	480
	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
a164	GQNVYPREIEEEIYKLDAVEAAVIGVKDRYADEEIVAFVQLKEGMDLGENEIRRHLRTV					
	430	440	450	460	470	480
m164.pep	490	500	510			
	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
a164	LANFKIPKQIHFKDGLPRNATGKVLKRVLKEQFDGNKX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 685>:

g165.seq

1 ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC

```

51  GACTTTGGGC GTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAagat gTGGCGTTGG AATCGTCAAA cGCGTGAAC
151 AACGcCGGca CGGGGCATTc CGcGCTGTGc GAATTGAACT AtgcgcGCT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCg cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgctgGTCGc GGAAGGCAAG
301 TTGGAagaCA ATTCCTTCAT CAATGCcgtg ccgcatatGT Ctttggtgat
351 gAacgaagac cactgCCgtt acCTGCAAAA ACGCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtccgCTGAT TATGCGCGGC CGGgacgaaA ACCAACCCGT
501 CGCCGCCAAC TATTCGCCG Aaggcacgga tgtcgATTc GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGGCA AGGGCGTAA AACCAGATTc
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCCGCACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTcG GTCCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGGTGGGGCG
1051 AATATGCCGC TGACCAAATA CcTGCTGGGc gAaTTGCgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 686; ORF 165.ng>:

g165.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCRYLQKRYD VFQTKLFEN MEFSTDNRKI
151 SDWAPLIMRG RDENQPVAA YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLOK
251 SGIPEGKGYG GLPVSGLFFR NSNPETAQEH NAKVYQASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 687>:

m165.seq (partial)

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGAAC
151 AACGCCGCA CGGGGCATTc CGcGCTGTGc GAATTGAACT ATGCGCGCTT
201 GGGTGCAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGc GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGTGTAT
351 GAATGAAGAC CATTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGgTACGGA TGTCGATTc GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAA AACCAGATTc
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTcG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGTGGGGCG
1051 AATATGCCGC TGACCAA...

```

This corresponds to the amino acid sequence <SEQ ID 688; ORF 165>:

m165.pep (partial)

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFQTKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDENQPVAA YSAEGTDVDF GRLTRQMVKY LQKGVKTEF

```

m165 / g165 97.2% identity in 356 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 689>:

```

a165.seq
1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGCTCTTG GAAATGACCC
101 TGATTGAACG TTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGCTGGAAC
151 AACGCCGGCA CGGGGCATTC CGCGCTGTGC GAATTGAACAT ATGCCCGCTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCCG GGAAGGCAAG
301 TTGGAAGACA ATTCTTCCAT CAATCCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTTGTTCT ATCTTCAAAA CGGTTATGAC GCGTTTAAAA
401 CCCAAAAACT TTTTGGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCGT
501 CGCGGCCAAT TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTT

```

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601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCGCA ACCCGACGG GCAGCTCACC CTCCGTACCC
701 GCTTCCTCTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGCTTTCCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAACCAGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTC GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCACTTATG GATTGCGCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGCGCGC CGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAGA
1101 AGAACGCTTC GCCTCCCTGC TGAATACTA CCCCAGGGCA AACCCTGACG
1151 ACTGGGAAC CATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAG GCGGCGTGT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCTGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA
```

This corresponds to the amino acid sequence <SEQ ID 690; ORF 165.a>:

a165.pep

```
1 MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCSYLOKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTRFLFLGA GGGALTLLQK
251 SGIEPGKGYG GFPVSGLFFR NSNPETAEOH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASILEYYPEA NPDDWELITA QORVQIIKND
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRKLKEL VPGYGIKLINE NPERADEIIA YTAKVLDI*
```

m165/a165 99.7% identity in 356 aa overlap

m165.pep	10	20	30	40	50	60
a165	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
m165.pep	70	80	90	100	110	120
a165	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVNED					
m165.pep	130	140	150	160	170	180
a165	HCSYLOKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGRDENQPVAA N YSAEGTDVDF					
m165.pep	190	200	210	220	230	240
a165	GRLTRQMVKYLQKGVKTEFNRHVEDIKRES DGAWVLKTADTRNPDGQLTLRTRFLFLGA					
m165.pep	250	260	270	280	290	300
a165	GGGALTLLQKSGIEPGKGYGGFPVSGLFFRNSNPETAEOHNAKVYQASV GAPPMSVPHL					



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	310	320	330	340	350
m165 . pep	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTK				
a165	DTRNVDGKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG				
	310	320	330	340	350
a165	ELRKTKEERFASLLEYYPEANPDDWELITAGQVRVQIIKKDSEKGGVLQFGTEIVAHADGS				
	370	380	390	400	410
	420				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 691>:

g165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGcCGca CGGGGCATTC CGcGCTGTGc GAATTGAACT AtgcgccGCT
201 GGGtgccgac ggcgtcatCA ATCCGGCGCG cgCCCTGAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGcga cgtggTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAACGAAGAC CACTGCCGTT ACCTGCAAAA ACCTATGAT GTGTTTAAAA
401 CGCAGAAACT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CtcgCTGAT TATGCCGCGC CGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TATTCGCCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAGAT GGTGAAATAT TTGCAGGCA AGGCGTAAA AACCGAGTTC
601 AACC GCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCAGACTG GCAGCTCACC CTCGCGACCC
701 GCTTCTCTTT CCTCGGCGCG GCGGCGGCG CACTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTACCCG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG
851 TGACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGACCTC
901 GACACACGCA ACGTAGACGG CAAACGACAC CTTATGTTTC GTCTTACGC
951 AGGTTTCCGT TCCAACCTCC TCAAGCAAGG CTCGTTTATG GATTTGCCGC
1001 TGTCATCCA TATGGACAAC CTCTATCCTA TGTCGCGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTtt gCCTCCCTGC TGgaatacta cccGaggcag acccGACGAC
1151 tggtaactcat cagcaggnc acGCGTcata tcattanata tgactCgaaa
1201 ctgcgcgtgc tgcagttgta cgagattgtg ccaCGCGacg ctcgctcgcg
1251 cattctggag cgctcgcgcg catcacgctn tgcgctgata tccgctgatg
1301 acactgctcc gaGCGcgccc gtcttgaaa gtgtctga

```

This corresponds to the amino acid sequence <SEQ ID 692; ORF 165-1.ng>:

g165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSALC ELNYAPLGAD GVINPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVNED HCRYLQKRYD VFKTQKLFEN MEFSTDRNKI
151 SDWAPLIMRG RDNQPVAAAN YSAEGTDVDF GRLTRQMVKY LQKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDWQLT LRTRFLFLGA GGGALTLLQK
251 SGIEPEGKGYG GLPVSGLFFR NSNPETAEOH NAKVYQOASV GAPPMSVPHL
301 DTRNVDGKRH LMFPGPYAGFR SNFLKQGSFM DLPLSIHMDN LYPMLRAGWA
351 NMPLTKYLLG ELRKTKEERF ASLLEYPRQ TRRLVLITQX TRHIIYDSK
401 LRLVLQLYEIV PRDARSRIE RRGASRXALI SADDTAPSAP VLESV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 693>:

m165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCGCGCA CGGGGCATTC CGCGCTGTGC GAATTGAACT ATGCGCGGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGCTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATTTGTTCTT ATCTTCAAAA ACCTTATGAC GCGTTTAAAA
401 CCAAAAACCT TTTTGAAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCGCTGAT GATGCCGCGC CGGACGAAA ACCAACCCGT
501 CGCCGCCAAC TACTCCGCCG AAGGTACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGCA AGGCGTAAA AACCGAGTTC
601 AACC GCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGGC GCAGCTCACC CTCGCTACCC
701 GCTTCTCTTT CCTCGGCGCG GCGGCGGCG CGCTGACCCT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGC GGCTTCCCGG TGTCCGGCCT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAAG

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851 TGTACGGGCA GGCTTCCGTC GCGCGCGCCG CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAACCTCC TCAAGCAAGG CTCGCTTATG GATTTCGCCG
1001 TGTCCATCCA TATGGACAAC CTCTATCCTA TGCTGTGCGC CGGCTGGGCG
1051 AATATGCCGC TGACCAAATA CCTGTGGGCG GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAACTACT CCGGAGGCA AACCCGACG
1151 ACTGGGAACAT CATCACCGCA GGGCAACGCG TCCAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGGCGTGCT CCAGTTTGGT ACGGAGATTG TCGCCACGC
1251 CGACGGCTCA CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CTGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAGCGCGCC
1351 CCGTCTTGGG AAGACCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCTGAAA GCGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTATTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 694; ORF 165-1>:

```

m165-1.pep
1 MAEATDVVLV GGGIMSATLG VLLKELEPSN EITLIERLED VALESSNAWN
51 NAGTGHSALC ELNYAPLGAN GIIDPARALN IAEQFHVSRQ FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDRNKI
151 SDWAPLMMRG RDENQPVAA N YSAEGTDVDF GRLTRQMVKY LQGGKGVKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LRTFLFLGA GGGALTLLQK
251 SGIPEGKGYG GPPVSGLFFR NSNPETAQH NAKVYQASV GAPPMSVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLCAGWA
351 NMPLTKYLLG ELRKTKEERF ASLEYYPEA NPDDWELITA GQRVQIIKDD
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMR LMHQCFPERA
451 PSWEDRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

m165-1/g165-1 89.7% identity in 428 aa overlap

	10	20	30	40	50	60
m165-1.pep	MAEATDVVLVGGGIMSATLGVLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
g165-1	MAEATDVVLVGGGIMSATLGVLKELEPSWEITLIERLEDVALESSNAWNAGTGHSALC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
g165-1	ELNYAPLGADGVINPARALNIAEQFHVSRQFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
m165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDRNKISDWAPLMMRGDENQPVAAANYSAEGTDVDF					
g165-1	HCRYLQKRYDVFKTQKLFENMEFSTDRNKISDWAPLIMRGDENQPVAAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m165-1.pep	GRLTRQMVKYLQGGKGVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTFLFLGA					
g165-1	GRLTRQMVKYLQGGKGVKTEFNHVEDIKRESGAWVLKTADTRNPDGQLTLRTFLFLGA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m165-1.pep	GGGALTLLQKSGIPEGKGYGGPPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
g165-1	GGGALTLLQKSGIPEGKGYGGLPVSGLFFRNSNPETAQHNAKVYQASVGAPPMSVPHL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m165-1.pep	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG					
g165-1	DTRNVDGKRHLMFGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m165-1.pep	ELRKTKEERFASLEYYPEANPDWELITAGQRVQIIKDDSEKGGVLQFGTEIVAHADGS					
g165-1	ELRKTKEERFASLEYYPR-QTRRLVLITQXTR-HIIXYDS-KLRVLQLYEIVPRDARSR					
	370	380	390	400	410	
	430	440	450	460	470	480

m165-1.pep LAALLGASPGASTAVPLMIRLMHQCFPERAPSWEDRLKELVPGYGIKLNENPERADEIIA  
:  
g165-1 ILERRGASRXALISADDTAPSAPVLESVX  
420 430 440

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 695>:

## a165-1.seq

```

1  ATGGCTGAAG CGACAGACGT TGTCTTGGTG GCGGCGCGCA TTATGAGCGC
51  GACTTTGGGC GTTTTGCTCA AAGAACTCGA ACCGTCTTGG GAAATCACCC
101 TGATTGAACG CTTGGAAGAT GTGGCGTTGG AATCGTCAAA CGCGTGGAAC
151 AACGCCGGCA CGGGGCATTG CGCGCTGTGC GAATTGAACT ATGCGCCGTT
201 GGGTGCAAAAT GGGATTATCG ATCCGGCGCG CGCCCTCAAT ATTGCCGAAC
251 AGTTTCATGT CAGCCGCCAG TTTTGGGCGA CGTTGGTCGC GGAAGGCAAG
301 TTGGAAGACA ATTCCCTTCAT CAATGCCGTG CCGCATATGT CTTTGGTGAT
351 GAATGAAGAC CATGTGTTCTT ATCTTCAAAA ACGTTATGAC GCGTTTAAAA
401 CCCAAAAAT TTTTGAAAT ATGGAATTTT CCACCGATCG GAACAAAATT
451 TCCGATTGGG CTCCGCTGAT GATGCGCGGC CGGGACGAAA ACCAACCCTG
501 CGCCGCCAAC TACTCCGCCG AAGGCACGGA TGTCGATTTC GGACGGCTGA
551 CGCGCCAAAT GGTGAAATAT TTGCAGGGCA AGGGCGTAAA AACCGAGTTC
601 AACCGCCACG TCGAAGACAT CAAACGCGAA TCCGACGGCG CGTGGGTGCT
651 CAAAACCGCC GATACCCGCA ACCCGACGCG GCAGCTCACC CTCCGTACCC
701 GCTTCTCTCT CCTCGGCGCG GCGCGCGCGC CGGTGACCTT GCTGCAAAAA
751 TCCGGCATCC CCGAAGGCAA AGGCTACGGT GGGTTTCCCG TGTCGGGCTT
801 GTTCTTCCGC AACAGCAACC CCGAAACCGC CGAACAACAC AACGCCAAG
851 TGTACGGGCA GGCTTCCGTC GCGCGCGCGC CGATGTCCGT CCCGCACCTC
901 GACACACGCA ACGTGGACGG CAAACGCCAC CTTATGTTCG GCCCTTACGC
951 AGGCTTCCGT TCCAATTCC TCAAGCAAGG CTCATTATG GATTGGCCGC
1001 TGTCCATCCA TATGACAAC CTCTATCCTA TGCTGCGCGC CGGCTGGGCG
1051 AATATGCCCG TGACCAAATA CCTGCTGGGC GAATTGCGTA AAACCAAAGA
1101 AGAACGCTTC GCCTCCCTGC TGGAATACTA CCCCAGGGCA AACCCGACG
1151 ACTGGGAAC TATCACCGCA GGGCAACGCG TTCAAATCAT TAAAAAGAC
1201 TCCGAAAAAG GCGCGGTGTT GCAGTTTGGT ACGGAGATTG TCGCACACGC
1251 CGACGGCTCG CTCGCCGCAT TGCTGGGCGC GTCGCCGGGC GCATCGACCG
1301 CCGTGCCGCT GATGATCCGG CTGATGCACC AATGCTTCCC CGAACGCACC
1351 CCGTCTTGGG AAGGCCGTCT GAAAGAGCTG GTACCGGGTT ACGGCATCAA
1401 GTTGAACGAA AACCCCGAAA GGGCGGATGA AATTATCGCC TATACCGCGA
1451 AAGTGTGGA TATTAA

```

This corresponds to the amino acid sequence <SEQ ID 696; ORF 165-1.a>:

## a165-1.pep

```

1  MAEATDVVLV GGGIMSATLG VLLKELEPSW EITLIERLED VALESSNAWN
51  NAGTGHSAIC ELNYAPLGAN GIIDPARALN IAEQFHVSRO FWATLVAEGK
101 LEDNSFINAV PHMSLVMNED HCSYLQKRYD AFKTQKLFEN MEFSTDNRKI
151 SDWAPLMMRG RDNQFVAAN YSAEGTDVDF GRLTRQMVKY LQKGVRKTEF
201 NRHVEDIKRE SDGAWVLKTA DTRNPDGQLT LTRFLFLGA GGGALTLLQK
251 SGIPEGKGYG GFPVSGLFFR NSNPETAEOH NAKVYGOASV GAPPMSPVPHL
301 DTRNVDGKRH LMFGPYAGFR SNFLKQGSIM DLPLSIHMDN LYPMLRAGWA
351 NMPLTRYLLG ELRKTKEERF ASLLEYYPEA NPDDWELITA GORVQIIKID
401 SEKGGVLQFG TEIVAHADGS LAALLGASPG ASTAVPLMIR LMHQCFPERT
451 PSWEGRLKEL VPGYGIKLE NPERADEIIA YTAKVLDI*

```

a165-1/m165-1 99.4% identity in 488 aa overlap

	10	20	30	40	50	60
a165-1.pep	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSAIC					
m165-1	MAEATDVVLVGGGIMSATLGVLLEKELEPSWEITLIERLEDVALESSNAWNAGTGHSAIC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a165-1.pep	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
m165-1	ELNYAPLGANGIIDPARALNIAEQFHVSROFWATLVAEGKLEDNSFINAVPHMSLVMNED					
	70	80	90	100	110	120
	130	140	150	160	170	180
a165-1.pep	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDENQFVAANYSAEGTDVDF					
m165-1	HCSYLQKRYDAFKTQKLFENMEFSTDNRKISDWAPLMMRGRDENQFVAANYSAEGTDVDF					
	130	140	150	160	170	180
	190	200	210	220	230	240

```

a165-1.pep  GRLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
m165-1      GRLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTLRTRFLFLGA
              190      200      210      220      230      240

              250      260      270      280      290      300
a165-1.pep  GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL
m165-1      GGGALTLLQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL
              250      260      270      280      290      300

              310      320      330      340      350      360
a165-1.pep  DTRNVGDKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG
m165-1      DTRNVGDKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLCAGWANMPLTKYLLG
              310      320      330      340      350      360

              370      380      390      400      410      420
a165-1.pep  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
m165-1      ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVAHADGS
              370      380      390      400      410      420

              430      440      450      460      470      480
a165-1.pep  LAALLGASPGASTAVFLMIRLMHQCFFPERTPSWEGRLKELVPGYGIKLNENPERADEIIA
m165-1      LAALLGASPGASTAVFLMIRLMHQCFFPERTPSWEDRLKELVPGYGIKLNENPERADEIIA
              430      440      450      460      470      480

              489
a165-1.pep  YTAKVLDIX
m165-1      YTAKVLDIX

```

## a165-1/p33940

sp|P33940|YOJH\_ECOLI HYPOTHETICAL 60.2 KD PROTEIN IN ECO-ALKB INTERGENIC REGION  
>gi|1736851|gnl|PID|d1016718 (D90850) ORF ID: o372#5; similar to [SwissProt Accession Number  
P33940] [Escherichia coli] >gi|1788539 (AE000310) f548; This 548 aa ORF is 100 pct identical  
to 490 residues of YOJH\_ECOLI SW: P33940 (492 aa) but contains 56 additional N-ter aa; 100 pct  
identical to GB: ECOHU49\_33  
ACCESSION: U00008 (490 aa) but contains 58 additional N-term resi... Length = 548  
Score = 458 bits (1167), Expect = e-128  
Identities = 233/490 (47%), Positives = 303/490 (61%), Gaps = 5/490 (1%)

```

Query: 3  EATDVVLVGGGIMSATLGVLLEPSWEITLIERLEDVALESSNAWNAGTGHSALCEL 62
          + TDV+L+GGGIMSATLG L+ELEP W +T++ERLE VA ESSN WNNAGTGHSAL EL
Sbjct: 30  QETDVLLIGGGIMSATLGTYLRELEPEWSMTMVERLEGVAQESSNGWNNAGTGHSALMEL 89

Query: 63  NYAPLGGANGIIDPARALNIAEQFHSRQFWATLVAEGKLED-NSFINAVPHMSLVMNEDH 121
          NY P A+G I +A+ I E F +SRQFWA V G L SFIN VPHMS V ED+
Sbjct: 90  NYTPQNADGSISIEKAVAINAEAFQISRQFWAHQVERGLRTPRSFINTVPHMSFVWGDN 149

Query: 122  CSYLQKRYDAFKTQKLFENMEFSTDNRNKISDWAPLMMGRDENQPVAANYSAEGTDVDFG 181
          ++L+ RY A + LF M +S D +I +WAPL+M GRD Q VAA + GTDV++G
Sbjct: 150  VNFLRARYAALQSSSLFRGMRYSEDHAQIKEWAPLVMEGRDPQKVAATRTEIGTDVNYG 209

Query: 182  RLTRQMVKYLGKGVKTEFNRHVEDIKRESDGAWVLKTADTRNPDGQLTXXXXXXXXXX 240
          +TRQ++ LQ K ++ V +KR D W + AD +N Q
Sbjct: 210  EITRQLIASLQKSNFSLQLSSEVRALKRNDNTWTVTVDLKNGTAG-NIRAKFVFIGA 268

Query: 241  XXXXXXXXQKSGIPEGKGYGGFPVSGLFFRNSNPETAEOHNAKVYGOASVGAPPMSVPHL 300
          Q+SGIPE K Y GFPV G F + NP+ H AKVYG+ASVGAPPMSVPH+
Sbjct: 269  GGAALKLLQESGIPEAKDYAGFPVGGQFLVSENPDVNVHHLAKVYGKASVGAPPMSVPHI 328

Query: 301  DTRNVGDKRHLMFPGPYAGFRSNFLKQGSIMDLPLSIHMDNLYPMLRAGWANMPLTKYLLG 360
          DTR +DGKR ++FGP+A F + FLK GSL DL S N+ PM+ G N L KYL+
Sbjct: 329  DTRVLDGKRVVLFPGPFATFSTKFLKNGSLWDLMSSTTTSNVPMHVLGDNFDLVKYLVS 388

Query: 361  ELRKTKEERFASLLEYYPEANPDDWELITAGQRVQIIKKDSEKGGVLQFGTEIVXXXXXX 420
          ++ ++E+RF +L EYYP+A +DW L AGQRVQIIK+D+EKGGVL+ GTE+V
Sbjct: 389  QVMLSEEDRFEALKEYYPOAKKEDWRLWQAGQRVQIIKRDAEKGGLRLGTEVVSDDQGT 448

Query: 421  XXXXXXXXXXXXXVPLMIRLMHQCFFERT--TPSWEGRLKELVPGYGIKLNENPERADEI 478

```

P+M+ L+ + F +R +P W+ LK +VP YG KLN + +  
 Sbjct: 449 IAALLGASPGASTAAPIMLNLEKVFGRVSSPQWQATLKAIVPSYGRKLNGDVAATERE 508  
 Query: 479 IAYTAKVLDI 488  
 + YT++VL +  
 Sbjct: 509 LQYTSEVLGL 518

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 697>:

g204.seq  
 1 atggcgccgg cggaaataaa acgccccctc gctgtcgatt tccagcacat  
 51 agcgtccgtt ctgcacggcg gcatagccgc ttttgccctgc ctgatagggg  
 101 tgcagggcgg aatgcgaaat caggtaatca gtcagtttgc cgccgtcttc  
 151 ggcgatattg cccaccagtt tggcaaaciaa ggtatggcac acgcccgttt  
 201 ccgcccagcc cgaaggcgcg tcctttccgt cggtttccat acatttgccg  
 251 acgacggcct ccaagtcggt gggatgcttt ccggtcagcc ggacggcgtt  
 301 ttgttccggc aagcctttaa tggataact gatttgtttt ttgcccgtct  
 351 tggttttgcc ttcgctactt tgtcccaaag ccaaaccggc aatcgccgta  
 401 ttgtcgaagt atttgacttt gaaaaccggg ttcggcgccg tttgtgccgc  
 451 attttgccgc tgttccgccc tattttcggg tttgccgcag gcggcaagca  
 501 gcaggcagcc gcccaacacg gcaaaaggta ttttcagcat tccgcactcc  
 551 tgatgggttc aaaatggcgt ctgaaatgcc gtctgaaacg tggcaggcgg  
 601 aggttcggac ggcattgggt ttatttcaac gggcggatgc cgaccgcac  
 651 gcgtacttta tccaacaatt cgcgcgcttc tttgcgcgct ttttgcgcgc  
 701 ctgcctgcaa aatctcttcg atttgcggaag gattagaggt caatgcggtg  
 751 tag

This corresponds to the amino acid sequence <SEQ ID 698; ORF 204.ng>:

g204.pep  
 1 MAAAEIKRPL AVDFQHIASV LHGGIAAFAC LIGLQGGMRN QVISQFAAVF  
 51 GDIAHQFGKQ GMAHAVFREPA RRRVLSVGFH TFADDGFQV GMLSGQPDGV  
 101 LFRQAFNRIT DLFFAVVGFA FATLSQSQTG NRRIVDVDF ENRFRRLCR  
 151 ILRLFRRIFG FAAGGKQQA AOHGKRYFOH SALLMVSKCR LKCRRLKRRR  
 201 RFGRHWVYFN GRMPTASRTL SNNSRASLRA FCAPACKISS ICEGLEVNAL  
 251 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 699>:

m204.seq  
 1 ATGGCGGCGG CGGAAATAAA ACGCCCCTTC GCTGTGCGATT TCCAGCACAT  
 51 AGCGTCCGTT CTGCACGGCG GCATAGCCGC TTTTGCCCTGC CTGATAGGGT  
 101 TGCAGGGCGG CATGCGAAAC TAGGTAATCC GTCAGTTTGC CGCCGTCTTC  
 151 GGCATATTG CCCACCAGTT TGGCAAACAA GGTATGGCAC ACGCCGTTTT  
 201 CTGCCCAACC TGCCGGACTG TCCTTATCAT CGGTTTCCAT ACATTGCGCG  
 251 CTGACGGCTT CCAAGTCGCC GGGATGCTTG CCGATCAGTC GGATAACATT  
 301 TTGTTCCGGC AAGCCTTTAA TCGGATAACT GATTGTGTTT TTGCCGTCGT  
 351 TGTTTTTGCC TTCGCTGCTT GTCCCAAAT CCAAACCGGC AATCGCCGTA  
 401 TTGTCGATAT ATATGACTTT GAAAACCGGT TTCGGCGCGC TTTGTACCGC  
 451 GTTTTGCGGC TGTACCGCG TATTTwCGGA TTTGCCGCaC GGCaaRGcAG  
 501 CAGGCAGCCG CCCAATACGG CAAAaAwGT wTTCAGCATT CCACaYTCCT  
 551 GATGGTTTCA AAATGCGGTC TGAAACGCGG CAGGCGGAGG TTCGGACGGC  
 601 ATCGGGTTCA TTTCAACGGG CGGATGcCGA CCGCATCgGT ACTTTGTCCA  
 651 ATAATTGCGG TGCTTCTTTA CGCGCTTTCG CCGCGCCTGC CTGCAAAATC  
 701 TCTTCGATT GCGAAGGGTC GCGGTCAGC TCGTTGTAG

This corresponds to the amino acid sequence <SEQ ID 700; ORF 204>:

m204.pep  
 1 MAAAEIKRPF AVDFQHIASV LHGGIAAFAC LIGLQGGMRN \*VIRQFAAVF  
 51 GDIAHQFGKQ GMAHAVFCPT CRTVLIIGFH TFAADGFQVA GMLADQSDNI  
 101 LFRQAFNRIT DLFFAVVGFA FAALSQIQTG NRRIVDIYDF ENRFRRLYR  
 151 VLRLYRRIXG FAATAXQQA AYGKXXXQH STXLMVSKCR LKRRRRFRGR  
 201 HRVHFNGRMP TASGTLNNS RASLRAFAAP ACKISSICEG SAVSSL\*

Computer analysis of this amino acid sequence gave the following results:

m204 / g204

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 701>:

**This corresponds to the amino acid sequence <SEQ ID 702; ORF 204.a>:**

a204.pap

1	MAAAEIKRPL	AVDFQHIASV	<u>LHGGIAAFAC</u>	<u>LIGLQGGMRN</u>	QVIRQFAAVF
51	GDIAHQFGKQ	GMAHAVCRPA	RRRLSVGFH	TFADDGFQV	GMLAGQPDV
101	LFRQAF....	.....	.....	.....	.....
151	.....	.....	.....	.....	.....KRFR
201	HWVYFNGRIP	TASRTLNNNS	RASLRAFAP	ACKISSICEG	SAVSSL*

478

**m204/a204 54.5% identity in 246 aa overlap**

	10	20	30	40	50	60
m204.pep	MAAAEIKRPFVDFQHIASVLHGGIAAFACLIQLGGMRNXVIRQFAAVFGDIAHQFGKQ					
a204	MAAAEIKRPLAVDFQHIASVLHGGIAAFACLIQLGGMRNOVIRQFAAVFGDIAHQFGKQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m204.pep	GMAHAVFCPTCRTLIIIGFHTFAADGFQVAGMLADQSDNILFRQAFNRITDLFFAVVGFA					
a204	GMAHAVCRPARRRALSFGFHTFADDGFQVVGMLAGQPDVLFQAF-----					
	70	80	90	100		
	130	140	150	160	170	180
m204.pep	FAALSQIQGTGNRRIVDIYDFENRFRRLYRVLRLYRRIXGFAATAXQAAAQYGKXXXQH					
a204	-----					
	190	200	210	220	230	240
m204.pep	STXLMVSKCRLKRGRRRFGRHVRHFNGRMPTASGTLNNSRASLRFAFAAPACKISSICEG					
a204	-----KRFGRHWVVFNGRIPTASRTLNNNSRASLRFAFCAPACKISSICEG					
	110	120	130	140	150	
m204.pep	SAVSSLX					
a204	SAVSSLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 703>:

g205.seq

```

1 atgctgaaaa taccttttgc cgtggtgggc ggctgcctgc tgcttgccgc
51 ctgcggaaca tccgaaaata cggcggaaca gccgcaaat gcggcacaaa
101 gcgcgccgaa accggttttc aaagtcaaat acatcgacaa tacggcgatt
151 gccggtttgg ctttgggaca aagtagcgaa ggcaaaacca acgacggcaa
201 aaaacaaatc agttatccga ttaaaggctt gccggaacaa aacgccgtcc
251 ggctgaccgg aaagcatccc aacgacttgg aagccgtcgt cgcaaatgt
301 atggaaaccg acggaagga cgcgccttcg ggctgggagg aaaacggcgt
351 gtgccatacc ttgtttgcca aactggtggg caatatcgcc gaagacggcg
401 gcaaactgac tgattacctg atttcgcatt ccgccctgca accctatcag
451 gcaggcaaaa gcggctatgc cgccgtgcag aacggacgct atgtgctgga
501 aatcgacagc gagggggcgt tttatttccg ccgccccat tattga

```

This corresponds to the amino acid sequence <SEQ ID 704; ORF 205.ng>:

g205.pep

```

1 MLKIPFAVLG GCLLLAACGK SENTAEQPON AAQSAPKPVF KVKYIDNTAI
51 AGLALGQSSE GKTNDGKKQI SYPIKGLPEQ NAVRLTGKHP NDLEAVVGKC
101 METDGKDAPS GWAENGVCHT LFAKLVGNTA EDGKLTGYL ISHSALQPYQ
151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 705>:

m205.seq

```

1 ATGCTGAAWA CwTyTTTTGC CGTATTGGGC GGCTGCCTGC TGCyTtGCCG
51 tCGGCGAAAT CCGwAAATAC GGCGGTACAG CCGCAAAACG CGGTACAAAG
101 CCGCGCCGAAA CCGGTTTTCA AAGTCATATA TATCGACAAT ACGGCGATTG
151 CCGGTTTGGG TTTGGGACAA AGCAGCGAAG GCAAAACCAA CGACGGCAAA
201 AAACAAATCA GTTATCCGAT TAAAGGCTTG CCGGAACAAA ATGTTATCCG
251 ACTGATCGGC AAGCATCCCG GCGACTTGGA AGCCGTCAGC GGCAATGTA
301 TGGAACCGA TGATAAGGAC AGTCCGGCAG GTTGGGCAGA AAACGGCGTG
351 TGCCATACCT TGTTTGCCAA ACTGGTGGGC AATATCGCCG AAGACGGCGG
401 CAAACTGACG GATTACCTAG TTTCGCATGC CGCCCTGCAA CCCTATCAGG
451 CAGGCAAAAG CGGCTATGCC GCCGTGCAGA ACGGACGCTA TGTGCTGGAA
501 ATCGACAGCG AAGGGGCGTT TTATTTCGCG CGCCGCCATT ATTGA

```

This corresponds to the amino acid sequence <SEQ ID 706; ORF 205>:

m205 . pep  
 1 MLXTXFAVLG GCLLXCRCGK SXNTAVQPON AVQSAPKPVF KVIYIDNTAI  
 51 AGLDLGQSSE GKTNDGKKQI SYPIKGLPEQ NVIRLIGKHP GDLEAVSGKC  
 101 METDDKDSPA GWAENGVCHT LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ  
 151 AGKSGYAAVQ NGRYVLEIDS EGAFYFRRRH Y\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 205 shows 88.4% identity over a 181 aa overlap with a predicted ORF (ORF 205.ng) from *N. gonorrhoeae*:

m205/g205

	10	20	30	40	50	60
m205 . pep	MLXTXFAVLGGCLLXCRCGKSXNTAVQPONAVQSAPKPVFKVIYIDNTAIAGLDLGQSSE					
g205	MLKIPFAVLGGCLLLAACGKSENTAEQPNAAQSAPKPVFKVIYIDNTAIAGLALGQSSE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m205 . pep	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKCMETDDKDSGWAENGVCHT					
g205	GKTNDGKKQISYPIKGLPEQNAVRLTGKHPNDLEAVVGKCMETDGKDAPSGWAENGVCHT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m205 . pep	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH					
g205	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQNGRYVLEIDSEGAFFRRRH					
	130	140	150	160	170	180

m205 . pep YX  
 |  
 g205 Y

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 707>:

a205 . seq (partial)  
 1 TCCGAACCTC TTAAAGGCTT GCCGGAACAA AACGTCGTCC GGCTGACCGG  
 51 CAAGCATCCC AACGACTTGG AAGCCGTCGT CGGCAAATGT ATGGAAACCG  
 101 ACGGAAAGGG CGCGCCTTCG GGCTGGGCGG CAAACGGCGT GTGCCATACC  
 151 TTGTTTGCCA AACTGGTGGG CAATATCGCC GAAGACGGCG GCAAACCTGAC  
 201 GGATTACCTG ATTTGCGATT CCGCCCTGCA ACCCTATCAG GCAGGCAAAA  
 251 GCGGCTATGC CGCCGTGCAG AACGACGCT ATGTGCTGGA AATCGACAGC  
 301 GAGGGGGCGT TTTATTTCCT CCGCCGCCAT TATTGA

This corresponds to the amino acid sequence <SEQ ID 708; ORF 205.a>:

a205 . pep (partial)  
 1 SEPLKGLPEQ NVVRLTGKHP NDLEAVVGKC METDGKGAPS GWAANGVCHT  
 51 LFAKLVGNIA EDGGKLT DYLVSHAALQPYQ AGKSGYAAVQ NGRYVLEIDS  
 101 EGAFYFRRRH Y\*

m205/a205 88.3% identity in 111 aa overlap

	50	60	70	80	90	100
m205 . pep	KVIYIDNTAIAGLDLGQSSE	GKTNDGKKQISYPIKGLPEQNVIRLIGKHPGDLEAVSGKC				
a205			SEPLKGLPEQNVVRLTGKHPNDLEAVVGKC			
			10	20	30	
	110	120	130	140	150	160
m205 . pep	METDDKDSGWAENGVCHT	LFAKLVGNIAEDGGKLT DYLVSHAALQPYQAGKSGYAAVQ				



g205-1.seq (partial)

**This corresponds to the amino acid sequence <SEQ ID 710; ORF 205-1.ng>:**

g205-1.pgp (partial).

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 711>:

m205-1.seq. .

1	ATGCTGAAAA	CATCTTTTGC	CGTATTGGGC	GGCTGCCTGC	TGCTTGCOCG
51	CTGCGGCAAA	TCCGAAAATA	CGCGGGAACA	GCCGCAAAC	GCGGTACAAA
101	GCGCGCCGAA	ACCGGTTTTC	AAAGTCAAAT	ATATCGACAA	TACGGCGATT
151	GCCGGTTTGG	ATTTGGGACA	AAGCAGCGAA	GGCAAAACCA	ACGACGGCAA
201	AAAACAAAAT	AGTTATCCGA	TTAAAGGCTT	GCCGGAACAA	ATGTTTATCC
251	GACTGATCGG	CAAGCATCCC	GGCGCATTTG	AAGCGCTCAG	CGGCAAAATG
301	ATGGAACCG	ATGATAAGGA	CAGTCCGGCA	GGTTGGGCAG	AAAACGGCGT
351	GTGCCATACC	TTGTTTGCCA	AACTGCTGGG	CAATATCGCC	GAAGACGGCG
401	GCAAACTGAC	GGATTACCTA	GTTTGCATCG	CCGCCCTGCA	ACCCATTACAG
451	GCAGGCAAAA	GCGGCTATGC	CGCCGTCGAC	AACGGACGCT	ATGTGCTGGA
501	AATCGACAGC	GAAGGGGCGT	TTTATTTCGG	CCGCGGCCAT	TATTGA

**This corresponds to the amino acid sequence <SEQ ID 712; ORF 205-1>:**

m205-1.pep

1	<u>MLKTSFAVLG</u>	<u>GCLLLAACGK</u>	SENTAEQPQN	AVQSAPKPVF	KVKYIDNTAI
51	AGLDLGQSSE	GKTNLDGKKQI	SYPIKGLNEA	NVIRLIGKHP	GDLEAVSGKC
101	METDDKDSAP	GWAENGVCST	LFAGLVYRIA	EDGGKLT DYL	VSHAALQPYQ
151	AGKTSVAAPV	NGRWYEI LDT	EFAKLYFRHR	Y*	

m205-1/g205-1 92.0% identity in 174 aa overlap

	10	20	30	40	50	60
<b>g205-1.pep</b>	MLKI PFAVLGGCLLLA	CGKSENTAEQ	PQNAAQ	SAPKPVFKV	KYIDNTA	IAGLALGQSSE
<b>m205-1</b>	MLKTSFAVLGGCLLLA	CGKSENTAEQ	PQNAVQ	SAPKPVFKV	KYIDNTA	IAGLDLGQSSE
	10	20	30	40	50	60
	70	80	90	100	110	120
<b>g205-1.pep</b>	GKTNDGKKQISYPIK	GLPEQNAVRLTGK	HPNDLEAVVGKCM	ETDGDAPSGWA	ENGVCHT	
<b>m205-1</b>	GKTNDGKKQISYPIK	GLPEQNVIRLIGK	HPGDLEAVSGKCM	ETDDKDS	PAGWAENGVCHT	

a205-1.seq (partial)

1	CCCTCTTAAG	GCTTGCCGGA	ACAAAACGTC	GTCGCGCTGA	CCGGCAAGCA
51	TCCCACACAC	TTGGAAACCG	TCGTCGGCAA	ATGTATGGAA	ACCGACGGAA
101	AGGGCCGCGC	TCGGGCTGG	CGGGCAACG	CGCTGTGCCA	TACCTTGTTT
151	GCCAAACTGG	TGGGCAATAT	CGCCGAAGAC	CGCGCCAAAC	TGACGGATTAT
201	CCCTGATTCC	CATTCCGCC	TGCAACCTCA	TCAGGCAGGC	AAAAGCGGCT
251	ATGCCGCGCT	CGAGAAACGA	CGCTATGTGC	TGGAATATCGA	CACGCAGGGG
301	CGCGTTTATT	TCCGACGCGC	CCATTATGTA		

a205-1.pap (partial)

1 PLKGLPEQNV VRLTGKHPND LEAVVGKCM TDKGAPSGW AANGVCHTLF  
51 AKLVGNIAED GGLTDYLYS HSALQPYQAG KSGYAAVQNG RYVLEIDSEG  
101 AFYFRRRHY\*

m205-1/a205-1 89.0% identity in 109 aa overlap

```

      50          60          70          80          90          100
m205-1.pep  KYIDNTAIAGLDLGQSSEGKTNDGKKQISYPYIKGLPEQNVIRLIGKHPGDLEAVSGKCM
              |||||
a205-1      PLKGLPEQNVVRLTGKHPNDLEAVVGKCM
              10          20          30

      110         120         130         140         150         160
m205-1.pep  TDDKDSFAGWAENGVCHTLFAKLVGNIAEDGGKLTDYLVSHAALQPYQAGKSGYAAVQNG
              |||||
a205-1      TDGKGAPSGWAANGVCHTLFAKLVGNIAEDGGKLTDYLIHSHALQPYQAGKSGYAAVQNG
              40          50          60          70          80          90

      170         180
m205-1.pep  RYVLEIDSEGAFFRRRRHYX
              |||||
a205-1      RYVLEIDSEGAFFRRRRHYX
              100         110

```

q206.seq

1	atgttttccc	cgcacaaaac	ccttttctct	tgtctcggcg	cactgtctct
51	cgctcatgc	ggcacgacct	cgggcaaaca	cgccaacog	aaaccctaac
101	agacagtcg	gcaaatccaa	gccgtccgca	tcagccacat	cggccgcaca
151	caaggctcgc	aggaactcat	gctccacagc	ctcggactca	tcggcacgcc
201	ctacaaatgg	ggcggcagca	gcaccgcaac	cggcttcgac	tgacgcggca
251	tgattcaatt	ggtttacaaa	aacgccctca	acgtcaagct	gccgcgcacc
301	gcccgcgaca	tgccggcggc	aagccgcaaa	atccccgaca	gccgcctcaa
351	ggccggcgac	atcgattctt	tcaacaccgg	cggcgcacac	cgctactcac
401	acgtcggact	ctacatctgc	aacggcgaa	tcacatgtc	ccccggcagc
451	ggcaaaacca	tcaaaaccga	aaaactcttc	acacggttt	acgccaaaaa
501	ctaccttgga	gcgcatacgt	tttttacaga	atga	

g206.pep

1 MFSPDKTLFL CLGALLASC GTTSGKHRQP KPKQTVROIO AVRISHIGRT

51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQLVYK NALNVKLPR  
 101 ARDMAAASRK IPDSRLKAGD IVFFNTGGAH RYSHVGLYIG NGEFIHAPGS  
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 717>:

m206.seq  
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT  
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC  
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA  
 151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC  
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA  
 251 TGATTCAATT CGTTTACAAr AACGCCCTCA ACGTCAAGCT GCCGCGCACC  
 301 GCCCGCGACA TGGCGGCGGC AAGCCGsAAA ATCCCGGACA GCCGCTCAA  
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC  
 401 ACGTCGGACT CTACATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC  
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA  
 501 CTACCTCGGC GCACATACTT TTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 718; ORF 206>:

m206.pep..  
 1 MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT  
 51 QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPR  
 101 ARDMAAASRK IPDSRXKAGD LVFFNTGGAH RYSHVGLYIG NGEFIHAPSS  
 151 GGTIKTEKLS TPFYAKNYLG AHTFFTE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 206 shows 96.0% identity over a 177 aa overlap with a predicted ORF (ORF 206.ng) from *N. gonorrhoeae*:

m206/g206

m206.pep	10	20	30	40	50	60
	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
g206	MFSPDKTLFLCLGALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIGRTQGSQELMLHS					
	10	20	30	40	50	60
m206.pep	70	80	90	100	110	120
	LGLIGTPYKWGGSSTATGFD CSGMIQFVYK NALNVKLPR TARDMAAASRK IPDSRXKAGD					
g206	LGLIGTPYKWGGSSTATGFD CSGMIQLVYK NALNVKLPR TARDMAAASRK IPDSRLKAGD					
	70	80	90	100	110	120
m206.pep	130	140	150	160	170	
	LVFFNTGGAHRYSHVGLYIG NGEFIHAPSSGKTIKTEKLS TPFYAKNYLGAHTFFTEX					
g206	IVFFNTGGAHRYSHVGLYIG NGEFIHAPSGKTIKTEKLS TPFYAKNYLGAHTFFTE					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 719>:

a206.seq  
 1 ATGTTTCCCC CCGACAAAAC CCTTTTCCTC TGTCTCAGCG CACTGCTCCT  
 51 CGCCTCATGC GGCACGACCT CCGGCAAACA CCGCCAACCG AAACCCAAAC  
 101 AGACAGTCCG GCAAATCCAA GCCGTCCGCA TCAGCCACAT CGACCGCACA  
 151 CAAGGCTCGC AGGAATCAT GCTCCACAGC CTCGGACTCA TCGGCACGCC  
 201 CTACAAATGG GCGGCGAGCA GCACCGCAAC CGGCTTCGAT TGCAGCGGCA  
 251 TGATTCAATT CGTTTACAAA AACGCCCTCA ACGTCAAGCT GCCGCGCACC  
 301 GCCCGCGACA TGGCGGCGGC AAGCCGCAAA ATCCCGGACA GCCGCCTTAA  
 351 GGCCGCGGAC CTCGTATTCT TCAACACCGG CGGCGCACAC CGCTACTCAC  
 401 ACGTCGGACT CTATATCGGC AACGGCGAAT TCATCCATGC CCCCAGCAGC  
 451 GGCAAACCA TCAAAACCGA AAAACTCTCC ACACCGTTT ACGCCAAAAA  
 501 CTACCTCGGC GCACATACTT TCTTTACAGA ATGA

This corresponds to the amino acid sequence <SEQ ID 720; ORF 206.a>:

```
a206.pep
1  MFPPDKTLFL CLSALLLASC GTTSGKHRQP KPKQTVRQIQ AVRISHIDRT
51  QGSQELMLHS LGLIGTPYKW GGSSTATGFD CSGMIQFVYK NALNVKLPRP
101 ARDMAAASRK IPDSRLKAGD LVFNTGGAH RYSHVGLYIG NGEFIHAPSS
151 GKTIKTEKLS TFFYAKNYLG AHTFFTE*
```

m206/a206 99.4% identity in 177 aa overlap

	10	20	30	40	50	60
m206.pep	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
a206	MFPPDKTLFLCLSALLLASC GTTSGKHRQPKPKQTVRQIQAVRISHIDRTQGSQELMLHS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m206.pep	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRPTARDMAAASRKIPDSRXKAGD					
a206	LGLIGTPYKWGGSSTATGFD CSGMIQFVYKNALNVKLPRPTARDMAAASRKIPDSRLKAGD					
	70	80	90	100	110	120
	130	140	150	160	170	
m206.pep	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
a206	LVFFNTGGAHRYSHVGLYIGNGEFIHAPSSGKTIKTEKLSTPFYAKNYLGAHTFFTEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 721>:

```
g209.seq
1  atgctgcggc atttaggaaa cgacttcgcc ttgggcgcgt tgtttttcga
51  tgctgcgggt gatgtgccac tgctgggcga tggtcaggag gttgttgacc
101 acccagtaga gaaccaaacc ggcagggaag aagaagaaca tgacggagaa
151 aaccaacggc atgattttca tcattttcgc ctgcatcggg tcggtcggcg
201 gcgggttcag ataggtttgg gcgaacatcg ttgccgccat aatgatgggc
251 aggatgtagt aggggtcggc gcggctgagg tcggtaatcc agcccagcca
301 aggtgcctgg cgcaattcta cggaggcgaa caatgccagc tacaagccga
351 tgaagacggg gatttgcaac agcataggca gacagccgcc cagcgggttg
401 atttcctcgt cttcgaaaag ctgcatcatc gcttgctgtt gcgccatacg
451 gtcgtgcgcg tatttttctt tgatggtctg cagttcgggt gcggcggcac
501 gcattttcgc catcgaaagg taggaggcgt tggtaaatgg atacagtacg
551 gctttgacga tgatggtcaa aacgacgatt gccagcccc agttgcccgt
601 aatgttgtgc agttggttca ggagccagaa gagcggcgat gcgaaccagt
651 gtactttacc gtagtctttt gccagttgca ggttgtcggc gatgtttgcg
701 ataacggatg tggtttgagg accggcatac aggttgaccg ccattttcgg
751 ttttggcccc cgggttgagg tagcgggttaa
```

This corresponds to the amino acid sequence <SEQ ID 722; ORF 209.ng>:

```
g209.pep
1  MLRHLGNDEA LGALFFDAV DVPLLGDGQE VVDHPVENQT GREEEEHDGE
51  NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPAQP
101 RCLAQFYGGE QCPVQADEDG DLQQHRTAA QRVDLVEFEK LHRLLLLRHT
151 VVAVFFFDGL QFGCGGTHFR HRTVGGVGQW IQYGFDDDGQ NDDCPAPVAD
201 NVVQLVQEP EERRCEPVYFT VVFCQLQVVG DVCNCGCLR TGIQVDRHFR
251 FWPPGWDG*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 723>:

```
m209.seq
1  ATGCTGCGGC ATTTAGGAAA CGACTTCGCC TTGGGCGGTT GTTTTTCGAT
51  GCTGCGGTTG ATGTGCCATT GCTGGGCGAT GGTCAAGAGG TTGTTGACTA
101 CCGAGTACAA TACCAGACCG GCAGGGAAGA AGAAGAACAT GACGGAGAAA
151 ACCAACGGCA TGATTTTCAT CATTTCGCC TGCCATCGGT CGGTCGGCGG
201 CGGGTTCAGA TAAGTTTGGG CGAACATCGT TGCCGCCATA ATGATGGGCA
251 GGATGTAGTA GGGGTCGGCG CGGCTGAGGT CGGTAATCCA ACCCAGCCAA
```

```

301 GGTGCCTGGC GCAATTCTAC GGAGGCGAAC AATGCCCAAT ACAATCCGAT
351 GAAGACGGGG ATTTGCAACA GCATAGGCAG GCAGCCGCCC AGCGGGTTGA
401 TTTTCTCGTC TGTGTAAAGC TGCATCATCG CCTGTTGTTG CGCCATACGG
451 TCGTCGCCGT ATTTCTCTTT GATGGCTTGC AGTTTGGGTG CGCGCGCACG
501 CATTTTCGCC ATAGAGCGGT AAGAGGCGTT GGTCAATGGA TACAGTACGG
551 CTTTGACGAT GATGGTTAAA ACGATAATCG CCCAGCCCCA GTTGCCGATG
601 ATGTTGTGCA GTTGGTTCAG GAGCCAGAAG AGCGGGGAGG CGAACCAGTG
651 TACTTTGCCG TAGTCTTTGG CCAGTTGCAG GTTGTGCGCG ATGTTTGC GA
701 TGACGGATGT GGTCTGCGGG CCGGCGTAGA GGTGATGGA GGCTTCGgTT
751 TCGCGCCGTT TTGGATGGCG GCTAAAGGCA CGCTGACGCT GGTGCTGTAC
801 AGCTTGTGCT TCGGCGGTTT GATGTCGATG TTGCACTCGC CTGCGGCGCA
851 AACGCTTTGT TGCCTTTTAG GTTGAGAAAT CCAGGTGGAC ATGAAGTGGT
901 GTTCAATCAT GCCGAGCCAG CCGGTCGGGG TTTTGGCGAT GTATTGCGCC
951 TCGGATTTGC CGGATTTGGC ATCGTCGTCC AAGTCGGAAA AGCTGACTTT
1001 TTGGAAGTTG CCTTCAGGGG TATAA

```

This corresponds to the amino acid sequence <SEQ ID 724; ORF 209>:

```

m209.pep
1 MLRHLGNDEFA LGALFFDAAV DVPLLGDGQE VVDYPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ ISLGEHRCRH NDQDQVVG VGAAEVGNPTQP
101 RCLAQFYGGE QCPIQSDG DLQHRQAAA QRVDFLVCVK LHHRLLLRHT
151 VVAVFLFDGL QFGCGGTHFR HRAVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQEP EERGEPVYFA VVFGQLQVVG DVCDDGCGLR AGVEVDGGFG
251 FAPFWMAAKG TLTVLVLSL LRLMSMLHS PAAQTLCLPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 209 shows 88.5% identity over a 253 aa overlap with a predicted ORF (ORF 209.ng)

from *N. gonorrhoeae*:

```

m209/g209
10      20      30      40      50      60
m209.pep MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
|||||
g209      MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVENQTGREEEEHDGENQRHDFHHFR
10      20      30      40      50      60

70      80      90      100     110     120
m209.pep LHRVGRRRVQISLGEHRCRHNDQDQVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSDG
|||||
g209      LHRVGRRRVQIGLGEHRCRHNDQDQVVGVGAAEVGNPAQPRCLAQFYGGEQCQVQADEG
70      80      90      100     110     120

130     140     150     160     170     180
m209.pep DLQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||
g209      DLQHRQTAAQRVDFLVEKLHHRLLLRHTVVAVFFDGLQFGCGGTHFRHRTVGGVGQW
130     140     150     160     170     180

190     200     210     220     230     240
m209.pep IQYGFDDDGKNDNRPAPVADDVVQLVQEP EERGEPVYFAVVFGQLQVVG DVCDDGCGLR
|||||
g209      IQYGFDDDGQNDPCAPVADNVVQLVQEP EERRCEPVYFTVVFQQLQVVG DVCDDGCGLR
190     200     210     220     230     240

250     260     270     280     290     299
m209.pep AGVEVDGGFGF-APFWMAAKGTLTLVLVLSLRLMSMLHSPAAQTLCLPLGWRIQVDMK
:||||
g209      TGIQVDRHFRFWPPGWDG
250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 725>:

```

a209.seq
1 ATGCTGCGGC ATTAGGAAA CGACTTCGCC TTGGGCGCGT TGTTTTTCGA

```

```

51 TGCTGCGGTT GATGTGCCAT TGCTGGGCGA TGGTCAGGAG GTTGTGATC
101 ACCCAGTACA ATACCAGACC GGCAGGGAAG AAGAAGAACA TGACGGAGAA
151 AACCAAAGGC ATGATTTTCA TCATTTTCGC CTGCATCGGG TCGGTCGGCG
201 GCGGGTTCAG ATAGGTTTGG GCGAACATCG TTGCCGCCAT AATGATGGGC
251 AGGATGTAGT AGGGGTCGGC GCGGCTGAGG TCGGTAATCC AACCAGCCA
301 AGGTGCCTGG CGCAATTCTA CGGAGGCGAA CAATGCCCAA TACAATCCGA
351 TGAAGACGGG GATTTGCAAC AGCATAGGCA GGCAGCCGCC CAGCGGGTTG
401 ATTTTCTCGT CTGTGTAAAG CTGCATCATG GCTTGTGTGCT GCGCCATACG
451 GTCGTCGCCG TATTTCTCTT TGATGGCTTG CAGTTTGGGC GCGCGGGCAC
501 GCATTTTCGC CATCGAACGG TAAGAGGCGT TGGTCAATGG ATACAGTACG
551 GCTTTGACGA TGATGGTTAA AACGATAATC GCCCAGCCCC AGTTGCCGAT
601 GATGTTGTGC AGTTGGTTCA AAAGCAGAAA GAGGGGGGAG GCGAACCAGT
651 GTACTTTGCC GTAGTCTTTG GCCAGTTGCA GGTGTGTCGGC GATGTTTGCG
701 ATAACGATG TGGTCTGTGG GCCGCGTAG AGGTTGATGG AGGCTTCGGT
751 TTCGCACCGT TTTGGATAGC GGCTAAAGGC ACGCTGACGC TGGTGCTGTA
801 CAGCTTGTCG TTGCGGCGTT TGATGTCGAT ACGGCAGTCG CCAGCGGCGC
851 AAACGCTTTG TCCGCCTTTG GGTGAGGA TCCAGGTGGA CATGAAGTGG
901 TGTTCATCA TGCCGAGCCA GCCGGTCGGG GTTTTGCGGA TGTATTGGC
951 CTCGGATTG CCGGATTGG CATCGTCGTC CAAGTCGGAG AAGCTGACTT
1001 TTTGGAAGTT GCCTTCAGGG GTATAA

```

This corresponds to the amino acid sequence <SEQ ID 726; ORF 209.a>:

```

a209.pep
1 MLRHLGNDFAL LGALFFDAAV DVPLLGDGQE VVDHPVQYQT GREEEEHDGE
51 NQRHDFHHFR LHRVGRRRVQ IGLGEHRCRH NDGQDVVGVG AAEVGNPTQP
101 RCLAQFYGGE QCPIQSEDEG DLQQHRQAAA QRVDFLVCVK LHHGLLLRHT
151 VVAVFLFDGL QFGRGGTHFR HRTVRGVGQW IQYGFDDDG* NDNRPAPVAD
201 DVVQLVQKPK EGGGEPVYFA VVFGQLQVVG DVCNCGGLW AGVEVDGGFG
251 FAPFWIAAKG TLTVLVLSL LRLMSIRQS PAAQTLCPPL GWRIQVDMKW
301 CSIMPSQPVG VLRMYSASDL PDLASSSKSE KLTFWKLPSG V*

```

m209/a209 95.6% identity in 341 aa overlap

```

m209.pep      10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDYPVQYQTGREEEEHDGENQRHDFHHFR
|||||
a209          10      20      30      40      50      60
MLRHLGNDFALGALFFDAAVDVPLLGDGQEVVDHPVQYQTGREEEEHDGENQRHDFHHFR

m209.pep      70      80      90      100     110     120
LHRVGRRRVQISLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSEDEG
|||||
a209          70      80      90      100     110     120
LHRVGRRRVQIGLGEHRCRHNDGQDVVGVGAAEVGNPTQPRCLAQFYGGEQCPIQSEDEG

m209.pep      130     140     150     160     170     180
DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRAVRGVGQW
|||||
a209          130     140     150     160     170     180
DLQQHRQAAAQRVDFLVCVKLHHRLLLRHTVVAVFLFDGLQFGCGGTHFRHRTVRGVGQW

m209.pep      190     200     210     220     230     240
IQYGFDDDGXNDNRPAFVADDVVQLVQEPPEERGGEVPYFAVVFGQLQVVGDVCDGCGLR
|||||
a209          190     200     210     220     230     240
IQYGFDDDGXNDNRPAFVADDVVQLVQKPKEGGEPVYFAVVFGQLQVVGDVCDNCGGLW

m209.pep      250     260     270     280     290     300
AGVEVDGGFGFAPFWMAAKGTLTLVLVLSLRLRLMSMLHSPAAQTLCLPLGWRIQVDMKW
|||||
a209          250     260     270     280     290     300
AGVEVDGGFGFAPFWIAAKGTLTLVLVLSLRLRLMSIRQSPAAQTLCPPLGWRIQVDMKW

m209.pep      310     320     330     340
CSIMPSQPVGVLRMYSASDLPLASSSKSEKLTFWKLPSGVX

```

```

a209      |||||
          CSIMPSQPVGLRMYASDLPDLASSKSEKLTFWKLPSGVX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 727>:

```

g211.seq
1  atgttgcgga ttgctgctgc caatcagttg ggcggtcgaa atggtgcggc
51  ggtgggaaac ggggtcgata agtttgggcg tgggtctgat aatcaggttg
101 agtttttggg aggaaacctg attgtagtcg gcgctccgg gcgtgccgct
151 gtaacggtag ccgtggcgca attcgagcgt gcgtttgttg tccttcagcg
201 agaagttacc ttctttggcg aagatgatgt tgcgcgcgcc gttttgttcc
251 tgttcgcgca ggaacagggt tttcatgatg ccggttcgg tgtcaaagg
301 ttcgacgaaa taaaccctgc cgttgcgctt gcccaagtta ttgaactcgc
351 cggcttcac caaagacaat tcctgcttct gttcaaaat ttcggcatat
401 tcgcggtcgc gcagctctgc ccacgggtatc acccaaagct gcattgacggc
451 aatcaggatg gcaaacggca cggcaaaactg catgacgggg cgtatccact
501 gtttcaacgc caatccgcag gatag

```

This corresponds to the amino acid sequence <SEQ ID 728; ORF 211.ng>:

```

g211.pep
1  MLRIAAANQL GGRNGAAVGN GVDKFRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVLQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFVKVG
101 FDEINPAVAL AQVIELAGFH QRQFLLLQD FGIFAAALC PRYHPKLHDG
151 NQDKRHKGL HDGAYPLFQ QSAG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 729>:

```

m211.seq
1  ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGTCGGA ATGGTACGGC
51  GGTGGGAAAC GGGGTCGATG AGTTTGGGCG TGGTCTGAT AATCAGGTTG
101 AGTTTGTGGA AGGAAACCTG ATTGTAAGTCG GCGGTCGCG GCCTGCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTGTGTG TCGTTCAGCG
201 AGAAGTTACC TTCTTTGGCG AAGATGATGT TGTGCGCGCC GTTTTGTCC
251 TGTTGCGGCA GGAACAGGTT TTTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAAGT TGAAGTCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GCAAACGGCA CGGCAAAGT CATCACGGG CGTATCCATT
501 GTTCAATGC CAATCCGAG GATAG

```

This corresponds to the amino acid sequence <SEQ ID 730; ORF 211>:

```

m211.pep
1  MLRVAAANQL GGRNGTAVGN GVDEFGRGAD NQVEFLEGNL IVVGASGRAA
51  VTVAVAQFER AFVVVQREVT FFGEDDVVAA VFVLFAQEQV FHDAGFGIEG
101 FDKINPAVAL AQTVELACLH QRQFLLLQD FSVFAAAXLC PRYHPKLHDG
151 NQNGKRHKGL HHRAYPLFQC QSAG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 211 shows 89.1% identity over a 174 aa overlap with a predicted ORF (ORF 211.ng) from *N. gonorrhoeae*:

```

m211/g211

          10      20      30      40      50      60
m211.pep  MLRVAAANQLGGRNGTAVGNVGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g211      MLRIAAANQLGGRNGAAVGNVVDKFRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER
          10      20      30      40      50      60

          70      80      90      100     110     120
m211.pep  AFVVVQREVTFFGEDDVVAAVFVLFAQEQVFHDAGFGIEGFDKINPAVALAQTVELACLH

```

	:                               :   :           :     :
g211	A F V V L Q R E V T F F G E D D V V A A V F L F A Q E Q V F H D A G F G V K G F D E I N P A V A L A Q V I E L A G F H
	70                  80                  90                  100                  110                  120
	130                  140                  150                  160                  170
m211.pep	Q R Q F L L L L Q D F S V F A A X L C P R Y H P K L H D G N Q N G K R H G K L H H R A Y P L F Q C Q S A G X
	:   :
g211	Q R Q F L L L L Q N F G I F A A A Q L C P R Y H P K L H D G N Q D G K R H G K L H D G A Y P L F Q R Q S A G
	130                  140                  150                  160                  170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 731>:

```
a211.seq
1 ATGTTGCGGG TTGCTGCTGC CAATCAGTTG GCGGGTCGGA ATGGTACGGC
51 GGTGGGAAC GGGGTCGATG AGTTTGGGCG TGGTGCTGAT AATCAGGTTG
101 AGTTTTTGA AGGAACCTG ATTGTAGTCG GCGCGTCCGG CCGTCCCGCT
151 GTAACGGTAG CCGTGGCGCA ATTCGAGCGT GCGTTTGTTG TCGTTCAGCG
201 AGAAGTTACT TTCTTTGGCG AAGATGATGT TGTCGCCGCC GTTTTTTTC
251 TGTTGCGCA GGAACAGGTT TTTCATGATG CCGGATTCGG TATCGAAGGT
301 TTCGACAAAA TAAACCCTGC CGTTGCGCTT GCCCAAAGT TTGAACCCGC
351 CTGCCTCCAC CAAAGACAAT TCCTGCTTCT GCTTCAGGAT TTCAGCGTAT
401 TCGCGGCTGC GTAGCTCTGC CCACGGTATC ACCCAAAGCT GCATGACGGC
451 AACCAAAACG GAAACGGCA CGGCAAACTG CATCACC GGTATCCATT
501 GTTTCATGCA CAATCCGAG GATAG
```

**This corresponds to the amino acid sequence <SEQ ID 732; ORF 211.a>:**

a211.pep

1	MLRVAAANQL	GGRNGTAVGN	GVDFEGRGAD	NQVEFLEGNL	<u>IVVGASGRAA</u>
51	<u>VTVAVAQFER</u>	AFVVVQREVT	FFGEDDVVAA	VFVLFAGEQV	FHDAGFGIEG
101	FDKINPAVAL	AQTVEPACLH	<u>QRQFLLLQD</u>	<u>FSVFAAA*LC</u>	PRYHPKLHDG
151	NQNGKRHGKL	HHRAYPLFOC	OSAG*		

**m211/a211 99.4% identity in 174 aa overlap**

	10	20	30	40	50	60
m211.pep	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
a211	MLRVAAANQLGGRNGTAVGNGVDEFGRGADNQVEFLEGNLIVVGASGRAAVTVAVAQFER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m211.pep	AFVVVVQREVTFFGEDDVVAAVFVLFAGEQVVFHDAGFGIEGFDKINPAVALAQTVELACLH					
a211	AFVVVVQREVTFFGEDDVVAAVFVLFAGEQVVFHDAGFGIEGFDKINPAVALAQTVEPACLH					
	70	80	90	100	110	120
	130	140	150	160	170	
m211.pep	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLLHHRAYPLFQCQSAGX					
a211	QRQFLLLLQDFSVFAAAXLCPRYHPKLHDGNQNGKRHGKLLHHRAYPLFQCQSAGX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 733>:

g212.seq (partial)

1	atggacaatc	tcgatgga	cggcattccc	gacatccgca	cactcgacca
51	aaccatccgc	aaacacgcac	acccgctcaa	cctgattgtc	tgccctccccg
101	ataatcagat	tcccgatttt	caaacgcac	aagatgcttc	ggactcggaa
151	tgccgtctga	agcaccggtt	ggatcaggca	accagtgcc	tccagttcga
201	cagcatcaac	ctcatcgaac	acatcctgcc	cgatgtccgc	ttctggctgg
251	ttcccccttc	acgcaccgcg	cgctgcacg	aacatttcca	ccacatttcc
301	tggcagacgg	aagccatccc	gcaaacggaa	agcaagtccg	acaaacctgt
351	gtttgcactt	ccacaaacat	ccgaacggaa	aaaaccggaa	cacgtcctcg



```

401 tcatcgggtgc aggcattgcc ggcgcatcga ccgcccacgc cttagcatca
451 caccggcattt ccgttaccgt attggaagcc cgaaaagccg ctcaagccgc
501 cagcggcaac cggcaagggc tgctttacgc caaaatctcg ccgcacgaca
551 ccggacagac cgaactgctg cttgccggct acggctacac caaacgcctg
601 ctcggacaca tcctgcccga ctcgcgacct tggggcggca acggcatcat
651 ccacctcaat tacagccgca ccgaacaaca acgcaatcac gaattgggtt
701 tgcaaaaaca ccataaccac ctctaccgca gcatacagtc tgcagaagcc
751 gaaaaaatcg ccggcatccc gctgaacacg ccctacgccc aaccattatg
801 cggactctac tggcaacacg gcgtatggct caatccgccc gcattcgtcc
851 gcacctcct cagccatccg ctgatcgaac tatatgaaa cacaacgtta
901 accggcattt cccacgacgg agaaaagtgg attgcaagca cgccaaacgg
951 caccatttacc gccacacaca tcatctactg caccggcgcg cacagcccct
1001 gcctgcccga aaccaacctc gccgccctac ccctcaggca aatacgcgga
1051 caaaccggcc tcacaccgtc caccgccgtt tccgaacaac tgcgttgccg
1101 cgttttcaggc gaaagctaca tcagcccgtc gtggcacgga ctgactgct
1151 acggcgcgag ttttattccc aacagcagca ataccggtg gaacgaagcc
1201 gaagaagcct caaaccgcca agcattggca caccttaacc ccgcccttgc
1251 cgaatcattg ttt...

```

This corresponds to the amino acid sequence <SEQ ID 734; ORF 212.ng>:

g212.pep (partial)

```

1 MDNLVWDGIP DIRTLDQIR KHAHPLNLIV CLPDNQIPDF QTAQDASDSE
51 CRLKHLRDLQA TQCLQFDSIN LIEHILPDVR FWLVPPSRTR RLHEHFHHIS
101 WQTEAIPQTE SKSDKPWFAL PQTSEKKPE HVLVIGAGIA GASTAHALAS
151 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTGQTELL LAGYGYTKRL
201 LGHILPDSDT WGGNGIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
251 EKIAGIPLNT PYAELCGLY WQHGVLNPP AFVRTLLSHP LIELVENTTL
301 TGISHDGEKW IASTPNGTFT ATHIIYCTGA HSPCLPETNL AALPLRQIRG
351 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGASFIP NSSNTGWNEA
401 EEASNRQALA HLNPALAESL F...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 735>:

m212.seq

```

1 ATGGACAATC TCGTATGGGA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AGCCATCCGC AAACACGCAC CCCCCTCAA CCTGATTATC TGCCTCCCCG
101 ATAATCAGAT TCCCGATTTT CAAACCGCAC AAGATGCTTC GGACGCGGAA
151 TGCCGTCTGA AGCACCGTTT GGATCAGGCA ATGCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTCATCGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCTTC ACGCACCCAC CACCTGCACG AACATTTCCA CCACATTTCC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGCAAGCCCG ACAAAACCTG
351 GTTTGCACTT CCACAAACAT CCGAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGCGC GGCATATCC GCGCGGGCAA CCGCCACGC CTTAGCATCA
451 CACGGCATT TCCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCAAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCAGGACA
551 CCGAACAGAC CGAACTTTTG CTGCGCGGCT ACGGCTACAC CAAACGCCGTG
601 CTCGGACACA TCCTGCCCGA ATCCGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACATC TGCAGAAGCC
751 GAAAAAATCG CCGGTATCCC ACTGTCCGTC CCATACGACC ACCCTTCATG
801 CGGACTCTAC TGGCAACAGC GCGTATGGCT CAATCCACCC GCATTCTGCC
851 GCACCCTCCT CAACCATCCG CTCATTGGAC TACACGAAGA CACACCCTTG
901 ACCGACATTT CCCACGACGG GGAAGAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCACCTC GCCGCCCTGC CTCTCAGGCA AATACGCGGA
1051 CAAACCGGCC TCACACCGTC CACCCCGTTT TCCGAACAAC TCGGTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCACGGA CTGCACTGCT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCCGCA ACCCAAACCC CCAAAAACAC CAAGGGCACG
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCTAGT CGGCGCACTC
1351 GCGGACATTG CCGCATGCG GCAGACCTAC ACCAAACTCG CGCTGGACAA
1401 AAATACCGC ATCGACACCC CATGCCATA CCTGCCTAAT GCCTACGTCA
1451 ACACCGCGCA CCGCACCCGC GACTCGCCA CCGCCCCAT CTGCGCCGCC

```

15 01 GmCAwTGCAG CCCAAATCst AGGCyTGCCC CATCCCTTTT yAcAAcGCCT  
 15 51 gCGCCACGCC cTAcACCCCA ACCGCACCAT CATCCGCGCC ATCGTCAGAA  
 16 01 GGAAGGATCT AACCCCTTAA

This corresponds to the amino acid sequence <SEQ ID 736; ORF 212>:

m212.pep

```

1 MDNLVWDGIP DIRTLDQAIR KHAPPLNLII CLPDNQIPDF QTAQDASDAE
51 CRLKHLRDLQA MQCLQFDSIN LIEHILPDVR FWLVPPSRTH HLHEHFHHIS
1 01 WQTEAIPQTE SKPDKPWFAL POTSERQKPE HILVIGAGIS GAATAHALAS
1 51 HGISVTVLEA RKAQAASGN RQGLLYAKIS PHDTEQTELL LAGYGYTKRL
2 01 LGHILPESET WGGNGIHLN YSRTEQQRNH ELGLQKHHNH LYRSITSAEA
2 51 EKIAGIPLSV PYDHPSCGLY WQHGVLNPP AFVRTLLNHP LIGLHEDTPL
3 01 TDISHDGEKW IASTPNGTFT ATHIIYCTGA NSPYLPETNL AALPLRQIRG
3 51 QTGLTPSTPF SEQLRCAVSG ESYISPSWHG LHCYGFASFP NSSHTGWNEA
4 01 EEASNQALA HLNPALESSE FAANPNPQKH QGHAAIRCD S PDHLPVGLAL
4 51 GDIAAMRQTY TKLALDKNYR IDTPCPYLPN AYVNTAHGTR GLATAPICAA
5 01 XXAAQIXGLP HPFXQRLRHA LHPNRTIIRA IVRRKDLTP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 212 shows 92.9% identity over a 421 aa overlap with a predicted ORF (ORF 212.ng) from *N. gonorrhoeae*:

m212/g212

	10	20	30	40	50	60
m212.pep	MDNLVWDGIPDIRTLDQAIRKHAPPLNLII CLPDNQIPDFQTAQDASDAECRLKHLRDLQA					
g212	MDNLVWDGIPDIRTLDQTIKHAHPLNLIVCLPDNQIPDFQTAQDASDSECRLKHLRDLQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m212.pep	MQCLQFDSINLIEHILPDVRFWLVPPSRTHHLHEHFHHISWQTEAIPQTESKPKDPWFAL					
g212	TQCLQFDSINLIEHILPDVRFWLVPPSRTRRLHEHFHHISWQTEAIPQTESKSDKDPWFAL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m212.pep	POTSERQKPEHILVIGAGISGAATAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
g212	POTSERKKPEHVLVIGAGIAGASTAHALASHGISVTVLEARKAAQAASGNRQGLLYAKIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m212.pep	PHDTEQTELLLAGYGYTKRLLGHILPESETWGGNGI IHLNYSRTEQQRNHELGLQKHHNH					
g212	PHDTGQTELLLAGYGYTKRLLGHILPDSDTWGGNGI IHLNYSRTEQQRNHELGLQKHHNH					
	190	200	210	220	230	240
	250	260	270	280	290	300
m212.pep	LYRSITSAEAEKIAGIPLSVPYDHPSCGLYWQHGVLNPPAFVRTLLNHP LIGLHEDTPL					
g212	LYRSITSAEAEKIAGIPLNTPYAEPLCGLYWQHGVLNPPAFVRTLLSHPLIELYENTTL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m212.pep	TDISHDGEKWIASTPNGTFTATHIIYCTGANSPLYLPETNL AALPLRQIRGQTGLTPSTPF					
g212	TGISHDGEKWIASTPNGTFTATHIIYCTGAHSPCLPETNL AALPLRQIRGQTGLTPSTPF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m212.pep	SEQLRCAVSGESYISPSWHGLHLCYGFASFI PNSSHTGWNEAEASNQALAHLPALSESSE					

```

a212.seq
1 ATGGACAATC TCGCATGGAA CGGCATTCCC GACATCCGCA CACTCGACCA
51 AACCATCCGC AAACACGCAC ACCCGCTCAA CCTGATTGTC TGCCTCCCCG
101 ATAATCAGAT TCCCAATTTT CAAACCGCAA AAGATGCTTC GGACCGGGAA
151 TGCCGTCGTA AGCACCGTTT GGATCAGGCA ACCCAGTGCC TCCAGTTCGA
201 CAGCATCAAC CTGATTGAAC ACATCCTGCC CGATGTCCGC TTCTGGCTGG
251 TTCCCCCTTC ACGCACCCGC CGCTGCAACG AACACTTCCA CCACATTTC
301 TGGCAGACCG AAGCCATCCC GCAAACCGAA AGTAAGCCCC ACAAAACCTG
351 GTTTGCATCT CCACAACATC CGCAACGGCA AAAACCGGAA CACATCCTCG
401 TTATCGGAGC GGGCATATCC GGGCGGGCAA CCGCCACGCG CTTAGCATCA
451 TACGGCATT TCCGTTACCGT ATTGGAAGCC CGAAAAGCCG CCCAAGCCGC
501 CAGCGGCAAC CGCCAAGGGC TGCTCTACGC CAAAATCTCG CCGCACGACA
551 CCGAACAAAC CGAACTGCTG CTTGCCGGCT ACGGGTACAC CAAACGCGCT
601 CTCGGACATA TACTGCTCGA ATCGGAAACC TGGGGCGGCA ACGGCATCAT
651 CCACCTCAAT TACAGCCGCA CCGAACAACA ACGCAATCAC GAATTGGGTT
701 TGCAAAAACA CCATAACCAC CTCTACCGCA GCATCACGCA GGCAGAAGCC
751 GAAAAAATCG CCGGCATCCC TCTGAACAGC CCCTACGCGC AACCATTATG
801 CGGACTGTTT TGGCAGTAGC GCGTATGGCT CAATCCTCCC ACATTCTGTC
851 GCGCCCTCCT CAGCCATCCG CTCATTGGAC TACACAAGAA CACACCGTTA
901 ACCGACATTT CCCACGACGG GGAAAAGTGG ATTGCAAGCA CGCCAAACGG
951 CACATTTACC GCCACACACA TCATCTACTG CACCGGTGCG AACAGCCCTT
1001 ACCTACCCGA AACCAACCCT GCCACCTCGC CCCTCAGGCA AATACGCGGA
1051 CCAACCGGCC TCAACCCGTC CACCCCGTTT TCCGAACAAC TGCCTTGCGC
1101 CGTTTCAGGC GAAAGCTACA TCAGCCCGTC GTGGCAGGGA CTGCATCTGT
1151 ACGGCGCGAG TTTTATTTCC AACAGCAGCC ATACCGGATG GAACGAAGCC
1201 GAAGAAGCCT CAAACCGCCA AGCATTGGCA CACCTTAACC CCGCCCTTTC
1251 CGAATCATTG TTTGCGCGCA ACCCAAACCC CCAAAAACAC CAAGGGCAGC
1301 CCGCCATACG CTGCGACAGC CCGGACCACC TTCCCCTAGT CGGCGCACTC
1351 GCGCAGATTG CGCCTATGCA ACAAACTTAC GCCAAACTCG CGCTGGACAA
1401 AAACATATCG ATCGATGCCC CCTGCCCGTA CCTGCCCAAT GCCTACGCCA
1451 ACACCGCCCA CGGCACACGC GGGCTTGCCA CCGCCCCCAT CTGCGCGGCC
1501 GCGGTTGCAG CCGAAATCTT AGGCTTGCCC CATCCCCTCT CAAAACGCCT
1551 GCCCAGCCG CTACACCCCA ACCGCGCCAT CATCCGCGCC ATCGTCAGAA
1601 GGAAGGATCT AACCCTTTAA

```

**a212.pep**

1	MDNLAWNIGIP	DIRTLDQITR	KHAHPLNLIV	CLPDNQIPNF	QTAQDASDAE
51	CRCLKHRLDQA	TQCLQFDSIN	LIEHILPDVR	FWLVPPSRTR	RLHEHFHHIS
101	WQTEAIPQTE	SKPKDPWFAL	PQTSERQKPE	HILVIGAGIS	GAATAHALAS
151	YGTSTVTLEA	RKAAQGAASN	RQGLLYAKIS	PHDTEQTELL	LAGYGYTKRL
201	LGHILPESET	WGGNGIIHLN	YSRTEQQRNH	ELGLQKHNNH	LYRSITQAEA
251	EKIAGIPLNT	PYAEPLCGLF	WQYGVWLNPP	TFVRALLSHP	LIGLHEDTPL
301	TDISHDGEKW	IASTPNGTFT	ATHIIYCTGA	NSPYLPETNL	ATLPLRQIRG
351	QTGLTPSTPF	SEQLRCAVSG	ESYISPSWHG	LHCYGASFIP	NSSHTGWNEA
401	EEASNRRQAL	HLNPALSES	FAANPNPQKH	QGHAAIRCDS	PDHLPLVGAL
451	GDIAMQQQTY	AKLALDKNYR	IDAPCPYLPN	YAAANTAHGR	<u>GLATAPICAA</u>
501	AVAAEILGLP	HPLSKRLRHA	LHPNRAIIRA	IVRRKDLTP*	

[illegible]

491

	10	20	30	40	50	60
m212.pep	70	80	90	100	110	120
a212	70	80	90	100	110	120
m212.pep	130	140	150	160	170	180
a212	130	140	150	160	170	180
m212.pep	190	200	210	220	230	240
a212	190	200	210	220	230	240
m212.pep	250	260	270	280	290	300
a212	250	260	270	280	290	300
m212.pep	310	320	330	340	350	360
a212	310	320	330	340	350	360
m212.pep	370	380	390	400	410	420
a212	370	380	390	400	410	420
m212.pep	430	440	450	460	470	480
a212	430	440	450	460	470	480
m212.pep	490	500	510	520	530	540
a212	490	500	510	520	530	540

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 739>:

g214.seq

```

1  atgatacaaa agatatgtaa gctatttggt ttaattgtaa tttttgcaac
51  ttctcccgtt tttgcccttc aaagcgacag cagacggccc atccaaatcg
101 aagccgacca aggttcgctc gatcaagcca accaaaggac cacatttagc
151 ggcaatgtca tcatcagaca gggtagctc aacatttccg cctcgtgtgt
201 caacgtcaca cgcggcaggc aaaggcggcg aatccgtgag ggcggaaggt
251 tcgcccgtcc gcttcagcca aacgttggac gggggcaaag ggacggtgcg
301 cggtcaggca aacaacgtta cctattcctc cgcaggaagc actgtcgttc
351 tgaccgcaa tgccaaagtg cagcgcggcg gcgacgttgc cgaaggtgcg
401 gtcattacct acaacaccaa aaccgaagtc tatacatca acggcagcac
451 gaaatcgggt gcgaaatccg cttccaaaac cggcagggtc agcgtcgtca
501 tccagccttc aagcacacaa aaaaccgaat aacccgatg ccgtctgaaa
551 cggaaacgca gttcagacgg catttgccga ccgaaatgcc gagaagagat
601 tattga

```

This corresponds to the amino acid sequence <SEQ ID 740; ORF 214.ng>:

g214.pep

m214.seq (partial)

m214.pep (partial)

m214/g214

a214.seq

1	ATGATACAAA	AGATATGTAA	GCTATTGTGT	TTAATAGCAT	TTTTTTCGGC
51	GTCCCCGCT	TTTGCCCTTC	AAAGCGACAG	CAGGCAGCCT	ATTCAGATTG
101	AGGCCGACCA	AGGTTTCGCTC	GATCAAGCCA	ACCAAAGCAC	CACATTCAAG
151	GGAAACGTCG	TCATCAGACA	GGGTACGCTC	AATATTTCCG	CCGCCCGCGT
201	CAATGTTACA	CCTGGC.GGC	AAAGGCGGCG	AATCCGTGAG	GGCGGAAGGT
251	TCGCGACATCC	GGCTCAGTCA	GACATTGGAC	GGCGGCAAAG	GCACGGTTCG
301	CGGACAGGCA	AACAACGTTG	CTTATTCATC	TGCAGGACAG	CCCGTAGTCT

```

351 TAACCGGTAA TGCCAAAGTA CAGCGCGGCG GCGATGTCGC CGAAGGTGCG
401 GTGATTACAT ACAACACCAA AACCGAAGTC TATACCATCA GCGGCAGCAC
451 AAAATCCGGC GCAAAATCCG CTTCCAAATC CGGCAGGGTC AGCGTCGTTA
501 TCCAGCCTTC GAGTACGCAA AAATCCGAAT AATCCCAATG CCGTCTGAAA
551 CATAAACCTG GTTCGGACGG CATTGCGCGA CCGAAATATT GAAGAGATAT
601 TTATGA

```

This corresponds to the amino acid sequence <SEQ ID 744; ORF 214.a>:

```

a214.pep
1  MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISAARVNVT RGXQRRRIRE GGRFASPLQ P DIGRRQRHGA
101 RTGKQRCLFI CRQHRSLNR* CQSTARRRCR RRCGDYIQH Q NRSLYHQRH
151 KIRRKIRFQI RQGQRRYPAF EYAKIRIIPM PSET*TWFG R HLPTEILKRY
201 L*

```

m214/a214 99.3% identity in 152 aa overlap

```

              10      20      30      40      50      60
m214.pep      MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
a214           MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS GNVVIRQGT L
              10      20      30      40      50      60

              70      80      90     100     110     120
m214.pep      NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCLFICRQHRSLNRX
a214           NISAARVNVT RGRQRRRIRE GGRFASPLQ PDIGRRQRH GARTGKQRCLFICRQHRSLNRX
              70      80      90     100     110     120

              130     140     150
m214.pep      CQSTARRRCRRRCGDYIQH QNRSLYHQRH K
a214           CQSTARRRCRRRCGDYIQH QNRSLYHQRH KIRRKIRFQI RQGQRRYPAF EYAKIRIIPM
              130     140     150     160     170     180

a214           PSETXTWFG RHLPTEILKRY L X
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 745>:

```

g214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATTGTAA TTTTGC AAC
51  TTCTCCCGCT TTGCCCCTTC AAAGCGACAG CAGACGGCCC ATCCAAATCG
101 AAGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGTAC CACATTAGC
151 GGCAATGTCA TCATCAGACA GGTACGCTC AACATTCCG CCTCGCGCT
201 CAACGTCACA CGCGCGGCA AAGCGGCGA ATCCGTGAGG GCGGAAGTT
251 CGCCCGTCCG CTTACGCCAA ACGTTGGACG GGGGCAAAGG GACGGTGCGC
301 GGTCAGGCAA ACAACGTTAC CTATTCCTCC GCAGGAAGCA CCGTCGTTCT
351 GACCGGCAAT GCCAAAGTGC AGCGCGGCGG CGACGTTGCC GAAGGTGCGG
401 TCATTACCTA CAACACCAA ACCGAAGTCT ATACCATCAA CGGCAGCAGC
451 AAATCGGGTG CGAAATCCGC TTCCAAAACC GGCAGGGTCA GCGTCGTCAT
501 CCAGCCTTCA AGCACACAAA AAACCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 746; ORF 214-1.ng>:

```

g214-1.pep
1  MIQKICKLFV LIVIFATSPA FALQSDSRP IQIEADQGS L DQANQSTTFS
51  GNVVIRQGT L NISASRVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGTVR
101 GQANNVTYSS AGSTVLTGN AKVQRGGDVA EGAVITYNTK TEVYTINGST
151 KSGAKSASKT GRVSVVIQPS STQKTE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 747>:

```

m214-1.seq
1  ATGATACAAA AGATATGTAA GCTATTTGTT TTAATAGCAT TTTTTCGGC
51  GTCCCCCGCT TTGCCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTTGCTC GATCAAGCCA ACCAAAGCAC CACATTAGC
151 GGAACGTCG TCATCAGACA GGTACGCTC AATATTCCG CCGCCCGCGT

```

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```

201 CAAATGTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCCG
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 748; ORF 214-1>:

m214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS
51 GNVVIRQGT L NISAARVNVT RGGKGGESVR AEGSPVRF SQ TLDGGKGTVR
101 GQANNVAYSS AGSTVVL TN AKVQRGGDVA EGAVITYNTK TEVYTISGST
151 KSGAKSASKS GRVSVVIQPS STQKSE*

```

m214-1/g214-1 93.8% identity in 176 aa overlap

	10	20	30	40	50	60
m214-1.pep	MIQKICKLFV	LIAFFSASPA	FALQSDSRQP	IQIEADQGS	L DQANQSTTFS	GNVVIRQGT
g214-1	MIQKICKLFV	LIVIFATSP	AFALQSDSR	PIQIEADQGS	L DQANQSTTFS	GNVVIIRQGT
	10	20	30	40	50	60
	70	80	90	100	110	120
m214-1.pep	NISAARVNVT	RGGKGGESV	RAEGSPVRF	SQTLDGGK	GTVRGQANN	VAYSSAGST
g214-1	NISASRVNVT	RGGKGGESV	RAEGSPVRF	SQTLDGGK	GTVRGQANN	VYSSAGST
	70	80	90	100	110	120
	130	140	150	160	170	
m214-1.pep	AKVQRGGDVA	EGAVITYNT	KTEVYTIS	GSTKSGAKS	ASKSGRVSV	VIQPSSTQK
g214-1	AKVQRGGDVA	EGAVITYNT	KTEVYTING	STKSGAKS	ASKTGRVSV	VIQPSSTQK
	130	140	150	160	170	

g214-1/p38685

sp|P38685|YHBN\_ECOLI 17.3 KD PROTEIN IN MURA-RPON INTERGENIC REGION PRECURSOR (ORF185)  
>gi|551336 (U12684) orf185 [Escherichia coli] >gi|606139 (U18997) ORF\_o185 [Escherichia coli]  
>gi|1789592 (AE000399) orf, hypothetical protein [Escherichia coli] Length = 185  
Score = 97.1 bits (238), Expect = 6e-20  
Identities = 57/126 (45%), Positives = 74/126 (58%), Gaps = 3/126 (2%)

Query: 19 PAFALQSDSRQPIQIEADQGS L DQANQSTTFS GNVVIRQGT L NISAARVNVT --GGKGG 76  
PAFA+ D+ QPI IE+DQ SLD TF+GNV++ QGT+ I+A +V VTR G +G  
Sbjct: 24 PAFAVTGD TDQPIHIESDQQLDMQGNVVTFTGNVIVTQGTIKINADKVVVTRPGGEQK 83

Query: 77 ESVRAEGSPVRF SQTLDGGKGTVRGQANNVAYSSAGSTVVL TN AKVQRGGDVAEGAVIT 136  
E + G P F Q D GK V G A+ + Y A VVLTGNA +Q+ +G IT  
Sbjct: 84 EVIDGYGK PATFYQMDNGK-PVEGHASQMHYELAKDFVVL TNAYLQQVDSNIRGDKIT 142

Query: 137 YNTKTE 142  
Y K +  
Sbjct: 143 YLVKEQ 148

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 749>:

a214-1.seq

```

1 ATGATACAAA AGATATGTAA GCTATTGT TTAATAGCAT TTTTTCGGC
51 GTCCCCCGCT TTTGCCCTTC AAAGCGACAG CAGGCAGCCT ATTCAGATTG
101 AGGCCGACCA AGGTCGCTC GATCAAGCCA ACCAAAGCAC CACATTACAGC
151 GGAAACGTCG TCATCAGACA GGGTACGCTC AATATTTCCG CCGCCGCGCT
201 CAATGTTTACA CGCGGCGGCA AAGGCGGCGA ATCCGTGAGG GCGGAAGGTT
251 CGCCAGTCCG CTTCAGCCAG ACATTGGACG GCGGCAAAGG CACGGTGCCG
301 GGACAGGCAA ACAACGTTGC TTATTCATCT GCAGGCAGCA CCGTAGTCTT
351 AACCGGTAAT GCCAAAGTAC AGCGCGGCGG CGATGTCGCC GAAGGTGCGG
401 TGATTACATA CAACACCAA ACCGAAGTCT ATACCATCAG CGGCAGCACA
451 AAATCCGGCG CAAAATCCGC TTCCAAATCC GGCAGGGTCA GCGTCGTTAT
501 CCAGCCTTCG AGTACGCAA AATCCGAATA A

```

This corresponds to the amino acid sequence <SEQ ID 750; ORF 214-1.a>:

a214-1.pep

```

1 MIQKICKLFV LIAFFSASPA FALQSDSRQP IQIEADQGS L DQANQSTTFS

```

51 GN<sup>V</sup>VIRQGT<sup>L</sup> NISAARVNVT RGGKGGESVR AEGSPVRFSQ TLDGGKGT<sup>V</sup>R  
 101 GQANNVAYSS AGSTVVL<sup>T</sup>TGN AKVQRGGDVA EGAVITYNTK TEVYTISG<sup>S</sup>T  
 151 KSGAKSASKS GRVSVVIQPS STQKSE\*

a214-1/m214-1 100.0% identity in 176 aa overlap

	10	20	30	40	50	60
a214-1.pep	MIQKICKL	FLVLI	AFSASP	FALQSD	SRQPIQ	IEADQGS
m214-1	MIQKICKL	FLVLI	AFSASP	FALQSD	SRQPIQ	IEADQGS
	10	20	30	40	50	60
	70	80	90	100	110	120
a214-1.pep	NISAARVN	VT	RGGKGG	ESVRAE	GS	SPVRFSQ
m214-1	NISAARVN	VT	RGGKGG	ESVRAE	GS	SPVRFSQ
	70	80	90	100	110	120
	130	140	150	160	170	
a214-1.pep	AKVQRGG	DVAE	GA	VITYNT	KTEVYT	ISG
m214-1	AKVQRGG	DVAE	GA	VITYNT	KTEVYT	ISG
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 751>:

g215.seq  
 1 atgaaagtaa gatggcggtta cgggaattgcg ttccattga tattggcgg  
 51 tgccttgggc agcctgtcgg catggttggg ccgtatcagc gaagtcgaaa  
 101 tgcaggaagt caggctcaat cccgacgaac ctcaatacac aatggacggc  
 151 ttggacggaa ggcggttga cgaacaggga tacttgaag aacatttgag  
 201 cgcgaaaggt gcgaaacagt ttccgaaaa cagcgacatc cattttgatt  
 251 cgccgcatct cgtgttcttc caagaaggca ggctgttgta cgaagtcggc  
 301 agcgatgaag ccgtttacca taccgaaaaa aaacaggttc ttttataaaa  
 351 caacgttggt ctgacaaaaa ccgccgacgg caggcgagcag gcgggtaaa  
 401 tcgaaaccga aaaactgcac gtcgataccg aatctcaata tgcccaaacc  
 451 gatacgcttg tcagtttcca atatggcgcg tcgcacggtc aggcgggcgg  
 501 tatgacctac aaccacaaa caggcatgtt gaacttctca tctaaagtga  
 551 aagccgcgat ttatgataca aaagatatgt aa

This corresponds to the amino acid sequence <SEQ ID 752; ORF 215.ng>:

g215.pep  
 1 MKVRWRYGIA FPLILAVALG SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS  
 51 LDGRRFDEQG YLKEHLSAKG AKQFPENSDI HFDSPLVFF QEGRLLYEVG  
 101 SDEAVYHTEN KQVLFKNV V LTKTADGRRQ AGKVETEK<sup>L</sup>H VDTESQYAQT  
 151 DTPVSFQYGA SHGQAGGMTY NHKTGMLNFS SKVKA<sup>I</sup>YDT KDM\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 753>:

m215.seq (partial)  
 1 ..AGCCTGTCGG CATGGTTGGG TCGTATCAGC GAAGTCGAGA TTGAAGAAGT  
 51 CAGGCTCAAT CCCGACGAAC CGCAATACAC AATGGACAGC TTGGACGGCA  
 101 GCGGTTTGA CGAACAGGGA TACTTGAAAG AACATTTGAG CGCGAAGGGC  
 151 GCGAAACAGT TTCCGAAAG CAGCGACATC CATTTTGATT CGCCGCATCT  
 201 CGTGTCTTC CAAGAAGGCA GGTGTTGTA CGAAGTCGGC AGCGACGAAG  
 251 CCGTTTACCA TACCGAAAAC AAACAGGTTC TTTTAAAAA CAACGTTGTG  
 301 CTGACCAAAA CCGCCGACGG CAAACGGCAG GCGGGTAAAG TTGAAGCCGA  
 351 AAAGCTGCAC GTCGATACCG AATCTCAATA TGCCCAAACC GATACGCCTG  
 401 CAGTTTCCA ATATGGTGCA TCGCAGGTC AGGCGGGCGG CATGACTTAC  
 451 GACCACa<sup>w</sup>A CAGGCATGTT GA<sup>A</sup>CTTCTCA TCTAAAGTGA AAGCCACGAT  
 501 TTATGATACA AAAGATATGT AA

This corresponds to the amino acid sequence <SEQ ID 754; ORF 215>:

m215.pep (partial)  
 1 ..SLSAWLGRIS EVEIEEVRLN PDEPQYTMDS LDGRRFDEQG YLKEHLSAKG  
 51 AKQFPESDI HFDSPLVFF QEGRLLYEVG SDEAVYHTEN KQVLFKNV V  
 101 LTKTADGK<sup>R</sup>Q AGKVEAEK<sup>L</sup>H VDTESQYAQT DTPVSFQYGA SHGQAGGMTY



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151 DHXTGMLNFS SKVKATIYDT KDM\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 215 shows 96.0% identity over a 173 aa overlap with a predicted ORF (ORF 215.ng) from *N. gonorrhoeae*:

m215/g215

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
g215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTM	DG	LDGRRFDEQG		
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD	
g215	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD	
	70	80	90	100	110	
	110	120	130	140	150	
m215.pep	LTKTADGKRQAGK	VEAEKLV	DTESQYAQ	TDTPV	SFOYG	
g215	LTKTADGKRQAGK	VEAEKLV	DTESQYAQ	TDTPV	SFOYG	
	130	140	150	160	170	
	170					
m215.pep	SKVKATIYDTKDMX					
g215	SKVKAAYDTKDM					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 755>:

a215.seq

1	ATGAAAGTAA	GATGGCGGTA	CGGAATTGCG	TTCCCATGTA	TATTGGCGGT
51	TGCCTTGGGC	AGCCTGTCGG	CATGGTTGGG	ACGCATCAGC	GAAGTCGAGA
101	TTGAAGAAGT	CAGGCTCAAT	CCCGACGAAC	CGCAATACAC	AATGGACGGA
151	TTGGATGGCA	GCGGGTTTGA	CGAACAGGGA	TACTTGAAAG	AACATTGAG
201	TTCGAAGGGC	GCGAAACAGT	TTCCCGAAAG	CAGCGACATT	CATTTCGACT
251	CACCGCATCT	CGTGTCTTC	CAAGAAGGCA	GGTTGTGTA	CGAAGTCGGC
301	AGCGATGAAG	CCGTTTACCA	TACCGAAAAC	AAACAGGTTT	TTTTTAAAAA
351	CAACGTTGTG	CTGACCAAAA	CCGCCGACGG	CAAACGGCAG	GCGGGTAAAG
401	TTGAAGCCGA	AAAGCTGCAC	GTCGATACCG	AATCTCAATA	TGCCCAAAACC
451	GATACGCCTG	TCAGTTTCCA	ATATGGTGCA	TCGCACGGTC	AGGCGGGCGG
501	CATGACTTAC	GACCACAAAA	CAGGCATGTT	GAACCTCTCA	TCTAAAGTGA
551	AAGCCACGAT	TTATGATACA	AAAGATATGT	AA	

This corresponds to the amino acid sequence &lt;SEQ ID 756; ORF 215.a&gt;:

a215.pep

1	MKVRWRYGIA	FPLILAVALG	SLSAWLGRIS	EVEIEEVRLN	PDEPQYTM
51	LDGRRFDEQG	YLKEHLSSKG	AKQFP	ESSDI	HFDS
101	SDEAVYHTEN	KQVLFKNNVV	LTKTADGKRQ	AGKVEAEKLV	DTESQYAQ
151	DTPVSFQYGA	SHGQAGGMTY	DHKTGMLNFS	SKVKATIYDT	KDM*

m215/a215 98.3% identity in 173 aa overlap

		10	20	30	40	
m215.pep		SLSAWLGRISEVEIEEVRLNPDEPQYTMDSLDGRRFDEQG				
a215	MKVRWRYGIAFPLILAVALG	SLSAWLGRISEVEIEEVRLNPDEPQYTM	DG	LDGRRFDEQG		
	10	20	30	40	50	
	50	60	70	80	90	
m215.pep	YLKEHLSAKGAKQFP	ESSDIHFDS	PHLVFFQEG	RLLYE	VGSD	

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```

a215      |||||:|||||
          YLKEHLSSKGAQKQFPESSDIHFDSPHLVFFQEGRLLYEVGSDEAVYHTENKQVLFKNVV
          70      80      90      100     110     120

          110     120     130     140     150     160
m215.pep  LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVVSFYQASHGQAGGMTYDHTGMLNFS
          |||||
a215      LTKTADGKRQAGKVEAEKLHVDTESQYAQTDTPVVSFYQASHGQAGGMTYDHTGMLNFS
          130     140     150     160     170     180

          170
m215.pep  SKVKATIIDTKDMX
          |||||
a215      SKVKATIIDTKDMX
          190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 757>:

g216.seq (partial)

```

1  ..atgatatcga tttcgagctc ggtacccagc gacgaaatca ccgccatcat
51  ccccgcactc aaacgcaaag acattaccct cgtctgcatc accgcccgcc
101 ccgattcaac catggcgcgc catgccgata tccacatcac cgcacggtt
151 tcgcaagaag cctgcccgtt ggggcttgcc ccgaccacca gcaccaccgc
201 cgttatggct ttgggcgacg cgttggcggt cgtcctgctg cgcgcccgcg
251 cgttcacgcc cgacgacttc gccttgatcc accctgccgg cagcctcggc
301 aaacgcctgc ttttgccgct tgccgacatt atgcacaaag gcggcgccct
351 gcccgccgct cgactcggca cgcccttgaa aggagccatc gtcagcatga
401 gcgagaaagg tttgggcatg tgggcgggaa cggacgggca aaggctgtct
451 gaaaggcctt tttactga

```

This corresponds to the amino acid sequence <SEQ ID 758; ORF 216.ng>:

g216.pep (partial)

```

1  ..MISISSVPS DEITAIIPAL KRKQITLVCI TARPSTMAR HADIIHITASV
51  SQEACPLGLA PTTSTTAVMA LGDALAVLL RARAFTPDDF ALIHPAGSLG
101 KRLLLRVADI MHKGGGLPAV RLGTPLKGA I VSMSEKGLGM WAGTDGQRLS
151 ERPFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 759>:

m216.seq

```

1  ATGGCAATGG CAGAAAACGG AAAATATCTC GACTGGGCAC GCGAAGTGTT
51  GCACGCCGAA GCGGAAGGCT TGCGCGAAAT TGCAGCGGAA TTGACAAAA
101 ACTTCGTCCT TGCGGCAGAC GCGTTGTTGC ACTGCAAGGG CAGGGTCGTT
151 ATCACGGGCA TGGTCAAGTC GGGACATATC GGGCGCAAAA TGGCGGCAAC
201 TATGGCCTCG ACCGGCACGC CTGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGCGA TTTGGGTATG ATTGTGGACA TCGACGTGGT CGTCGCGATT
301 TCCAATTCGG GCGAAAGCGA CGAAATCGCC GCCATCATCC CCGCACTCAA
351 ACGCAAAGAC ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TCATGGCTTT
501 GGGCGATGCG TTGGCGGTG TCCtGCTGCG CgcACGCGCG TTCACGCCCG
551 ACGATTTCGC CTTGAGCCAT CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGCGCCTGC CTGCCGTCGG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GGCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTTGCGCGC CCTGTTTCAA GAATGCGACA ATTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTG CTGGCGGCAC GGATGTGATA G

```

This corresponds to the amino acid sequence <SEQ ID 760; ORF 216>:

m216.pep

```

1  MAMAENGKYL DWAREVLHAE AEGLEIAAE LXKNFVLAA ALLHCKGRVV

```

```

51  ITGMVKS GHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDXDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN
301 GLLVTDADGV LIGALNMHDL LAARIV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 216 shows 91.8% identity over a 147 aa overlap with a predicted ORF (ORF 216.ng) from *N. gonorrhoeae*:

m216/g216

	70	80	90	100	110	120
m216.pep	TMASTGTPAFFVHPAEAAHGD LGMIVDXDVVVAISNSGESDEIAAIIPALKRKDITLVCI					
g216	MISISSVSPSDEITAIIPALKRKDITLVCI					
				10	20	30
	130	140	150	160	170	180
m216.pep	TARPDSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDF					
g216	TARPDSTMARHADIHITASVSQEACPLGLAPTTSTTAVMALGDALAVVLLRARAFTPDDF					
	40	50	60	70	80	90
	190	200	210	220	230	240
m216.pep	ALSHPAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKEAIVSMSEKGLGMLAVTDGQGR L					
g216	ALIH PAGSLGKRLLLRVADIMHKGGLPAVRLGTPLKG AIVSMSEKGLGMWAGTDGQR L S					
	100	110	120	130	140	150

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 761>:

a216.seq

```

1  ATGGCGATGG CAGGAAACGA AAAATATCTT GATTGGGCAC GCGAAGTGTT
51  GCACACCGAA GCGGAAGGCT TGCGCGAAAT TGCGGCGGAT TTGGACGAAA
101 ACTTCGCCCT TGCGGCGGAC GCGTTGTTGC ACTGCAAAGG CAGGGTCGTT
151 ATCACGGGCA TGGGCAAGTC GGGACATATC GGGCGCAAAA TGCGGCGAAC
201 CATGGCCTCG ACCGGCACGC CCGCGTTTTT CGTCCACCCT GCGGAAGCGG
251 CACACGGCGA TTGGGCGATG ATTGTGGACA ACGACGTGGT CGTCGCGATT
301 TCCAATTCGG GTGAAAGCGA CGAAATCGCC GCCATCATCC CCGCGCTCAA
351 ACGCAAAGAT ATCACGCTTG TCTGCATCAC CGCCCGCCCC GATTCAACCA
401 TGGCGCGCCA TGCCGACATC CACATCACGG CGTCGGTTTC CAAAGAAGCC
451 TGCCCGCTGG GGCTTGCCCC GACCACCAGC ACCACCGCCG TTATGGCTTT
501 GGGCGATGCG TTGGCGGTTG TCCTGCTGCG CGCCCGCGCG TTCACGCCCG
551 ACGACTTCGC CTTGAGCCAC CCTGCCGGCA GCCTCGGCAA ACGCCTACTT
601 TTGCGCGTTG CCGACATTAT GCACAAAGGC GCGCGCTGCG CTGCCGTCGG
651 ACTCGGCACG CCCTTGAAAG AAGCCATCGT CAGCATGAGT GAAAAAGGGC
701 TGGGCATGTT GCGGTAACG GACGGGCAAG GCCGTCTGAA AGGCGTATTC
751 ACCGACGGCG ATTGCGCGCG CCTGTTTCAA GAATGCGACA ATTTTACCGG
801 TCTTTCGATA GACGAAGTCA TGCATACGCA TCCTAAAACC ATCTCCGCCG
851 AACGTCTCGC CACCGAAGCC CTGAAAGTCA TGCAGGCAAA CCATGTGAAC
901 GGGCTTCTGG TTACCGATGC AGATGGCGTG CTGATCGGCG CGCTGAATAT
951 GCACGACCTT TTGGCGGCGC GGATTGTATA G

```

This corresponds to the amino acid sequence <SEQ ID 762; ORF 216.a>:

a216.pep

```

1  MAMAGNEKYL DWAREVLHTE AEGLREIAAD LDENFALAAD ALLHCKGRVV
51  ITGMGKSGHI GRKMAATMAS TGTPAFFVHP AEAHGD LGM IVDNDVVVAI
101 SNSGESDEIA AIIPALKRKD ITLVCITARP DSTMARHADI HITASVSKEA
151 CPLGLAP TTS TTAVMALGDA LAVVLLRARA FTPDDFALSH PAGSLGKRLL
201 LRVADIMHKG GGLPAVRLGT PLKEAIVSMS EKGLGMLAVT DGQGR LKGVF
251 TDGDLRRLFQ ECDNFTGLSI DEVMHTHPKT ISAERLATEA LKVMQANHVN

```

3 O1 GLLVTDADGV LIGALNMHDL LAARIV\*

m216/a216 97.2% identity in 326 aa overlap

m216.pép	10	20	30	40	50	60
	MAMAENGKYLDWAREVLHAEAEGLREIAAEELXKNFVLAADALLHCKGRVVITGMVKSCHI					
a216	MAMAGNEKYLDWAREVLHTEAEGLREIAADLDENFALAADALLHCKGRVVITGMGKSGHI					
	10	20	30	40	50	60
m216.pép	70	80	90	100	110	120
	GRKMAATMASTGTTPAFFVHPAEAAHGDLMIVDXDVVVAISNSGESDEIAAIIIPALKRKD					
a216	GRKMAATMASTGTTPAFFVHPAEAAHGDLMIVDNDVVVAISNSGESDEIAAIIIPALKRKD					
	70	80	90	100	110	120
m216.pép	130	140	150	160	170	180
	ITLVCITARPDPSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
a216	ITLVCITARPDPSTMARHADIHITASVSKEACPLGLAPTTSTTAVMALGDALAVVLLRARA					
	130	140	150	160	170	180
m216.pép	190	200	210	220	230	240
	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
a216	FTPDDFALSHPAGSLGKRLLLRVADIMHKGGGLPAVRLGTPLKEAIVSMSEKGLGMLAVT					
	190	200	210	220	230	240
m216.pép	250	260	270	280	290	300
	DGQGRLLKGVFTDGLRRLFQECNFTGLSIDEVMHHPKTI SAERLATEALKVMOANHVN					
a216	DGQGRLLKGVFTDGLRRLFQECNFTGLSIDEVMHHPKTI SAERLATEALKVMOANHVN					
	250	260	270	280	290	300
m216.pép	310	320				
	GLLVTDADGVLIGALNMHDLAARIVX					
a216	GLLVTDADGVLIGALNMHDLAARIVX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 763>:

g217.seq

```

1  atggcggatg acggtttgtt gcggaactg tccgaaaaac ccagccaaag
51  tgctctcttc ctgccatttg acccattcgt ttctcaggtt ttggactgcc
101 ttttggtcat cgggcccggc ttgaaacaat gtttcaagca aatcccggca
151 acgcgccacc cattcgccga ccgtcgcagg ttgccgcat atccgggcaa
201 tatccgacag gtttccgagg aaggcggcaa aacgtccgaa catggcgggt
251 tgattcacgt cggcatacca cgcgctgaca tcctgccaca tcgggttgcc
301 gccttcgggc agcatccagc ccaatatcat acggtctgcc gcctgcttcc
351 aggtaaacag ctgatccgtg ccgcccgcga tttctccgtc caatccccc
401 tggacgttca aatcggcaac catatcgtgc aaaagcggca aatcgtcccc
451 ggtcagtcgc aaacggcgca acacggcggc ggtttccaaa agcgcgagca
501 ctttgccgac ttcaaaacgg ctttccagca agtcggacac gcactccaac
551 gcataaaaaa acggttgccg gcggtcgatt ttcacgtccg aaacggaata
601 cggcaatgcc tgcgcgccgg gttgcgcctg tccgaacacg gcttccataa
651 aaggcgataa ggttcgataa ttcgggggta a

```

This corresponds to the amino acid sequence &lt;SEQ ID 764; ORF 217.ng&gt;:

g217.pép..

```

1  MADDGLLRQL SEKPSQSALF LPFDPFVFEV LDCLLVIGPG LKQCFKQIPA
51  TRHPFADRRR LPPYPGNIRQ GFEEGGKTSE HGGLIHVGIP RADILPHRVA
101 AFGQHQAQYH TVCRLLPGKQ LIRAAHFSV QSPMDVQIGN HIVQKRQIVP
151 GQSETAQHGR GFQKREHFAD FKTAQQVGH ALQRIKKRLP AADFHVNRGI

```

m217.seq

1	ATGGCGGATG	ACGGTGTGCG	GCGGCAACTG	TCCGGAAAAA	TGCGCCAATT
51	CGGTTTCCGC	CTTCCATTG	ACCCATTCTG	TTTCAAGGTT	TTGGAAGTAC
101	TTTTGTGCAT	CGGCTTCAGC	TTGGAACAAT	GTTTCAAGCA	AATCCCGGC
151	ACGCGCCACC	CATTGCGCGA	CGTTGCGGG	CTGCCGCCAT	ATCCGTACAA
201	TATCCGTCAG	GGTTTCGAGG	AAGGCGGCAA	AACGTCGGAA	CATGGCGGTT
251	TGATTACAGT	CGGCATACCA	CGCGCTGACA	TCCTGCCACA	TCCGATTGCC
301	GCCTTTGGCG	AGCATCCAGC	CCAAATATCAT	CGGTTCTACC	TGGTGCTTCC
351	AGGTGAACAG	CTGATCCGTG	CCGCCGCGCA	TTTCTCCGTC	CAAACCCAG
401	TGGACGTTCA	AATCGGCAAC	CATGTCGTGC	AAAAGCGGTA	AATCGTCTCT
451	AGTCAGTCCG	AAACGGCGCA	ACACGGGCGC	GGTTTCTAAA	AGCACAGCA
501	CTTTATCGAC	TTCAAATCGG	CTTTCCAACA	AGTCGAACAG	GCATGACAAA
551	GCATGAAACA	GCGGTTGGCG	GCGGCTGATT	TTCACGTCGT	ACACGGAATA
601	CGGCAATGCC	TGCGCAACGg	GctGCGCTG	TCCGAACACG	GCTTCGATAA
651	AAGGCGTATA	GGATTTCGATA	TTCCGGGTTA	A	

m217.pep

```

1  MADDGVRRL SGKLRQGFGR LPFDPFVFKV LDXLLVIGFS LEQCFKQIPA
51 TRHPFADRCG LPPYPYNIQ GFEEGGKTSE HGGLIHVGIP RADILPHRIA
101 AFGQHPAQYH AFYRLLPGE LIRAAAHFSV QTPVDVQIGN HVVQKRXLVL
151 SQSETAQHGR GFXXKHKFID FKSAQQOVEQ AXQSMKQRLA AADFHVXHGI
201 RQCLRTLGLR SHHGDKKRI GFDIRG*

```

**Homology with a predicted ORF from *N. gonorrhoeae***

m217/q217

		10	20	30	40	50	60
m217.pep		MADDGVRRLQSGKLRQGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHPPFADRCG					
		:     : : :     :     : :					
g217		MADDGLLRQLSEKPSQSALFLPFDPFVFEVLDCLLVIGPGLKQCFKQIPATRHPPFADRRR					
		10	20	30	40	50	60
		70	80	90	100	110	120
m217.pep		LPPYPYNIRQGFEEGGKTSEHGGLIHVGI PRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
		:     :					
g217		LPPYPGNIRQGFEEGGKTSEHGGLIHVGI PRADILPHRVA AFGQHPAQYHTVCRLLPGKQ					
		70	80	90	100	110	120
		130	140	150	160	170	180
m217.pep		LIRAAAHFSVQTPVDVQIGNHVQKRXIVLSQSETAQHGRGFXKHKHFIDFKSAFQVVEQ					
		: :     :        :     :     :					
g217		LIRAAAHFSVQSPMDVQIGNHIVQKRQIVPGQSETAQHGRGFGKREHFADFKTAFAQVQVGH					
		130	140	150	160	170	180
		190	200	210	220		
m217.pep		AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
		: :     :     :     :     :     :					
g217		ALQRIKKRLPAADFHVVRNGIRQCLRAGLRRLSEHGFKRRIGFDIRG					
		190	200	210	220		

a217.seq

1	GTGGCGGATG	ACGGTGTGCA	GCGGCAACTG	TCCGGAATAA	TGCGCCAATT
51	CGGTTTCCGC	CTGCCATTGT	ACCCATTTCG	TTTCGAGGCT	TTGACATGCC
101	TTTTGGTCAT	CGCCTTCGAC	TTGGAACAAT	GTTTCAAGCA	AATCCCGGCA
151	ACGCGCCACC	CATTTCGTC	CCGTCGCAGG	TTGCCGCCAT	ATCCGTACAA

501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGCGGGTT
251 TGGTTACAGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTCTTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TGC GCGCGCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTCGATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEEA LDCLLVIAFD LEQCFKQIPA
51 TRHPFVNRRR LPPYPYNIRQ GFEEGGKTSE QGGLVHVGIIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KKHFID FKSFAQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRRRI GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

m217.pep	10	20	30	40	50	60
	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHHPFADRCG					
a217	10	20	30	40	50	60
	VADDGVQRQLSGKLRQFGFRLPFDPFVFEEALDCLLVIAFDLEQCFKQIPATRHHPFVNRRR					
m217.pep	70	80	90	100	110	120
	LPPYPYNIRQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
a217	70	80	90	100	110	120
	LPPYPYNIRQGFEEGGKTSEQGGLVHVGIIPRADPLPHRIA AFGQHPAQYHAFYRLLPGEQ					
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQTPVDVQIGNHVVQKRQIVLSQSETAQHGRGFXKKHFIDFKSAFQQVEQ					
a217	130	140	150	160	170	180
	LIRAAAHFSVQTPADVQIGNHVVQKRQIVLSQSEMAQHGRGFXKKHFIDFKSAFQQVEQ					
m217.pep	190	200	210	220		
	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
a217	190	200	210	220		
	AXQSMKQRLSAADFHIRNGIRQCLRAGLRLSEHGFDKRRIGFDIRGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg.
51 caatcagggt tggatcaca ctatggatga aatccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttgaaa cggcagcttc actgaccatt
151 attatggttg tcagcggtt gtacctttgg tggcgaaac agcgcgcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tggtgccgga
251 atctgcacgg cgcgtttgga acttggtgtt cggtgatttt actgttggtc
301 tgcctgtcgg gtattgcttg ggcaggtatt tggggcgcca aatcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggggtgtcga ccgaaccccg
401 tttcaatcgt gccgaccac ggcgaggtat tgaatgacgg caaggtaag
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggacgac
501 tgtgggtgaa aacggcatta accccaccga gcccaataac attggaaacc
551 gtcgaccggt tcgcgcggga aatcggtttc aaagggcgtt atcagttgaa
601 tttgccaaa ggcgaggacg gggatggac tttgtcgac gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

51 IMVVSGLYLW WAKQRGIKAM LLPPKSRARS WWRNLHGAFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWN QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWILELMP MPVSGTTVGE NGINPTEPNN IGNRRPFRAF NRFRALSVE  
 201 FAQRRRGRMD FVAGFYEL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 771>:

m218.seq

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCGCGG  
 51 CAATCAGGGT TGGTATTACA CGATGGATGA AATCCACAGC GATATGATGC  
 101 TCGGTGCGGC AGGCGATTAT CTTTGGGAAA CGGCAGCTTC ACTGACCATT  
 151 ATTATGGTTG TCAGCGGCTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT  
 201 CAAGGCGATG CTGCTGCCGT CAAAAGGCAr GGC CGCTTCT TGGTGGCGGA  
 251 ATCTGCACGG CACGTTTGA ACTTGGGTGT CGTTGATTTT GCTGTGTTC  
 301 TGCTGTCCG GTATTGCTTG GCGGGTATT TGGGGCGGCA AGTTCGTACA  
 351 GGCTTGGAGT CAGTTCCTG CCGGTAAATG GGGTGTGAA CCGAACCCCG  
 401 TTTCAGTCGT GCCGACCCAC GCGAGGTAT TGAATGACGG CAAGTTAAG  
 451 GAAGTGCCGT GGGTTTGA GCTTACGCCT ATGCCTGTTT CAGGGACGac  
 501 yGtgGGCAA GACGGCATT ACCCTGACGA GCCGATGACA TTGGAAACCG  
 551 TCGACCGCTT TCGCGGnGA AATCGGTTT AAAGGGCGTT ATCAGTTGAA  
 601 TTTGCCCAA GCGAGGACG GCGTATGGAC TTTGTGCGAG GATTCTATGA  
 651 GTTA

This corresponds to the amino acid sequence <SEQ ID 772; ORF 218>:

m218.pep

1 MVAVDPYTAK VVSTMPRNQG WYYTMDIHS DMMLGAAGDY LLETAASLTI  
 51 IMVVSGLYLW WVKRRGIKAM LLPSKGXARS WWRNLHGTFG TWVSLILLLF  
 101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSIVPTH GEVLNDGKVK  
 151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFRALSVE  
 201 FAQRRRRMD FVAGFYEL

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 218 shows 87.2% identity over a 218 aa overlap with a predicted ORF (ORF 218.ng) from *N. gonorrhoeae*:

m218/g218

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQG WYYTMDIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
g218	MVAVDPYTAKVVNTMPRNQG WYHTMDIHS DMMLGAAGDY LLETAASLTI IMVVSGLYLW					
	10	20	30	40	50	60
70	80	90	100	110	120	
m218.pep	WVKRRGIKAMLLPSKGXARS WWRNLHGTFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWS					
g218	WAKQRGIKAMLLPPKSRARS WWRNLHGAFGTWVSLILLLFCLSGIAWAGIWGGKFVQAWN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m218.pep	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVPEPWVLELTPMPVSGTTVGK DGINPDEPMT					
g218	QFPAGKWGVEPNPVSIVPTHGEVLNDGKVKVPEPWILELMPMPVSGTTVGE NGINPTEPNN					
	130	140	150	160	170	180
	190	200	210			
m218.pep	LETVDRFARXNRFRALSVEFAQRRRGRMD FVAGFYEL					
g218	IGNRRPFRAFNRFRALSVEFAQRRRGRMD FVAGFYEL					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 773>:

## a218.seq

```

1   ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCCGC
51  CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGC CGCGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CCGGTTTGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTT
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCCGG CAGGCAAATG GGGTGTGCGA CCGAACCTG
401 TTTCAGTCGT GCCGACCCAC GGCAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAAACCG
551 TCGACCGTTT TCGCGG.GA AATCGGTTT AAAGGCGGT ATCAGCTGAA
601 TTTGCCCAAA GCGGAGGACG GCGTATGGAC TTGTGCGCAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

## a218.pep

```

1   MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51  IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRRQALSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

	10	20	30	40	50	60
m218.pep	MVAVDPYTAKVVSTMPRNQGWYYTMD	DEIHS	DMMLGAAGDYL	LLETAASLTI	IMVVSGLYLW	
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDYL	LLETAASLTI	IMIISGLYLW		
	10	20	30	40	50	60
m218.pep	WVKRRGIKAMLLPSK	SGXARS	WWRNLHGT	FGTWVSLILLF	FCLSGIAWAGI	WGGKFVQAWS
a218	WVKRRGIKAMLLPPKGRARS	WWRNLHGA	FGTWVSLILLF	FCLSGIAWAGI	WGGKFVQAWS	
	70	80	90	100	110	120
m218.pep	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVK	KEVPWVLELTP	MPVSGTTVGK	DGINPDEPMT		
a218	QFPAGKWGVEPNPVSVVPTHGEVLNDGKVK	KEVPWVLELTP	MPVSGTTVGK	DGINPDEPMT		
	130	140	150	160	170	180
m218.pep	LETVDRFARXNRRQAL	SVEFAQRRGRMD	FVAGFYEL			
a218	LETVDRFARXNRRQAL	SAEFAQRRGRMD	FVAGFYEL			
	190	200	210			



1	atgacggcaa	ggttaaggaa	gtgccgtgga	ttttggagct	tatgcctatg
51	cctgtctcag	ggacgactgt	gggtgaaaac	ggcattaacc	ccaccgagcc
101	caataacatt	ggaaaaccgtc	gaccgtttcg	cgcgggaaat	cggtttcaaa
151	gggcgttatc	agttgaattt	gcccaaaggc	gaggacgggg	tatggacttt
201	gtcgcaggat	tctatgagtt	atgacatgat	cagcccggtt	gccgacgcga
251	cggtacatat	cgaccagtcg	agcggcgaga	tctctgcgga	catccgtttt
301	gacgattaca	acccgttcgg	caaatttatg	gcggcaagca	ttgcgtctga
351	<u>tatggggact</u>	ttgggctggg	ggagcgtgtt	ggcgaacgct	gtgttctgcc
401	ttgccgtgat	ttttatcggc	atcagcggct	gcgtgatgtg	gtggaaaacgc
451	cgtcgcgtcg	gcgtggcggg	cattgttcct	ccggcgcaaa	aaatcaaaact
501	gcccgtctcg	tgggcgatag	cattgcgcgt	gtgtgtgat	gcactgcttt
551	tcccgacccg	ggctctgtgc	attgccgtga	tttgctgtgt	ggataccttg
601	ctgcgtctcg	ggattcctgt	gttagcgtaaa	tggtttaaat	ga

1	MTARLRKCRG	FWSLCLCLSQ	GRLVVKTALT	PPSPITLETV	DRFAREIGFK
51	GRYQLNLPKG	EDGVWTLSQD	SMSYDMISPF	ADRTVHIDQY	SGEILADIRF
101	DDYNPFGKFM	AASIALHMG	LGWWSVLNV	VFCLAVIFIG	ISGCVMMWKR
151	RPSGVAGIVP	PAQIKLPVW	WAMALPILLI	ALLFPTALLA	IAVIWLLDTL
201	LLSRIPVLRK	WFK*			

1	ATGACGGCAA	GGTTAAGGAA	GTGCCGTGGG	TTTTGGAGCT	TACGCCTATG
51	CCTGTTTCAG	GGACGaCyGt	gGGCAAGAGC	GGCATTAAAC	CTGACGAGCC
101	GATGACATTG	GAACCCGTGC	ACCCGCTTTG	GCGGnGAAAT	CGGTTTCAA
151	GGGCGTTATC	AGTTGAATTG	GCCCAAAGGC	GAGGACGGCG	TATGGACTTT
201	GTCGCAGGAT	TCTATGAGTT	ACGACATGAT	CAGCCCGTTT	GCCGACCGCA
251	CGGTACATAT	CGACCAGTAC	AGCGGCAAAA	TCCTTGCCGA	CATCCGTTTT
301	GACGATTACA	ACCCGTTCCG	CAAATTTATG	GCGGCAAGCA	TTGCGCTGCA
351	TATGGGGACT	CTGGGCTGGT	GGAGCGTGTT	GGCGAAGCTC	TTGTTCTGCC
401	TTGCCGTCAT	TTTTATCGGT	ATCAGCGCGT	GCGTGATGTG	GTGGAAACGC
451	CGTCCGACCG	GAGCGGTGGG	CATCGTTCCG	CCGGCGCAGA	AAGTCAAGCT
501	GCCGGTTTGG	TGGATGATGT	CATTGCCCGT	ATTGGCAATC	GCACTGCTCT
551	TCCCGATTCG	ACTGCTTGCC	ATTGCCGTGA	TTTGGCTGTT	GGATACGCTG
601	CTGTTTGTCG	GGATTCTCTG	TTTGAGGAGA	TGGTTTAAAT	GA

1	MTARLRKCRG	FWSLRRLCLFQ	GRXWAKTALT	LTSRXHWKPS	TALRGEIGFK
51	GRYQLNLPGK	EDGVWTLSDQ	SMSYDMISFF	ADRTVHIDQY	SGKILADIRF
101	DDYNPFGKIV	AASIALHMGF	LGWWSVLAVN	<u>LFCLAVIFIG</u>	ISGCVMMWKR
151	RPTGAVGIVP	PQAKVKLPVW	WMMALPLLA	<u>ALLFPTSLA</u>	IAVIWLLDTL
201	LLSRIPVLR	WFK*			

m219/g219

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSRLCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	:       : :					
g219	MTARLRKCRGFWSRLCLCLSQGLRWVKTALTPPSPITLETVDRFAREIGFKGRYQLNLPKG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLTSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG					
	:					
g219	EDGVWTLTSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG					

505

	70	80	90	100	110	120
m219.pep	130	140	150	160	170	180
	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	:     :     :     :     :					
g219	130	140	150	160	170	180
	LGWWSVLANVVFCLAVIFIGISGCVMMWKRRPSGVAGIVPPAQKIKLPVWWAMALEPLLLI					
	130	140	150	160	170	180
m219.pep	190	200	210			
	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	:     :     :					
g219	190	200	210			
	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTTC GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCACTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTT GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCCTGT TTTGAGGAGA TGGTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMMWKR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRW WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRGFWSLRCLFQGRXWAKTALTLSRXHWKPSTALRGEIGFKGRYQLNLPKG					
	:     :     :     :     :					
a219	MTARLRKCRGFWSLRCLFQGRWAKTVLTLSRXHWKPSTVLRXEIGFKGRYQLNLPKG					
	10	20	30	40	50	60
m219.pep	70	80	90	100	110	120
	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKEMAASIALHMG					
	:     :     :     :     :					
a219	EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKEMAASIALHMG					
	70	80	90	100	110	120
m219.pep	130	140	150	160	170	180
	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPTGAVGIVPPAQKVLPVWMMALPLLAI					
	:     :     :     :     :					
a219	LGWWSVLANVLFCLAVIFIGISGCVMMWKRRPSGAVGMVPPAQKIKLPVWWAMAVPLLLI					
	130	140	150	160	170	180
m219.pep	190	200	210			
	ALLFPTSLLAIAVIWLLDTLLLSRIPVLRWFKX					
	:     :     :					
a219	ALLFPTALLAIAVIWLLDTLLLSRIPVLRWFKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaaac adatcgacgc tgacggattt gaaccctgcc
101 tcacggggcg catcgatgac ttctttggtt tcttcgtagc tttggatgcg
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgctca
201 tgcggttgaa gccgagtctg ccgagcatga ggacggtgtc gcggctgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgccg aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcggcg cggcctttgt ctttggatg gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcgg
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHFFFKIFDV
151 GIGAAFVFGD DFVAAAVVAD GVAKRNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACCTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCCG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC
301 ACGTTCGATC TGTTTCGTCG TCAAAAAGGt GCGTGCCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCATT
401 TCTTTTTCAA GATATTCGAT GTAGGCATCG GCGCGGCTTT TGTCTTTGGT
451 GATGATTTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGAAAAGC GGTTTGTTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHFFFKIFD VGIGAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE				
	: :                :				
g221	MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAHYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGI FAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

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m221.pep CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK  
 |||||  
 g221 AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK  
 130 140 150 160 170 180

m221.pep GKRFBVX  
 |||||  
 g221 GKRFBVX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

a221.seq  
 1 ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT  
 51 CGACGCTGAC GGATTGTAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT  
 101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG  
 151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA  
 201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG  
 251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TGCGGAAGAC  
 301 ACGTTCGATT TGGTCGTCGC TCAAAAAGGT CGGCGTGCCG CCGCCGAAGT  
 351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC  
 401 ATTTCTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT  
 451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG  
 501 GAATGTGAAT GTAAAGGGAA AGCGGTTTGT TTAA

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

a221.pep  
 1 MVLMLRSLV RQAVNQIDAD GFEPFARRI DDFGFFVTL DAVDRRLHFG  
 51 VEILNADHA VEAESAHEH GVAADFARVD FDGVFAGGD\* LEMFAYHAED  
 101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMW S EQFHFFFKF DVGIGAAAFV  
 151 GDDFVAAAVV ADGVAERNVN VKGKRFV\*

m221/a221 95.5% identity in 177 aa overlap

	10	20	30	40	50	60
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFARRIDDFGFFVTLDAVDRRLHFGVEILNADHA					
a221	MVLMLRSLVRQAVNQIDADGFEPFARRIDDFGFFVTLDAVDRRLHFGVEILNADHA					
	10	20	30	40	50	60
m221.pep	VEAESAHEHGDVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGA-CPAEVQLG					
a221	VEAESAHEHGDVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGRRAAAEVQLG					
	70	80	90	100	110	120
m221.pep	KLVPVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFBVX					
a221	KLVPVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFBVX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

g223.seq  
 1 atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca  
 51 ttctgatggc gaattggtct ttgttgccgc ggcaccagttg gaagaattgt  
 101 tccaaaggca ggttttggct atcgaagccg aaacggcgcg gaatcgcgcc  
 151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta  
 201 cagcaacgta atcagcgta ggagcagctt ggtgtttcca gtttttctcg  
 251 cgcaggtctt tggcaacgta gagcagctct tgttactga tctcttgcg  
 301 ccagtatttt tcttggcgca atttcaattc acggaaggcg ccgacacgcy  
 351 ggaagcctga

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

1 MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA  
 51 RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA  
 101 PVFFLGEFQF TEGADTREAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

m223.seq  
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTGCAAC CATTGCGTCA  
 51 TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT  
 101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC  
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC  
 201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTCCAG TTTTCTCGC  
 251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC  
 301 CAGTATTTTT CTTGTGCGAA TTCAATTCTG CGGAAGGCGC CGACACGCGG  
 351 GAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

m223.pep  
 1 VEFRHQVVVV GVEPFGHFDG ELVFVTARQL EELFQRQVLA VEAAGGNRA  
 51 GGDQVEDV VESEIXYNE IGVGSDLVFP VFLAQVFSNS QQFLADFFA  
 101 PVFFLGEFQF AEGADTREAA\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

m223/g223

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLA VEAAGGNRAGGDQVEDV					
g223	MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLA IEAETGGNRARGYLQVEDVM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYNEIGVGSDLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX					
g223	VESEITYSNVISVRSSLVFPVFLAQVFGNV EQLLFTDLFAPVFFLGEFQFTEGADTREAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

a223.seq  
 1 GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTGCAAC CATTGCGTCA  
 51 TTTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT  
 101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC  
 151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA  
 201 CGCAACGTA ATCGGCGTTG GCAGCGCCTT GGTGTTTCCA GTTTTCTCG  
 251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG  
 301 CCAGTATTTT TCTGTGCGA ATTTCAATTC GCGGAAGGCA CCGACACGCG  
 351 GGAAGCCTGA

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

a223.pep  
 1 VEFRHQVVVV GVEPFGHFDG ELVFVTARQL EELFQR\*VLA VEAAGGNRA  
 51 GGDQVEDV VESEIAYGNV IGVGSLVFP VFLAQVFSNS QQFLADFFA  
 101 PVFFLGEFQF AEGDTREAA\*

m223/a223 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
m223.pep	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLA VEAAGGNRAGGDQVEDV					
a223	VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRXVLA VEAAGGNRAGGDQVEDV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m223.pep	VESEIXYNEIGVGSDLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX					
a223	VESEIAYGNVIGVGSLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGDTREAX					



510

	10	20	30	40	50	60
m225.pep	60	70	80	90	100	110
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA					
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA					
				70	80	90
m225.pep	120	130	140	150	160	170
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225	DKLIGSAMRLGLIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225.pep	180	190	200	210	220	230
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225.pep	240	249				
	VKKN DPSRFLNX					
g225	VKKN DPSRFLN					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 797>:

```

a225.seq
1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCGGCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGCGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACCTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCGCCC GCGCGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCTT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGATGG GTACGCCGGT TGCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTGCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTTCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 798; ORF 225.a>:

```

a225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQPVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQPVLPVN RVPARRAGNA DELIGNAMGL NEQPVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR S ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKN DPSRFLN *

```

m225/a225 87.4% identity in 277 aa overlap

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG				
a225	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG				
	10	20	30	40	50
m225.pep	60	70	79	80	
	NADELIGSAMGLNEQPVLPVNR-----VPARRAGNA				

```

a225      |||||
          NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
              70          80          90          100          110          120

          90          100          110          120          130          140
m225.pep  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSVSTGFDCSGF
          |||||
a225      DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAIYRYGGTSISTGFDCSGF
              130          140          150          160          170          180

          150          160          170          180          190          200
m225.pep  MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
          |||||
a225      MQHIFKRAMGINLPRTSAEQARMGTFVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
              190          200          210          220          230          240

          210          220          230          240          249
m225.pep  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSPRFLNX
          |||||
a225      IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSPRFLNX
              250          260          270          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

**g225-1.seq**

1	atggattctt	ttttcaaacc	ggcagtttgg	gcggttttgt	ggctgatgtt
51	tgcgcgtcgc	cccgcgcctg	ccgacgaagt	gaccaaacctg	ctcagcagcc
101	gcgagcagat	tctcagacag	tttgcggaag	acgaacacctg	cgttttacc
151	gtcaaccgag	ccccgcggcg	gcggggcgggc	aatgcgcgacg	aactcatcgg
201	cggcgcgcat	gggcttaacg	aacagcccgt	tgtacgcgtc	aaccgagccn
251	ccgcgcggcg	ggcggggcaat	gcgcgacaaac	tcatcgcgcag	cgcgatcggg
301	cttttgggta	tgtcctaccg	ctacgcggcgc	acatcgtgtg	ctccggttt
351	tgaactgcagc	ggattcatgc	agcacatctt	caaacgcgcgc	atgggcatca
401	acctgcgcgc	cacgtcggcg	gaacagggcgc	ggatgggcgc	accggttgcg
451	cgaagcgcaat	tgcagcccg	ggatatggtg	tttttcgcga	cgctcggcgc
501	cagccgcgat	tcccatgtcg	gactttatat	cgccaacaac	gcgttcctcc
551	acgcgcgcgc	cacggggaaa	aatatcgaaa	tcaccagcct	gagccacaaa
601	tattggagcg	cgaaatatgc	gttcgcccgc	cgggtcaaga	aaaacgacct
651	gtccagcttt	ctgaactga			

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pap

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51 VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYRG TSVSTGFDSC GFMQHLYFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV PFRTLGGDSRI LN*GLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNDSPRF SHV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

**m225-1.seq**

1	ATGGATTCTT	TTTTCAAACC	GGCAGTTTGG	GCGGTTTTGT	GGCTGATGTT
51	TGCCGTCGCG	CCCGCCCTTG	CGACAGAGTT	GACCAACyTG	CTCAGCAGCC
101	GCGAGCAGAT	TCTCAGACAG	TTTGCAGAAG	ACGAACACGCC	CGTTTATCCC
151	ATCAACCGAG	CCCGCGCCCG	CGGGCGGGCG	AATGCCGACG	ACATCATCGG
201	CAGCGCGATG	GGGCTTAAAC	AACAGCCCGT	TTTACCCGTC	AACCGAGTCC
251	CCGCCCCGCG	GGCGGGCAAT	GCGCAAGCAAC	TCATCGGCAA	CGCGATGGGG
301	CTTAAACGAAC	AGCCGTTTAT	ACCCGTCAAC	CGAGCCCCCG	CCGGCGGGCG
351	GTCGCAATGCC	CGCGAACTCA	TGCGCAACGC	GATGGGACTT	TTGGGTATTG
401	CCTACCGCTA	CGGCGGCACA	TCGGTTTCTA	C CGGTTTTGA	CTGCAGCGGC
451	TTCATGCAGC	ACATCTTTCAA	AGCGCGCATG	GGCATCAACC	TGCGCGGCAC
501	TCGCGCGAGA	CAGGCACCTGA	TGGGTACGCC	GGTGCCCCGA	AGCGAATTGC
551	AGCCCCGAGAA	TATGTGTGTT	TTCCGACAGC	TCGCGCGCAG	CGCGATTCCC
601	CATGTCCGAC	TTTATATCGG	CAACAACCGC	TTCATCCACG	CGCGCGGCAC
651	GGGGAAAAAT	ATCGAAATCA	CCAGCCTGAG	CCACAAATAT	TGGAGCGGCA
701	AATACGCGTT	CGCCCGCCCG	GTCAAGAAAA	ACGACCCGTC	CCGCTTTCGT
751	AACTGA				



This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQVLPV NRVPARRAGN ADELIGNAMG
101 LNEQVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

	10	20	30	40	50	60
m225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
g225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPVNRAPARRAG					
	10	20	30	40	50	60
m225-1.pep	NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA					
g225-1	NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA					
	70	80	90	100	110	120
m225-1.pep	DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR					
g225-1	DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR					
	100	110	120	130	140	150
m225-1.pep	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR					
g225-1	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR					
	160	170	180	190	200	210
m225-1.pep	VKKNDPSRFLNX					
g225-1	VKKNDPSRFLNX					
	250					
m225-1.pep	VKKNDPSRFLNX					
g225-1	VKKNDPSRFLNX					
	220					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCGCG CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTGCGGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCC CGCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGCGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCGC CCCGGCGGGC
351 GGGCAATGCC GACGAACTCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CCGCACATCG ATTTCTACCG GTTTGACTG CAGCGGCTTC ATGCAGACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGNTTTC CGCACGCTCG GCGGCAGCCG CATTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGCGTTCGC
801 CCGCCGGGTC AAGAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXFARRAG NADELIGSAM GLNEQVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQVLPVN RVPARRAGNA DELIGNAMGL NEQVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAIYRYGGTS ISTGFDCSGF MQHIFKRAM INLPRTSAEQ
201 ARMGTPVARS ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNNDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWVWLMPFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWVWLMPFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA					
	70	80	90			
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSABQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSABQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLNX					
m225-1	IHAPRTGKNIETSLSHKYWSGKYAFARRVKKNDPSRFLNX					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1   ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggtcgg
351 gccggatacc caattctcct tcccgctcgt tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccgcca
451 tttctgttgc ctccgctct cctgcgcgcg ctcggccgcg atacattgcy
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Cggggcctcg cccctccct cttataa

```

This corresponds to the amino acid sequence &lt;SEQ ID 806; ORF 226.ng&gt;:

g226.pep

```

1   MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFRLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIIVTGM YFAAWLGPDY QFSFPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLR LGPHTLRRFT ILPKLRPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1   ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTGCGGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCC TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

5 01 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG  
 5 51 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC  
 6 01 CGTATGGCGG CACACGCGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 6 51 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep

1 MNEILRQPSV LLFLTAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
g226	MSEILRQPSVLLFLTAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSOLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
g226	QFSFPPRLQYLLFTPSGIPHTLYARVLPFPFLPPPLPRLGPHTLRRFTILPKKLRFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq

1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC  
 51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT  
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC  
 151 CTCGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT  
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC  
 251 GCCGTAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTGCG  
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG  
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC  
 401 CTATCGCCAT CGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC  
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA  
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG  
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC  
 601 CGCATGGCGG CACACGCGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC  
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep

1 MNEILRQPSI LLFLTAVYA LAIVRTRTG NIFCNPVLVS TIVLIAYLKI  
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSOLA  
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT  
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR  
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF \*

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

m226. pep	MNEILRQPSVLLFLT	LAVYALAIIV	VRTRTGNIF	FCNPVLVST	IVLIAYLKIL	GIDYAVYHN
a226	MNEILRQPSILLFLT	LAVYALAIIV	VRTRTGNIF	FCNPVLVST	IVLIAYLKIL	GIDYAVYHN
	10	20	30	40	50	60
m226. pep	AAQFIDFWLKP	AVVVLAVPLY	QNRKIFNQ	WL	LPVIVSQL	AGSVTGIVT
a226	AAQFIDFWLKP	AVVVLAVPLY	QNRKIFNQ	WL	LPVIVSQL	AGSVTGIVT
	70	80	90	100	110	120
m226. pep	GMFYAKWLGA	ER				
a226	GMFYAKWLGA	ER				
	70	80	90	100	110	120
m226. pep	EVVLSLASKSV	TNP	IAIEITRS	IGGIPAITA	ATVIIAGLV	GQIAGYKML
a226	EVVLSLASKSV	TNP	IAIEITRS	IGGIPAITA	ATVIIAGLV	GQIAGYKML
	130	140	150	160	170	180
m226. pep	KNTVMPSSVG					
a226	KNTVMPSSVG					
	130	140	150	160	170	180
m226. pep	MSLGTASHAM	GIAASLERS	RRMAAYAG	LGLTFNGV	L	TAL
a226	MSLGTASHAM	GIAASLERS	RRMAAYAG	LGLTFNGV	L	TAL
	190	200	210	220	230	
m226. pep	LIAPLLIPV	L	GF			
a226	LIAPLLIPV	L	GF			
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```
g227.seq
1  atgaacatca tccgcgcgct cctcatcatc ctcggtcgcc tcgccgccgg
51  cgaaacgccg gttttcctag cagggcatcaa actgcccggc agcatcgctg
101 gcatgggcgt gctggtttgc cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttctt
201 cgtgccgccc tgctgtggcg tcactagcta tttggattgt attgcgcagc
251 attggttttc gactactggt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgtggata ccagcatta tctqa
```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

g227.pap  
1 MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLF A LLQAGWLKTS  
51 WLQQLTDALM ANLTFLVPP CVAVISYDL IADWFSILV SASASTLCVL  
101 LVTGKVHRWI RSII\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```
m227.seq      (partial)
1      . ACGTCTTtKGC TGCAACAGCT TACCGACGCG CTGATgTCGA ACCTGACGCT
51     GTtCCTCTGTCG CCgCC. TGCG TGGCGGTAT CAGCTATTtTG GATTtGATTG
101    CCGACGATTG GTtTTTCGATA CTGGtTTTCG CCTCCGCCAG cACTTTGTGC
151    GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201    ATGA
```

**This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:**

```
m227.pep (partial)
1  ..TSXLQQLTDA LSMNLTLFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51 VLLVTGKVHR WIRGIIR*
```

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

m227/g227

```

                                10      20      30
m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
                || |||||:||:|||||:|||||
g227      TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
            20      30      40      50      60      70
                40      50      60

```

516

```

m227.pép    DLIADDWFSILVSASASTLCVLLVTGKVRWIRGIIRX
            |||||
g227        DLIADDWFSILVSASASTLCVLLVTGKVRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGGC CTTTTCAGG CGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TGGCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATGGGTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATTA TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pép
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLOAGWVKTS
51 WLQQLTDALM ANLTFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pép                                10      20      30
                                TSXLQQLTDALMSNLTFLVPPCVAVISYL
                                || |||||
a227        TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTFLVPPCVAVISYL
            20      30      40      50      60      70

m227.pép    DLIADDWFSILVSASASTLCVLLVTGKVRWIRGIIRX
            |||||
a227        DLIADDWFSILVSASASTLCVLLVTGKVRWIRSIIX
            80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pép
1  MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTTCGCAAGAA GCCAAACAGG AGGTTAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

a228.pep  
 1 MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA  
 51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD  
 101 KMKDAAK\*

m228/a228 100.0% identity in 107 aa overlap

	10	20	30	40	50	60
m228.pep	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
a228	MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD					
	10	20	30	40	50	60
	70	80	90	100		
m228.pep	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
a228	AAADAKASAEAEVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

g229.seq  
 1 atggctgccc tatcgggcgg cggtgcggtc ttcctgataa tgcttcacac  
 51 tattgcccgc gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag  
 101 aaatcgccat tgaagccgcc ggcgaaattg tatcggtgcg cgcccaagag  
 151 gttttgcccc acaaacggca cggtgccgaa cgagcgcgtt accgaacggt  
 201 tttgatggcc gaacgacagg cgcaggttct gttcgtgaa atctttgtta  
 251 tcccaataat gcacgcccgc gctgatgccg ccgtagagga aatgatgccc  
 301 gcccgccattg atttcgcgcg acacgcccac gccgtagcgc aaaccgtgtg  
 351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat  
 401 tcaatcgttt ttcggacga agcgttggtt atagcggatt aacaaaaatc  
 451 aggacaaggc ggcggggcgc aggcagtagc gatggtacgg aaccggttcg  
 501 cccggtgctt ggacgcctta gggaaccgtt ccctttgagc cggggcgggg  
 551 caaccgtac cggtttttgt tcatccgcca tattgtgttg a

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

g229.pep  
 1 MAAVSGGGAV FLIMLPFIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAQAE  
 51 VLPDKRHGAE RARYRTVLMA ERQAQVLFAR IFVIPIMHAA ADAAVEEMMP  
 101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKI  
 151 RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

m229.seq (partial)  
 1 ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC  
 51 GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG  
 101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC  
 151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC  
 201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG  
 251 CCCTAGCGCA AACCCTGTGC CTTTTCGCGC AGGCTGTTCG CGGTTTTTCGT  
 301 CCAGCTTCTG CCGCAAATT CAATCGTTTT TTCGGACGAA GCGTTGTTTA  
 351 TAGCGGATTA AAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA  
 401 AATAGTACGG AACCATTCA CTGGTGCTT CAGCACCTTA GAGAATCGTT  
 451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

m229.pep (partial)  
 1 ..AQALGEIGIE AADEIVSAAA KEVLLDKRHD AERARYRTVF IAERQAQALF  
 51 AEIFVIPIMH AAAADAAYEE MPMARIDFAR HAXALAQTVC LLRQAVGGFR  
 101 PASARKFNRF FGRSVVYSGT TKIRTRQRSA DSTNSTEPIH LVLQHLRESR  
 151 SLFCSSAILC \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

m229.pep				10	20	30
				AQALGEIGIEAADEIVSAAAXEVL	LDKRHDAE	
g229	MAAVSGGGAVFLIMLPHIARVQRPPAF	QAASGEIGIEAAAGEIVSAAAEVL	PKRHGAE			
	10	20	30	40	50	60
m229.pep	40	50	60	70	80	90
	RARYRTVFIAERQAQALFAE	IFVPIPMHAAAADA	AVEEMMPARIDFARHAXALA	QTVCLL		
g229	RARYRTVLMARQAQVLF	AEIFVPIPMHAAA-DA	AVEEMMPARIDFARHAQ	AVAQTVCLL		
	70	80	90	100	110	
m229.pep	100	110	120	130	140	
	RQAVGGFRPASARKFN	RFFGRSVVYSGLTKIR	TRQRSADSTNSTEPIHL	VLQHLRE----		
g229	RQAVGGFRPASARKFN	RFFGRSVVYSGLTKIR	TRRRAGSTDGT	EPVLPVLRGLREPFPL		
	120	130	140	150	160	170
m229.pep	150	160				
	-----S	RS	LCSSAILCX			
g229	SRGGATRTG	FCSSAILC				
	180	190				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

a229.seq (partial)

```

1  ATGGCTGTCG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51  TATTGCCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCGTGA
401 AATTCAATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTTCAGCACC TTAGAGAATC GTCTCTTTGA GCTAAGGCCA
551 GGCAACGCCG TACTGGTTTT TGTCATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

a229.pep (partial)

```

1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51  VLLDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADVSEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTK
151 ITRRRRSADS TDSTEPHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

m229.pep				10	20	30
				AQALGEIGIEAADEIVSAAAXEVL	LDKRHDAE	
a229	MAVVSGGGAVFLITLPHIAHVQRQPPX	FAQASGEIGIEAADEIVSAAAXEVL	LDKRHDAE			
	10	20	30	40	50	60
m229.pep	40	50	60	70	80	90
	RARYRTVFIAERQAQALFAE	IFVPIPMHAAAADA	AVEEMMPARIDFARHAXALA	QTVCLL		
a229	XARYXTVFIAERQAQALFAE	IFVILIVHAAAADVSEEMMPARIDFARHAQ	AVAQTVCLL			
	70	80	90	100	110	120

	100	110	120	130	140	149
m229.pcp	RQAVGGFRPASARKFNRRFFGRSVVYSGLTkIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTkIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pcp	-----RSLFCSSAILCX					
a229	AKARQRRTGFCSSSTI					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccatcgaaaa atacagaaca cccgcccag tcttattagg
51  cctgattgca ttaacttttg tcggcttcgg cgtcagcacg gtttcccatc
101 cgggcgcgca ctacatcgtc caagtggcg acgaaaaaat cagcgagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 gcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccgaatt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag ttgctctgca agaatttggg aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggtc aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgcccc agtcaaaagc tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tgggaatatgt
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgcttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaagaa aagctgggag
851 acgatgcgtt caatcatccc tcctcgcttg ccgaagccgc caaaaacagc
901 gggttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaac acctaataca tgccgtattc agcgacgagc
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaacc
1051 gcgtgggtcg tccgcgcaa agaagtcgcg gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tgcgtcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pcp
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSEIQKM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHME DQFVEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFPN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCC.GACGCG GTGTTCGAAT CCCTGCTGCA ACGCGCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC

```



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```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCCGA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCAATTGAA GAGCGCGTGG CGCGTTTGCC GGCAAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGC.GT CAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 CGGTGGGTGC TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

m230.pep (partial)

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPPSPDA VFQSLQRAY LKQGAALMGI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFPY
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRAKEVR EEKTLPPAEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPPSPDAVFQSLQRAYLKQGAALMGISVSSEIQKIIVDDPNFHDAANGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAALMGISVSSEIQKQIMVDDPNFHDAANGKFSHALLS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m230.pep	RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
g230	QYLSQRHMSDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRTIRSHTFN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m230.pep	PDEFIAQVKVSEADLQKFPYNANKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFPYNANKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m230.pep	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m23 0.pep	GLKVVETQETWLSRQDAQMSGMPENLINA VFSDDVLKKKHNSVLTINSETAWVVRKEVR					
g23 0	GLKVVETQETWLSRQDAQMSGMPENLINA VFSDDVLKKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m23 0.pep	EEKTLPF AEAKDAVRQAYIRTEAAKL					
g23 0	EEKNLLFEEAKDAVRQAYIRTEAAKLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a23 0.seq (partial)	
1	ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51	CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101	CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151	TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201	GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251	GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301	ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351	GCTTTTAAAC CGCTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401	TCAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451	CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501	GACGCAGGTC AACCGCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAAT
551	TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601	GCAAACAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651	CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701	AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAATGAA
751	GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801	AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851	ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901	GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951	AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001	TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051	GCGTGGGTCTG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101	TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151	CCAAACTT

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a23 0.pep (partial)	
1	MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51	SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGA LMG I SVSSEQIKQI
101	IVDDPNFHDA NGKFDHALLN RYLSQRH MSE DQFVEEIRDQ FALQNLVNLV
151	QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201	ANKKDYL LFK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251	AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGD DAFNHP SSLAEAAKNS
301	GLKVETQETW LSRQDAQMSG MPENLINA V SDDVLKKKH NSVLTINSET
351	AWVVRKEVR EEKTLPF AEAKDAVRQAYIR TEAAKL

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m23 0.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a23 0	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m23 0.pep	ADGGGPSRDAVFQSLQRAYLKQGA LMG ISVSSEQIKQIIVDDPNFH DANGKFDHALLN					
a23 0	ADGGGPSRDAVFQSLQRAYLKQGA LMG ISVSSEQIKQIIVDDPNFH DANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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m230.pep	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRLT	QVNR	TIRSH	TFN
a230	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGDA	QAEQLIRLT	QVNR	TIRSH	TFN
	130	140	150	160	170	180			
m230.pep		190	200	210	220	230	240		
		PDEFIAQVKV	SEADLQKF	YNANKKDY	LLPQAVKLE	YVALNLKDF	ADKQTVSE	TEVKNAFE	
a230		PDEFIAQVKV	SEADLQKF	YNANKKDY	LLPQAVKLE	YVALNLKDF	ADKQTVSE	TEVKNAFE	
	190	200	210	220	230	240			
m230.pep		250	260	270	280	290	300		
		ERVARLPANE	AKPSFEQE	KA AVENEL	KMKKAVAD	FNKAKEKL	GDDAVNHP	SSSLAEAA	KNS
a230		ERVARLPANE	AKPSFEQE	KA AVENEL	KMKKAVAD	FNKAKEKL	GDDAVNHP	SSSLAEAA	KNS
	250	260	270	280	290	300			
m230.pep		310	320	330	340	350	360		
		GLKVTQETW	LSRQDAQM	SGMPENLI	NAVFSDDV	LKKKHNS	EVLTINSE	TAWVVR	AKEVR
a230		GLKVTQETW	LSRQDAQM	SGMPENLI	NAVFSDDV	LKKKHNS	EVLTINSE	TAWVVR	AKEVR
	310	320	330	340	350	360			
m230.pep		370	380						
		EKTLPF	AEAKDAVR	QAYIRTEA	AKL				
a230		EKTLPF	AEAKDAVR	QAYIRTEA	AKL				
	370	380							

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACA CCCGCCCAAG TCTTTATTAGG
51  CCTGATTGCA TTAACTTTTC TCGGCTTCGG CGTCAGCAGC GTTTCCTATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCTTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAGCCTCGTC
451 CAAACCGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACCGCACCA TCCGTTTCGA CACTTTC AACCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCGA GCGGTCAAAT TGGAAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GAAAAAGGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TGGAACCCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCGGCG ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TCGCTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAAACAAG GCAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAACCGGCG AAACGGCAAA CCCGCCTATG TCAGACTGAC CGGTCGCGCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pap

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGAKLMI SVSSESIKQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHMS DQFVEEIRDQ FALQNLVSLV

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```

151  QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVRA SEADLQKFYN
201  ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251  AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301  GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351  AWVVRRAKEVR EEKNLLFEFA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401  GKAVDVKWE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451  APVIVEAQAV TPPEDIAAQL PPAKQALAAQ QSANTFDLLI RYFNGKIKQT
501  KGAQSVDNQD GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCGTATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCCG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTGCA CACTTCAAC CCGGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 TCGAACAAAA AAGACTATCT GCTGCCGAG GCGGTCAAAT TGGAAATATG
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAACGG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCCTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACATCCTT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATT AGCGACGAGC
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCTGCGCTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAG GCAAAGACG TGCTTACCCA ACTGAACGGC
1201 GGCAGGGTGT TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 CAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTA TTGTGCAAGT ACAGGCTGTA ACCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTTCA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTACAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMI SVSSEIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVRA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRRAKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAQ QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVDNQD GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

```

10      20      30      40      50      60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHINNAIQNEQ
|||||
g230-1      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
10      20      30      40      50      60

70      80      90      100     110     120
m230-1.pep ADGGGPSRDAVFQSLQRAYLKQGAKLMI SVSSEIKQI IVDDPNFHDANGKFDHALLN
|||||
g230-1      ADGGSPWRDAVFQSLQRAYLKQGAKLMI SVSSEIKQI QMIVDDPNFHDANGKFSHALLS
70      80      90      100     110     120

130     140     150     160     170     180
m230-1.pep RYLSQRHMESEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRIRSHTFN

```

**a230-1.seq**

1	ATGTTCCATT	CCATCGAAAA	ATACAGAACG	CCCGCCCAAG	TCCTTTTGGG
51	CCTGATTGCA	TTAACCTTCG	TCGGCTTCGG	GGTCAGCACG	GTATCCCATC
101	CGGGTGCCGA	TACATCTCGT	CAGGTGGGCG	ACGAAAAAAT	CAGCGACCAC
151	TCCATCAACA	ACGCCATACA	GAACGAACAG	CGCGACGGCG	CGCGCCCTTC
201	CGCGCAAGCG	GTGTTCCAAAT	CCCTGCTTACA	ACGGCGCTTAC	CTGAACACAGG
251	CGCGGAAGCT	GATGGGCATT	TCGGTTTCTT	CCGAACAAAT	CAAGCAGATT
301	ATCGTGGACG	ATCCCCAATT	CCACGACGCA	ACGGCAAAAT	CTGACACAGC
351	GCTTTTAAAC	CGCTACCTTT	CCCAACGTCA	TATGTCTGAA	GACCAAGTTG
401	TCGAAGAAT	CCGCGATCAG	TGTGCCCTTC	AGAATTTGGT	AAACCTCTGC
451	CAAAACGGCG	TATTGTCGG	CGACGCGCAG	CGGCAACAG	TGATCAGGCT
501	GACGCAGGTC	AACCGCACCA	TCCGTTTCGCA	CACTTTCAAC	CCCGACGAAAT
551	TCATCGCCCA	AGTCAAAGTC	TCCTGAAGCCG	ATTTCGAGAA	GTTTTATATAC
601	CGAAACAAA	AAGACTACCT	GCTTCCCAA	CGCGTCAAAAT	TGGAATATGT
651	CGCCTTGAAT	CTGAAAGACT	TTTCGACACA	ACAGACCGTC	AGCGAAACAG
701	AAGTGAAGAA	TGCGTTTGAA	GAGCGCAATG	CGCGTTTGCC	GGCAAATGAA
751	GCCAAACCTT	CTTTTCGAGCA	GGAAAAAGCC	CGCGTCGAAA	ACGAATGAA
801	AATGAAAAAG	CGGGTTGCCG	ACTTCAATAA	GGCAAAAAGAA	AGCTGTGGCG
851	ATGACGCGTT	CAACCATCCT	TCCTCGCTTG	CCGAAGCCGC	CAAAACACGC
901	GGTTTGAAG	TGCAAAACCA	AGAAACTTGG	CTGACGAGGC	AGGATGCCTCA
951	AATGTCGGGT	ATGCCCGAAA	ACCTGATCAA	TGCCGTATTCT	AGCGACGACG
1001	TATTGAAGAA	AAAACACAAT	TCCGAAGTGC	TGACCATCAA	CAGCGAAACC
1051	CGGTGGGTGC	TCCGCGCCAA	AGAAAGTCCG	GAAGAGAAAA	CCCTGCGCTT
1101	TGCCGAAGCC	AAAGACGCGG	TACGTCAGGC	TTATATCCGT	ACCGAAGCCG
1151	CCAAACTTGC	CGAAAACAAG	GCAAAAGACG	TGCTTACCCA	ACTGAACGCG
1201	GGCAAGGCTG	TTGACGTGAA	ATGGTCGGAA	GTGTCCGTTT	TGGGCGCACA
1251	CGAGGCAAGG	CAGTCCATGC	CGCCCGAGGC	TTATGCGGAA	CTGCTGAAGG
1301	CAAAACCGCG	AAAGCGCAAA	CCCGCCTACG	TCAGGCTGAT	CGGCTCTGCC
1351	GCACCCGTGA	TTGTCGAAGT	ACAGGCTGTA	ACCCCGCGGG	ATGATATTCG
1401	CGCACAGCTT	CGCGTTTGAA	AAACAGGCTT	GGCGCAACAG	CAGTCTGCCA
1451	ATACTTTCTA	CTGTTTGATA	CGTTATTTCA	ACGGCAAAAT	CAAAACAGACC
1501	AAAGGAGCGC	AATCGGTCGA	CACCGCGCAC	GGTCAGTAA	

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```
1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAQMGI SVSSEQIKQI
101 IVDDPNFHD NGKFDHALLN RYLSQRHME DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEK AAVENELKMK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKH SEVLINSET
351 AWVVRKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQA QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGQSVNDGD GQ*
```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```

g231.seq
1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
51  gccgccgttg caaataatc cgccatttta ccgtaaaaac cgccgcctga
101 acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151 gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtcttt
201 accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgccc
251 ccgcgcgtcc tgcctgcccg gcggtacgcc cacggcgctt gcggattttt
301 agctttccac aatcctttgc gttccctttc cgcctgaatt tgagcgtcgg
351 catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401 taatgccacg ccgcccgcgc ctgcacctgc atcagggttca aatcgggttt
451 gccggcggat acctgcgcca cttcgcgctg atagcggctg gtttcaaaca
501 cagctacact gactttccta ccctccgcgc ccgcgcgcag gttgtcgcgc
551 gaacgtgtac cgtaagcctg tttcatctcc ggtgcgtcga tatacggcat
601 ccgaatttta tgtttcgcgc cgtcgcgcgc gatgacgtga aggggtatcgc
651 cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701 gatgcccgtc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751 gagtacgtcg agtacggcaa ccgcgcgtcc caccgcctca ctgtcatatc
801 ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851 atgatttttt taatctgcat atttttcaaa tgccgatgcc gtctgaacat
901 ctctga

```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```

g231.pep
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201 PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251 EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301 L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```

m231.seq (partial)
1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGCGCGAACT
51  GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG GC....

```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```

m231.pep (partial)
1  MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51  ARGFQTAFV QGRAVSLPNA QPFG.....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```

m231/g231
          10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          |||||||||||||||||||||||||||||||||||||||||||||||||||
g231      MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          10      20      30      40      50      60

          70
m231.pep  QGRAVSLPNAQPFG
          |:|||||||||:
g231      QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIVG
          70      80      90     100     110     120

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

**a231.seq** (partial)

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGNGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTGCGCTG GTAGCGGTCG GTGTCGAACA
501 CGCGGACGCT GACTTTCCTG CTTCCGCGC CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACCCCAT
601 CCGGATTTTG TGTTTCGCGC CGTCGCGTGC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GGCGGGCGGG CGCGTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACGCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

**a231.pep** (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPOKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRLNRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVD FGHRAVAVA GFRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 I

```

**m231/a231** 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

**g231-1.seq**

```

1 ATGTCAAAAC GAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACCTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgcCAG GTTgtcgcGC
551 GAACgTGTAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTtTa tGtttcgcgc cgtcgcCgtc gATGACGTGA AGGgtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGAttctcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

**g231-1.pep**

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
51 ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```



101 SFQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF  
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH  
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC  
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA  
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG  
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT  
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC  
 251 CCGCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTT  
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG  
 351 CATAATCGGC AAAATCCGCC TTATCTGCT GTTCTTTAGC ATAACTTTAA  
 401 TAATGCCACG CCGCCCGTCC CTGCACCTGC ATCAGGTTCA AATCGGTTT  
 451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTG GTATCGAACA  
 501 CGCGCACGCT GACTTTCCTG CCTTCCGCGC CCGCGCGCAG GTTGTGCGGC  
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GCGCGTCTGA TATACGCCAT  
 601 CCGGATTTTG TGTTCGCGC CGTCGCGTGC GATAACGTGA AGGGTGTGCG  
 651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC  
 701 GATGCTCGGC GCGGGCGGG GCGCTCGGAA CCCGCGTCCC CTGCCGCGCC  
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCGG CACCGCTCG CTGCCGTACC  
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC  
 851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT  
 901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSNRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR  
 51 ARGFQTAFAV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF  
 101 SFQSFAPFF RLNLVGIIVG KIRLILFFS ITFIMPRRPV LHLHQVQIGF  
 151 ADRLNRHFAL VAVGIEHAHA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH  
 201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRCSAAGG RVGTRVPCRA  
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH  
 301 IIGIFQTAS\*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSNRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFAV				
m231-1	MSKRKSNRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCAS	PQKCRARGFQTAFAV				
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFS	SFQSFAPFRLNLVGIIVG				
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFS	SFQSFAPFRLNLVGIIVG				
	70	80	90	100	110	120
g231-1.pep	KIRLILFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRLNRHFALVAVGIEHAHADFPFRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHNFNMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDNDVKGVAVIDFGHRACVAVAGFRCSAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC  
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA  
 101 ACTTTTTTAT CGCGGCAGAC GCGGTTGCG CGTCTCCGCA AAAATGCAGG

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGCTTTT
201 ACCAAATGCC CAACCATTGC CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTC GTTCCCTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTA
401 TAATGCCAGC CGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCGGACAGAA ACCTGCCGCA CTTCCGCTG GTAGCGGTG GTGTCGAACA
501 CGCGGACGCT GACTTTCTG CCTTCCGCG CCGCGCGCAG GTGTGCGCGC
551 GAACGCGTGC CGTAAGCCTG TTTTATCTCC GCGCGGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGTC GATAACGTGA AGGGTGTCGC
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GCGGCTCGGC GCGGGGCGGG CGCGTCGGAA CCGCGCTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGCTCC CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTC
851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAACP AVRPRLRIF
101 SFPQSFAFP RLNLVGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRFAL VAVGEHADA DFPFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVD FGHRACVAV GFRRCSAAG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a231-1.pep	QSRVSLPNAQPFAHGIHPILIAAPACPAVRPRLRIFSFPQSFAFPRLNLVGIIG					
m231-1	QSRVSLPNAQPFAHGIHPILIAAPACPAVRPRLRIFSFPQSFAFPRLNLVGIIG					
	70	80	90	100	110	120
	130	140	150	160	170	180
a231-1.pep	KIRLILFFSITFIMPRRPVHLHQVQIGFADRNLRHFALVAVGEHADADFPFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVHLHQVQIGFADRNLRHFALVAVGIEHADADFPFRRRAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
a231-1.pep	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDQNVKGVAVIDFGHRACVAVAGFRRC SAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDQNVKGVAVIDFGHRACVAVAGFRRC SAAGG					
	190	200	210	220	230	240
	250	260	270	280	290	300
a231-1.pep	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
	310					
a231-1.pep	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgcgcct tatattgtcg
101 ggatactggt tttgctgggc gccgtcggag gaacggccgg cagcctgttt

```

```

151 atgccgtccg taccgcgcaa ggctgccgat acccaaatcg agtggaaat
201 tgtccgtggt acaaaatccc tgctgctga aacggtgagg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt ttggtttgt cggcgagggt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttgtt ttccatcggg attgccgagg
401 gttcggtagt gtgtgccaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacgggtg gtgctgtggg ttcgacggtt tgcggcctgg ttttgggtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttgggttt
551 tatcgcaagg atggggcatac cccgtgatgg cgggtgatgac gctgatcggc
601 tttttcggcg gatttttctc cgttccgctc tatacctggc tgcaaacgcg
651 cagcagcgag actttccgag cccgcggcgt tgcggccaac aatatcggtta
701 acggcatctt tatggtttcc gccgcggtt tgagcgagg attgctgttt
751 ttggttgaca gcatttccct gctgtatctg attgtcgcct tgggcaatat
801 tccgttggcg gtatttttga ttaagcgca aaggcggtt ttaggcgagg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g23 2. pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NIVNGIFMVS AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m23 2. seq

```

1  ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTGTGCG CCATCCTGTT
51  CGGTCAGATT TTGGGAACGG CGGTGGCAGG TGTACCGCCT TATATTGTCG
101 GGATACTGGT TTTGCTGGTC GCCGTCGGAG GCACGGTCGG CAGCCTGTTT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGGAAATAT
201 TGTCGGTGGC ACAAATCCC TGCTGCGTGA AACGGTGGCG CACAAGCCCG
251 TTTTACCGC CATTATCGGT ATTCGTGGT TTTGGTTTGT CCGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTT AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACCGCTGAT GTTGGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TGC GGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTGTGTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CGGTGATGAC GCTGATCCGC
601 TTTTTCGGCG GATTTTCTC CGTCCGCTC TATACCT (g) TG CAAACCGCCA
651 TAGCGAGATT TCCGCGCCCg GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGG TTTCCGCTGC CGTTTGTAGC GCGGTGTTGC TGTTTTTGT
751 TGACAGCATT TCCTTGTGT ATCTGATTGT CGCTTGGGC AATATCCGT
801 TGTCGGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m23 2. pep

```

1  MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51  MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAVMTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10      20      30      40      50      60
m23 2. pep  MMGNSLIESGTFVAILFGQILGTA VAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g232       MMGNSLIESGTFVAILFGQILGTA VAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
m232.pep	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	70	80	90	100	110	120
	TQIEWNIVRGTKSLLRETVRHNVPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
m232.pep	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	130	140	150	160	170	180
	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
m232.pep	190	200	210	220	230	
	FXFLSQGWAYPVMAMVMTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	190	200	210	220	230	240
	FWFLSQGWAYPVMAMVMTLIGFFGGFFSVPLYTWLQTASSETFRARAVAANNIVNGIFMVS					
m232.pep	240	250	260	270	280	289
	AAVLSAVLLFLFDSISLLYLIVALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	250	260	270	280	290	
	AAVLSAVLLFLFDSISLLYLIVALGNIPLAFLIKRERRFLGAAAIRKKP					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

a232.seq	1	ATGTACGCTA	AAAAAGGCGG	TTTGGGACTG	GTTAAAAGCC	GCCGTTTCGC
	51	ACCTCTTTTC	GCTACGCAGT	TTCTCGGCGC	GTTCAACGAC	AATGTGTTCA
	101	AAACCGCGCT	GTTTGTGATG	ATTGGGTTTT	ACGGTTTGGG	GCAAAACGGC
	151	TTCTCGCCTG	CCGGACAGAT	GTTGAACTTG	GGCGCGTTGC	TGTTTATTTT
	201	GCCGTATTTT	CTGTTTTCTT	CGCTGTCGGG	GCAGTTGGGT	AACAAATTCG
	251	ACAAGGCCGT	TTGGCGCGCT	TGGGCCAAGG	TGCTGGAAAT	GATCATTATG
	301	GCGGTGGCGG	CATACGGGTT	TTATATCCGG	TCTGCCCCGC	TGCTTTTGGC
	351	GTGTCTGTTT	TGCATGGGCG	CGCAATCGAC	GCTGTTCCGG	CCGCTGAAAT
	401	ACGCCATCCT	GCCCCATTAT	CTCGACGACA	AAGAGTTGAT	GATGGGCAAC
	451	AGCCTGATTG	AATCGGGTAC	GTTTGTGCGC	ATCCTGTTTC	GTCAGATACT
	501	GGGGACTGCG	GTGGCAGGTG	TACCGCCTTA	TATTGTCGGG	ATACTGGTTT
	551	TGCTGGTCCG	CGTAGGAGGC	ACGGTCGGCA	GCCTGTTTAT	GCCGTCCGTA
	601	CCCGCCAAGG	CTGCCGATAC	ACAAATTGAG	TGGAATATTG	TCCGGGGTAC
	651	AAAATCCCTG	CTGCGTGAAA	CGGTGCGGCA	CAAGCCCGTT	TTTACCGCCA
	701	TTATCGGTAT	TTCTGGTTT	TGGTTTGTTC	GCGCGGTTTA	TACCACGCCA
	751	CTGCCGACCT	TTACCCAAAT	CCATCTAGGC	GGCAACGACA	ATGTTTTCAA
	801	CCTGATGCTT	GCCCTGTTTT	CCATCGGTAT	TGCCGCCGGT	TCGGTACTGT
	851	GTGCCAAGTT	CAGCAGGGAA	CGGCTGAGGT	TGGCTTGGGT	AACGGTTGGT
	901	GCGTTGGGTT	TGACGGTTTG	CGGCTTGGTT	TTGGTGTGGC	TGACGCACGG
	951	ACACCGTTTT	GAAGGGCTGA	ACGGCATTTT	TTGGTTTTTA	TCGCAAGGAT
	1001	GGGCATATCC	CGTGATGGCG	GTGATGACGC	TGATCGGCTT	TTTCGGCGGA
	1051	TTTTTCTCCG	TTCCGCTCTA	TACCTGGCTG	CAAACCGCCA	GTAGCGAGAC
	1101	TTTCCGCGCC	CGCGCCGTTG	CCGCCAACAA	TATCGTTAAC	GGTATTTTTA
	1151	TGGTTTCCGC	TGCCGTTTTG	AGCGCGGTGT	TGCTGTTTTT	GTTTGACAGC
	1201	ATTTCTTGT	TGTATCTGAT	TGTCGCTTTG	GGCAATATTC	CGTTGTCGGT
	1251	ATTTTGTATT	AAGCGCGAAA	GGCGGTTTTT	AGGCGCGGCG	GCAATCAGGA
	1301	AAAAACCTTG	A			

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

a232.pep	1	MYAKKGGGLGL	VKSRRFAPLF	ATQFLGAFND	NVFKTALFVM	IGFYGLGQNG
	51	FLPAGQMLNL	GALLFILPYF	LFSSLSGQLG	NKFDKAVLAR	WAKVLEMIIM
	101	AVAAYGFYIR	SAPILLACL	CMGAQSTLFG	PLKYAILPDY	LDDKELMMGN
	151	SLIESGTFFVA	ILFGQILGTA	VAGVPPYIVG	ILVLLVAVGG	TVGSLFMPSV
	201	PAKAADTQIE	WNIVRGTKSL	LRETVRHKPV	FTAIIGISWF	WFGAVYTTQ
	251	LPTFTQIHLG	GNDNVFNML	ALFSIGIAAG	SVLCAKFSRE	RLRLAWVTVG

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG  
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS  
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP\*

m232/a232 95.9% identity in 290 aa overlap

m232.pep				10	20	30
				MMGNSLIESGTFVAILFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILEDYLDDELMGNSLIESGTFVAILFGQILGTAVAGVPP					
	120	130	140	150	160	170
m232.pep		40	50	60	70	80
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG				
a232	YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
	180	190	200	210	220	230
m232.pep		100	110	120	130	140
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSKERLMLAW				
a232	ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSRERLRLAW					
	240	250	260	270	280	290
m232.pep		160	170	180	190	200
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL				
a232	VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
	300	310	320	330	340	350
m232.pep		220	230	240	250	260
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS				
a232	YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
	360	370	380	390	400	410
m232.pep		270	280	289		
		VFLIKRERRFLGAAAIRKKPX				
a232	VFLIKRERRFLGAAAIRKKPX					
	420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

```

1  atgaaacgca aaaatatcgc gctgattccc gccgccggca tcggggtgcg
51  tttcgggtgcg gacaaaccca agcaatatgt cgaaatcgga agcaaaacgg
101 ttttagaaca tgtacttggg atttttgaac ggcattgaggc cgtcgatttg
151 accgtcgttg tcgtctcgcc cgaagacacg ttgcccgata aggttcagac
201 ggcatttcca caggttcggg tgtggaaaaa cgggtggacag acccgcgccg
251 aaactgtccg caacgggtgtg gcaaaactgt tggaaaccgg tttggcgggc
301 gaaaccgaca atattctggt acacgatgcc gcccgctgct gcctgccgtc
351 tgaagctctg gcgcgggtga tagaacaggc gggcaacgcc gccgaaggcg
401 ggattttggc agttcccgtt gccgatacgc tcaagcgcgc agaaagcgga
451 caaatcagtg caactgtcga ccgttcgggg ctttggcagg cgcaaacgcc
501 gcagcttttt caagcgggtt tgctgcaccg cgattggct gcggaaaact
551 tgggcggcat taccgatgaa gcgtccgccg tggaaaaact ggggtgtcgt
601 ccgctactga tacagggcga cgcgcgcaat ttgaaactga cgcagccgca
651 ggacgcatac atcgtcaggc tgctgctcaa tgcgtctga
```

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

```

1  MKRKNIALIP AAGIGVRFGA DKPKQYVEIG SKTVLEHVLG IFRHEAVDL
51  TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL ARLIEQAGNA AEGGILAVPV ADTLKRAESG
```

151 QISATVDRSG LWQAQTPQLF QAGLLHRLA AENLGGITDE ASAVEKLGVR  
 201 PILLIQGDARN LKLTQPDAY IVRLLNNAV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 859>:

m233.seq (partial)

1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCCT CAGGTTTCGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG  
 251 AAACCGTCCG CAACGGTGTG GCAAACTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCC GCCGAAGGCG  
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GC GACCGTGGG  
 451 AACATT....

This corresponds to the amino acid sequence <SEQ ID 860; ORF 233>:

m233.pep (partial)

1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL  
 51 TVVVVSPEDT FADKVQTAFF QVRVWKNNGQ TRAETVRNGV AKLLETGLAA  
 101 ETDNILEVHDA ARCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG  
 151 NI....

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 233 shows 93.4% identity over a 152 aa overlap with a predicted ORF (ORF 233.ng) from *N. gonorrhoeae*:

m233/g233

	10	20	30	40	50	60
m233.pep	MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
g233	MKRKNIALIP AAGIGVRFADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
	70					
m233.pep	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILEVHDAARCLPSEAL					
g233	FADKVQTAFFQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILEVHDAARCLPSEAL					
	70	80	90	100	110	120
	130					
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
	:					
g233	ARLIEQAGNA AEGGILAVPVADTLKRAESQISATVDRSGLWQAQTPQLFQAGLLHRLA					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 861>:

a233.seq

1 ATGAAGCGCA AAAATATCGC GCTGATTCCC GCCGCCGGCA TCGGGGCGCG  
 51 TTTCGGTGCG GACAAACCCA AGCAATATGT CGAAATCGGA AGCAAAACCG  
 101 TTTTAGAACA TACGATTGGG ATTTTGAAC GGCATGAGGC CGTCGATTG  
 151 ACCGTCGTTG TCGTCTCGCC CGAAGACACG TTTGCCGATA AGGTTTCAGAC  
 201 GGCATTTCCT CAGGTTTCGGG TGTGGAAAAA CGGCGGACAG ACCCGCGCCG  
 251 AAACGTCCG CAACGGTGTG GCAAAATTGT TGGAAACCGG TTTGGCGGCG  
 301 GAAACCGACA ATATTCTGGT ACACGATGCC GCGCGTTGCT GCCTGCCGTC  
 351 TGAAGCTTTG ACGCGGTTGA TAGAACAGGC GGGCAACGCT GCCGAAGGTG  
 401 GGATTTTGGC AATTCCTATT GCCGATACGC TCAAGTGC GC GACCGTGGG  
 451 AACATTAGTG CAACCGTCTGA GCGGACGAGC CTTTGGCAGG CGCAAACGCC  
 501 GCAGCTTTTC CGCGCCGGGC TGCTGCACCG CGCATTGGCT GCGGAAACT  
 551 TGGACGGCAT TACCGATGAA GCGTCCGCCG TGGAAAAATT GGGCATCCGC  
 601 CTTTGTCTGG TGCAGGGCGA CGCGCGCAAT TTGAACTGA CGCAGCCGCA  
 651 GGACGCATAC ATCGTCAGGC TGCTGCTCGA TGCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1 MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51 TVVVVSPEDT FADKVQTAFP QVRVWKNNGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDAV*
```

m233/a233 99.3% identity in 152 aa overlap

	10	20	30	40	50	60
m233.pep	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
a233	MKRKNIALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
	10	20	30	40	50	60
m233.pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
a233	FADKVQTAFPQVRVWKNNGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
	70	80	90	100	110	120
m233.pep	TRLIEQAGNA AEGGILAIPIADTLKCADGGNI					
a233	TRLIEQAGNA AEGGILAI PVADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA					
	130	140	150	160	170	180
a233	AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDAVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1 atgaaaaccg tttccgcgcg catcgctttt gccgcgcgctg ccgtttcact
51 gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcgcg caaagcgcgag aacctgaaa ggcgagatta
351 tgtcggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggtcgcggca aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaat acgcacttcc caaccgcgaa atcatcggtt
551 tcggcgccac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagccgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1 MKTVSAAIAF AAAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51 TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFN V LNRTNLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALS NRE IIGFGGTSY DATLNGKVL D
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1 ...GGCGCGGGCG AATACGCACT TTCCAACCGT GAAATCATCG GTTTCGGCGG
51 CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTGA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)

1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIKREAVNS LVQAVDNGAW  
51 QPNR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

					10	20	30
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL		
g234	LGRGKSQIAYAKVALNIVNVNTSEIVYSTQ	GAGEYALSNREIIGFGGTSGYDATLNGKVL					
	140	150	160	170	180	190	

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
	::		
g234	DLAIREAVDNLVQAVDNGAWQSNRX		
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)

1 AACCGCACCT ATTTGAACGC ATTAAACAG GAATCCGGCA TTTCCGGCAA  
51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG  
101 AATTCGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT  
151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA  
201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG  
251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGCTACGAT  
301 GCGACTTTGA ACGGCAAAGT TTAGACTTGC GCAATCCGCG AAGCCGTCAG  
351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)

1 NRTYLNALKQ ESGISGKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG  
51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD  
101 ATLNGKVL DL AIKREAVNSLV QAVDNGAWQP NR\*

m234/a234 100.0% identity in 54 aa overlap

					10	20
30						
m234.pep					GAGEYALSNREIIGFGGTSGYDATLNGKVL	
a234	LGRGKSQIAYAKVALNIVNVNTSEIVYSAQ	GAGEYALSNREIIGFGGTSGYDATLNGKVL				
	50	60	70	80	90	100

		40	50
m234.pep	DLAIREAVNSLVQAVDNGAWQPNRX		
a234	DLAIREAVNSLVQAVDNGAWQPNRX		
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq



536

```

1  atgaaacctt tgatttttagg gcttgccgcc gtggtggctc tgtctgcctg
51  ccaagttcga aaagctcccc acctcgacta cacgtcattc aaagaaagca
101 aaccggcttc aattttggtg gttccgccgc tgaacgagtc gcctgatgtc
151 aacggcactt gggggatgct ggcttcgacc gccgcgccga ttccgaagc
201 cggctattac gtctttcccg ccgcagtcgt ggaggaaacc ttcaaagaaa
251 acggcttgac caatgccgcc gatattcacg ccgtccggcc ggaaaaactg
301 catcaaattt tcggcaatga tgcggttttg tacattacgg ttaccgaata
351 cggcacttca tatcaaattt tagacagcgt gacgaccgta tccgccaaag
401 cacggcttgt cgattcccgc aacgggaaag agttgtggtc ggggttcggcc
451 agcatccgcg aaggcagcaa caacagcaac agcggcctgt tgggggcttt
501 ggtcggcgca gtggtcaatc agattgcaa cagcctgacc gaccgcggtt
551 atcaggtttc caaaaccgcc gcatacaacc tactgtcgcc ctattccgcc
601 aacggtatct tgaaagggtc gagattcgtc gaagagcagc ccaaataa

```

This corresponds to the amino acid sequence <SEQ ID 870; ORF 235.ng>:

g235.pep

```

1  MKPLILGLAA VLALSACQVR KAPDLDTYTSF KESKPASILV VPPLNESPDV
51  NGTWGMLAST AAPISEAGYY VFPAAVVEET FKENGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTG YQILDVTTV SAKARLVDSR NGKELWGSQA
151 SIREGSNNSN SGLLGLALVGA VVNQIANSLT DRGYQVSKTA AYNLLSPYSR
201 NGILKGPRFV EEQPK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

```

1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGTTTGTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATTCCCGC AACGGAAGAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTGAGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC CAAAACCGCC GCATACAACC TGCTGTGCGC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTT GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 872; ORF 235>:

m235.pep

```

1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAI DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTG YQILDVTTV SAKARLVDSR NGKELWGSQA
151 SIREGSNNSN SGLLGLALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 235 shows 96.7% identity over a 215 aa overlap with a predicted ORF (ORF 235.ng) from *N. gonorrhoeae*:

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
g235	MKPLILGLAAVLALSACQVRKAPDLDTYTSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTG					
g235	AAPLSEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTG					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130      140      150      160      170      180

          190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||||||||||||||||:|||||||||||||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
          190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTTCAA AAAGCGCCCG ATTTCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GAAAAACTG
301 CATCAGATT TCGGCAATGA TCGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAG
401 CACGCTGGT CGATTCCCGC AACGAAAAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGCCTGT TGGGGGCTTT
501 GGTACGCGCA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAAACCGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

          10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
          10      20      30      40      50      60

          70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLVYITVTEYGTS
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLVYITVTEYGTS
          70      80      90      100     110     120

          130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
          130     140     150     160     170     180

          190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          |||||||||||||||||||:|||||||||||||||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
          190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1 ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGACAG
51 CGGTTTCATA ACCTGCAACC GCGCCACAT CGCGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCGGGCGC GGTAATTTCTG
251 GCTTCCGCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcg9cg gTTACTGCTT CGCGCGCTTC GCGATTGCC GTCCATTTTT
351 TCACCAGTTC GGCTTCGGCT TTTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTCGCGC TGCGCGGGC GCGGCTGTCG
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGGAAAG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTGCAG CCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCCACC ATATCCGCCT GTTGACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAAT GGCAAAcagG AAGCTCAAGG
801 TATTCGGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgcccgt gTAATCGGTG GATGCCGCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1 MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAFAFFAV AGFGNGKFI
51 TDFHFCFRHQ QGKAQFFAQs IQIAGHFFRR GNFGRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGVEA VFQDVEVERA
201 QVFRAERNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAQ
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1 ..TTGCACGGAC GAACCGACGG TTTTGTCCGC GCGCAAAGGC TCGATGGCGG
51 CGGTTACCGC TTCGCGGGCT TCGCGGATG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TCTCTTCGC CGCCGCCGwT GAYGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAACT GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACAaTG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG ACACTCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTG AGGATTTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1 ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVSME
51 EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFRAE RNKVYFGKVE XITRIVIAQ TLLQLTCQYH
151 GVAVDFHHR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

539

m236.pep					10	20	30
					LHGR	TDFVGAQRLDGGGYRFAGFADCRPF	
g236					:	:	:
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
		FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXDVP	PRFFAGEAQNRCNQENQ	TACDVIQ	QSLC	
g236		:	:	:	:	:	:
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
		AAACMAVCFGGVEAVFQDVE	VERTQVFRAERNXVFY	GKVEKITRIVIA	CQTLQLCQYH		
g236		:	:	:	:	:	:
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
		GVAVDFH	IRLLHGIFNRIKVAQV	GKQKQAGIADTAVAF	GYAFEDFFGNRQFAA	VIGRCR	
g236		:	:	:	:	:	:
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
		PQAQDVCAEFVINLLRCNDVADG	FRHF	FAFVDNETMGQQLF	IRRATHX		
g236		:	:	:	:	:	:
	300	310	320	330	340		
		PQAQDVRAEFVIDFLRDDVADG	FRHFAAVLVNHETV	GQQLFIRCASHG			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 879>:

a236.seq	1	ATGGCGCGTT	TCGCCTTCTC	CGCCGACATT	CTCTGCACAG	CGTTTGCGAG
	51	CGGTTTCATG	GCCTGCAACC	GCGCCACAT	CGCGGGTGTA	GTGCCAGCAG
	101	CGTTCGCATT	TTTCAACATC	ACTGGCTTTA	GCGGCAACGG	CAAGTTCGCT
	151	GCCTACTTTC	ACTTCTGCTT	TAGACACCAG	CAAAGCAAAG	CGCAATTCTT
	201	CGCCCAAAGC	ATTGAGATAG	CCGGCCATTT	CTTCCGGGCG	GGTAATTTTCG
	251	GCTTCGGCTT	GCAAGGACGA	ACCGACGGTT	TTGTCCGGCG	GCAAAGGCTC
	301	GATGGCGGCG	GTTACCGCTT	CGCGGGCTTC	GCGGATTGCC	GTCCATTTT
	351	TCACCAAGTC	GGCTTCGGCT	TTTTCGTTGA	TGGTCCGGAA	CTCGTGCCAA
	401	GTATGGAATA	GCACGCTGTC	TTCTGCGCCG	CCGCCGATGA	TGTCCCACGC
	451	TTCTTCGCGG	GTGAAGCACA	AAATCGGTGC	AATCAAGAGA	ACCAGGCTGC
	501	GCGTGATGTG	GTACAGGGCG	GTTTCCGGCG	TGCGGCGGGC	GCGGCTGTGC
	551	GCTTTGGTGG	TATAGAGGCG	GTCTTTCAGG	ATATCGAGGT	AGAAGCGGCC
	601	CAAGTCTTCC	GAGCAGAAAG	AAACCATTTT	TTTACGGCA	AAGTGAAGG
	651	CATAACGCGG	ATAAAATCA	CCGGCAACGC	GTTCTTGCG	CCGCCTTGCC
	701	AACACCAAGG	CATAGCGGTC	GATTTCCACC	ATATCCGCCT	GTTGCACGGC
	751	ATCTTCAATA	GGATTGAAGT	CGCTCAAGTT	GGCAAACAAA	AAGCTCAAGG
	801	TATTGCGGAT	ACGGCGGTAG	CTTTCGGTTA	CGCGCTTGAG	GATTTCTTTG
	851	GAAATCGCCA	ATTCGCGGCT	GTAATCGGTG	GATGCCGCGC	ACAGGCGCAG
	901	GATGTCCGCG	CCGAACGCT	TATACACTTC	TTGCGGCGCG	ACGACGTTGC
	951	CGATGGATTT	CGACATTTTG	CGCCCGTTTT	GATCCACCAC	GAAACCATGG
	1001	GTCAGCAGCT	GTTGTACGG	CGCGCGACCC	ATTGA	

This corresponds to the amino acid sequence <SEQ ID 880; ORF 236.a>:

a236.pep	1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFTTI	TGFSNGKFA
	51	AYFHF CFRHQ	QSKAOFFAQS	IQIAGHFFRR	GNFGFGLQGR	TDGFVGAQRL
	101	DGGGYRFAGF	ADCRPFFHQF	GFGFFVDGRE	LVPSMEKHAV	FCAAADDVPR
	151	FFAGEAQNRC	NQENQAARDV	VQGLRAAAG	AAVGFGGIEA	VFQDIEVERA
	201	QVFRAERNHF	FHGKVEGTR	IKITGNAFLQ	PPCQHQGIIV	DFHHRLLHG
	251	IFNRIEVAQV	GKQKAQGIAD	TAVAFGYALE	DFFGNRQFAA	VIGGCRPQAG
	301	DVRAELVIHF	LRRDDVADGF	RHFAPVLIHH	ETMGQQLFVR	RATH*

540

m236/a236 81.0% identity in 258 aa overlap

m236.pep					10	20	30
					LHGRTDGFVGAQRLDGGGYRFAGFADCRPF		
a236	FRHQSKAQFFAQSIQIAGHFFRRGNFGFGLQGRTDGFVGAQRLDGGGYRFAGFADCRPF						
	60	70	80	90	100	110	
m236.pep		40	50	60	70	80	90
	FHQFGFGFFVDGRELVP	SMEEDAVXFAAAXDVPRFFAGEAQNRCNQENQTACDVIQSSLC					
a236	FHQFGFGFFVDGRELVP	SMEKHAVFCAAADDVPRFFAGEAQNRCNQENQAARDVVQGGLR					
	120	130	140	150	160	170	
m236.pep		100	110	120	130	140	150
	AAACMAVCFGGVEAVFQDVEVERTQVFRAERNXVFYGVKXITRIVIACTLLQLTCQYH						
a236	AAAGAAVGFGGIEAVFQDIEVERAQVFRAERNHFFHGKVEGITRIKITGNAFLQPPCQHQ						
	180	190	200	210	220	230	
m236.pep		160	170	180	190	200	210
	GVAVDFHHIRLLHGI	FNRIKVAQVGKQKAQGIADTAVAFGYAFEDFFGNRQFAAVIGRCR					
a236	GIAVDFHHIRLLHGI	FNRIEVAQVGKQKAQGIADTAVAFGYALEDDFFGNRQFAAVIGGCR					
	240	250	260	270	280	290	
m236.pep		220	230	240	250	259	
	PQAQDVCAEFVINLLRCNDVADGFRHFFAFVDNETMGQQLFIRRATHX						
a236	PQAQDVRAELVIHFLRRDDVADGFRHFAPVLIHETMGQQLFVRRATHX						
	300	310	320	330	340		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

g237.seq

```

1  atgctgggaca aggttgccgg taatatcgca ctccccgcc caccgaatatt
51  cgattctaac atcggaagc tgcggaaaaa ctttaagcat atcttgccgg
101 acaagctcgg tcatacgcg aggattgtcg ataaattcgt tacccttacc
151 gccgaaaagc agcctgccgt ccgcgctgag gcgtaataa tccaaaatat
201 ggcggttgtc gcatactgcc atattgttgc ggataagccc tttgtgccc
251 gcgcccagg gttcgggtgc aataataaag gtgctgacgg caatcgccct
301 gcgttccaaa ggccggaata tcgggttcaa accgacataa gtattgacgg
351 catagaccac atttttacac tcgacgctgc cttcgggcgt gtaaacaccg
401 caaccgtttt gatacggttc gatgcgctgc atcggggatt gctcgaaaat
451 ctgcgcgcgc gcttcggcag cgcgctggc aacacccaac gtgtaattga
501 gcggatgaag atgcccggac aagggatcga actgtgcgcc ttggtacata
551 tcgctgtcaa gctgctgtt caactcggct ttatcccaa gttgataatg
601 actcgacccg taatgccgtt gggcgtgttc atgccactgc tgcaactctt
651 cccaatgctg cggacggacg gcaaccgttg cataaccgcg ctgccaatcg
701 caatcgatgg catgtttgcg gacgcgttcg tccaccagtt cgaccgctcg
751 caaagactgt tgccaaaacc attgcgcctg ctccaagccg acctgttttt
801 caatttcccc cataccgcag gcgtagtcgc tgataacctg cccgccactc
851 ctgccggacg cgccgaagcc gatacgtgcg gcttccaaaa cgacggcttc
901 atgtccgtgt tccgccagcg gcaatgcggt acacaaaccg ctcaaaccgc
951 cgccgataat gcaggtttcg gctttcagac ggcattggag tttcggataa
1001 acagtatgcy gattaaccga actaaaataa taagaaggca gatattcttg
1051 aaaatcaggc cgaatcattg tgtttgcttt atcgggtata ttttcggacg
1101 gaatgataca gactgtcggg ccatatcgtc caaacagaaa atcgggtga

```

This corresponds to the amino acid sequence &lt;SEQ ID 882; ORF 237.ng&gt;:

g237.pep

```

1  MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51  AEQPAVRAE AVIIQNMAVV AYCHIVADKP FCARQGGFGG NNKGADGNRL

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNOPTVLIRF DARHRGLEN  
 151 LRAGFGSGAG NTQVIERMK MPQGIELCA LVHIAVKLLF QLGFI PKLIM  
 201 TRTVMLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRABE DTCGFQNDGF  
 301 MSVFRQRQCG TQTAQTAADN AGFGFQTALE FRINSMRINR TKIIRRQIFL  
 351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m23 7.seq  
 1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT  
 51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG  
 101 ACAAGCTCGG TCATACGCTC AGGATTGTCG ATAAACTCGT TATCCTTACC  
 151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAATAA TCCAAAATAT  
 201 GGCGGTGTC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTTGGCGCG  
 251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT  
 301 GCGTTCCAAA GGCGGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG  
 351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTGCGGCGT GTAAACCAGC  
 401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAA  
 451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCAA GTGTAAGTGA  
 501 GCGGATGCAG GTGTCCGAT AAGGGTTCGA ATTGTGCCCC TTGGTACATA  
 551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG  
 601 ACTCGCACCG TAATGCCGTT GGGCGTGTTT ATGCCACTGC TGCAACTCTT  
 651 CCCAATGCTG CGGACGGACG GCAACCGTGG CATAACCGCG CTGCCAATCA  
 701 CAATCGACCG CATGTTTTCG GACGCGTTTC TCCACCAGTT CGACCGCCTG  
 751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT  
 801 CAATTTCCTC CATAACGCGC nCGTAATCGC TGATAACCTG CCCGCCACTC  
 851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC  
 901 ATGTCCTGCG TCCGCCAAGG GCAATGCAGT GCACAAACCA CCCAATCCGC  
 951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA  
 1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG  
 1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCAGGTGTA TTTTCGGACG  
 1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAWACAGAAA ATCGGTTGA

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m23 7.pep  
 1 MRDKVGGNVA LPAPRIFFD IGLRKNFKH ILADKLGHTL RIVDKLVILT  
 51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NNGGADSNRL  
 101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNOPTVLMRF DARHRGLEN  
 151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFI PKLIM  
 201 TRTVMLGVF MPLLQLFPML RTDGNRGITA LPIAIDGMFA DAFVHQFDRL  
 251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPSRAET DTRGFQHNRF  
 301 MSLRQGCQS AQTTQSAADD TGIGFQTALE FRINSMRINR TEIIRRQIFL  
 351 KIRANHCVCF IRCIFGRNDT GCRAISSKQK IG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m23 7/g237

	10	20	30	40	50	60
m23 7.pep	MRDKVGGNVALPAPRIFFD	DIGLKRKNFKHILADKL	GHTLRIVDKLVILTAEKQ	SAVRAE		
g23 7	MRDKVGGNIALPAPRIFFD	SNIGLKRKNFKHILADKL	GHTLRIVDKLVILTAEKQ	PAVRAE		
	10	20	30	40	50	60
	70	80	90	100	110	120
m23 7.pep	AVIIQNMAVVAYCHIVTD	KPFCARPQGFGRNNGGAD	SNRLAFQRPEYRVQTCI	SIDSIDH		
g23 7	AVIIQNMAVVAYCHIVAD	KPFCARAQFGGNNKGAD	GNRLAFQRPEYRVQTDI	SIDGIDH		
	70	80	90	100	110	120
	130	140	150	160	170	180
m23 7.pep	IFALDAAFGRVNOPTVLM	RFDARHRGLENLRTGFG	SGTSDAQSVSERMQVSG	XGVELCP		

```

a237. seq
1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCTCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATACGCGC GGGATTGTGC ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGGTAAATA TCCAAATATA
201 GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTCCCAA GGCTTGAATA TCGGATTCAA ACCGGCAGTA GTATTGACGG
351 CGTACACCA AGTTTTCAT TCGACCTGTC CTTCCGGGAT GTAAACCAAG
401 CAACCGTTTT GATAAGGTTT ATCGCTATC ATGGGAGAAT GCTCAAAATC
451 CTTGTAACCA GCTTCGGCAG CGGCGCGGGC GATGCCAAC GTGTAATTGA
501 GCGGATGGAG AGTCCCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTCAGTG TTATCCCAAG GTTGATAATG
601 AGTTGCACCG TAATATTTTT GCGCGTGCTC ATGCCATTGT TGC AATTCTT
651 CCAATGCTG CGAACGGATG GCAACCGTGG CATAAACCGG CTGCCAATCG
701 CAATCAATGG CATGTTTGCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACG ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801 CAATTTCCTC CATACCGGAC GCGTAATCGC TGATAACCTG CCGCGCACTC
851 CGTCCCGACG CGCCGGAACC GATACGCGCG TCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTTCGGATAA
1001 ACAGATGAGG GATTAACCGA ACTGAAATAA TAGAAGGCA GATAATCTTG
1051 AAAATCAGG CGAATCATTG TGTATTGCTTT ATCGGGTATA TTTTCCGACG
1101 GAATGATACA GGCTGTCGAG CCGATATGTC CAACACGAAA ATCGGTTTGA

```

a237.pep

1	MRDKVGGNVA	LPAPRIFDFD	IGKLRKNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIQNMTHV	AYCHIVADKP	FCFTRAQGGFCG	NNKGADSNRL
101	ALQRLEYRIQ	TGISIDGVHQ	IFAFDAFAFG	VNQPTVLIRF	NAYHGRMLKN
151	LRTSFGSGAG	DAQRVIERME	MPGQGIELCA	LVHIAVKLLR	QFSVIPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQDTLFFNFL	HTAGVIADNL	PATFSRRAET	DTRGFOHNR
301	MSLLRHQGCQ	AQTQSAADD	TGIGFQTALK	FRNSMRNRL	TEIIRRQIFL
351	KIRANRGVCF	IGYIFGRNDT	GCAISSKOK	IG*	

m237/a237 85.6% identity in 382 aa overlap

m237.pep	10	20	30	40	50	60
	MRDKVGGNVALPAPRI	FD	DIGKLRKNFKHILADKLGHTLRIVDKLVILTAEQSAVRAE			
a237	10	20	30	40	50	60
	MRDKVGGNVALPAPRI	FD	DIGKLRKNFKHILADKLGHTRGIVDKLVILTAEQSAVRAE			
m237.pep	70	80	90	100	110	120
	AVIIQNMVAVYCHIVTDKPF	CAR	QGGFGRNNKGADSNRLAFORPEYRVQTCISIDSIDH			
a237	70	80	90	100	110	120
	AVIIQNMVAVYCHIVADKPF	CTRA	QGGFGRNNKGADSNRLALQRLQLEYRIQTGISIDGVHQ			
m237.pep	130	140	150	160	170	180
	IFALDAAFGRVNQPTVLMR	FDARH	RGLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP			
a237	130	140	150	160	170	180
	IFAFDAAFGRVNQPTVLI	RFNAYHGRMLKNLRTS	FGSGAGDAQRVIERMEMPGQGIELCA			
m237.pep	190	200	210	220	230	240
	LVHIAVKLLFQLGFIPKLI	MTRTV	MPPLGVMPLQLFPMRLTDGNGRITALPITIDGMFA			
a237	190	200	210	220	230	240
	LVHIAVKLLQFSVIPELIM	SCTVI	FLGVLMPLQLFPMRLTDGNGRITALPIAINGMFA			
m237.pep	250	260	270	280	290	300
	DAFVHQFDRQLRLLPKPL	RLLQADL	FFNFPH	TAXVIADNLPATPSRRAETDTRGFQHNRF		
a237	250	260	270	280	290	300
	DAFVHQFDRQLRLLPKPL	RLLQD	LDLFFN	FLHTAGVIADNLPATPSRRAETDTRGFQHNRF		
m237.pep	310	320	330	340	350	360
	MSLLRQGQCSAQTTSAA	DDTGIG	FQTALKFRINSMRINRTEIIR	RQIFLKIRANHCVC		
a237	310	320	330	340	350	360
	MSLLRQGQCSAQTTSAA	DDTGIG	FQTALKFRINSMRINRTEIIR	RQIFLKIRANHCVC		
m237.pep	370	380				
	IRCI	FRNDTGCRAISSXQKIGX				
a237	370	380				
	IGYI	FRNDTGCRAISSXQKIGX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcatgatgat gcaggcaaaa cactacgaac cgggttggca ataccatctg
151 tttggtaatg ctgcgcgcag tgtaaaaaat cgggttggcg ccgtccaaac
201 atttgatgca actgcggtcg gcccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtcggtt cgataatcat gattcaaaaa gcacttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttaccaa cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacggggc tcaaggcggc
451 ggttatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tgttccgcaa gcccttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcagg ttttctcagc
601 cgtgcgggat aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgtatgg atgatattcg cggcatcgtc caaggtgcgg
701 ttaatccttt ttaacgggt tttcaagggt tagggattgg ggcaattaca
751 gacagtgcgg taagcccggt cacagatata gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgccgcgc

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544

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgccttgccc gtagcagagg ccgcaggtac ggtttgccgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg ttaaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcgga aggaaaagct aatgctgcaa
1151 cctatcctaa gttgggttaat cagctaaatg agcaaaactt aaataacatt
1201 gcggtcctaa atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacattt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAIISMLH IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51 FGNARGSVKN RVCVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGS TTKINTVPQ APFSDRWLKE NAGAASGFSL
201 RADEAGKLIW ENDPKNWRA NRMDDIRGIV QGAVNPFLTQ FQGVGIGAIT
251 DSAVSPVTDI AAQQTLOGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKVELNPTK WDWVKNTGYK
351 KPAARHMQTV DGEAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYI IDSNEKRNKI KNHGLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGCAG CAGCAATATC
51 GTTGCTGCAA ATCCCATTAA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCAAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACGGA
251 CAGGGTTTGA AGGTGTTATC GGTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GGTGTAGACG CCGGTTTAC TGTTTACCAA CTTTCATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACCTCA ACAAACAAAG AGACTAATAT TGTCCTCAA GCCCATTTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCCGTG CCGCCTCTGG TTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTTG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTAGGAA AATTAAGTCC GGAAGCACAA CTTGTGCGCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCAG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCAAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TAAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAISLLQ IPISHANGLD ARLRDDMQAK HYEPGGKYHL
51 FGNARGSVK RYVAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

151 DYPPPGGARD IYSYYVKGTS TKTKTNIVPQ APFSDRWLKE NAGAASGFFS  
 201 RADEAGKLIW ESDPNKNWWA NRMDDVRGIV QGAVNPFLMG FQGVGIGAIT  
 251 DSAVSPVTD TAAQQTLOGIN DLGKLSPEAQ LAAASLLQDS AFAVKDGIN  
 301 AKQWADAHNP ITATAQTALS AAEAAGTVWR GKKVELNPTK WDWVKNTGYK  
 351 KPAARHMOTL DGEMAGGNKP IKSLPNSAAE KRKQNFKEFN SNWSSASFDS  
 401 VHKTLPNAP GILSPDKVKT RYTSLDGKIT IIKDNENNYF RIHDNSRKQY  
 451 LDSNGNAVKT GNLOGKQAKD YLQQQTHIRN LDK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 238 shows 86.0% identity over a 401 aa overlap with a predicted ORF (ORF 238.ng) from *N. gonorrhoeae*:

m238/g238

m238.pep	10	20	30	40	50	60
	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
g238	MNLPIQKFMMLLAAASMLHIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	70	80	90	100	110	120
	RVYAVQTFDATAVSPVLPITHERTGFEVIGYETHFSGHGHEVHSPFDHSDSKSTSDFSG					
g238	RVCAVQTFDATAVGPILPITHERTGFEVIGYETHFSGHGHEVHSPFDNHSDSKSTSDFSG					
	70	80	90	100	110	120
m238.pep	130	140	150	160	170	180
	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS DYPPPGGARDIYSYYVKGTSTTKTNIVPQ					
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGYEPQGGARDIYSYHIKGTSTTKINTVPQ					
	130	140	150	160	170	180
m238.pep	190	200	210	220	230	240
	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMDDVRGIVQGAVNPFLMG					
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPKNWRANRMDDIRGIVQGAVNPFLTG					
	190	200	210	220	230	240
m238.pep	250	260	270	280	290	300
	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGIN					
g238	FQGVGIGAITDSAVSPVTD TAAQQTLOGINDLGKLSPEAQ LAAASLLQDS AFAVKDGIN					
	250	260	270	280	290	300
m238.pep	310	320	330	340	350	360
	AKQWADAHNPITATAQTALSAAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMOTL					
g238	ARQWADAHNPITATAQTALAVAEAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHMOTV					
	310	320	330	340	350	360
m238.pep	370	380	390	400	410	420
	DGEMAGGNKPIKSLPNSAAEKRKQNFKEFNSNWSSASFDSVHKTLPNAPGILSPDKVKT					
g238	DGEMAGGNRPPKSI-TSEGKANAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP					
	370	380	390	400	410	
m238.pep	430	440	450	460	470	480
	RYTSLDGKITIIKDNENNYFRIHDNSRKQYLDNSNGNAVKTGNLOGKQAKDYLQQQTHIRN					
g238	IGTATYEEADRLGKIWVGEGARQTSGGGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY					
	420	430	440	450	460	470

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 891>:

**a238.seq** (partial)

```

1 ATGAATTGTC CTATTCAAAA ATTCATGATG CTGTTTGCGAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCCCGTTTGC
101 GCGATGATAT GCAGGCCAAA CACTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAT CGGGTTTACG CCGTCCAAAC
201 ATTTGATGCA ACTGCGGTCG GCCCCATACT GCCTATTACA CACGAACGGA
251 CAGGATTGTA AGGCATTATC GGTATGAAA CCCATTTTTC AGGACATGGA
301 CATGAAGTAC ACAGTCCGTT CGATAATCAT GATTCAAAAA GCACCTCTGA
351 TTTCAGCGGC GCGGTAGACG GTGGTTTAC CGTTTACCAA CTTATCGGA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCAGGAGG AGCAAGGGAT ATATACAGCT ACTATGTCAA
501 AGGAATTCA AAAAAACAA AGAGTAATAT TGTTCCCGCA GCCCCATTTT
551 CAGACCGCTG GCTAAAAGAA AATGCCGCTG CCGCCTCTGG TTTTTCAGC
601 CGTGCTGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATATCG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT CATTTAGGAA ATTTAAGTCC CGAAGCACAA CTTGCGGCTG
851 CAACCGCATT ACAAGACAGT GCTTTTGGCG TAAAAGACGG TATCAATTCC
901 GCCAGACAAAT GGGCTGATGC CCATCCGAAT ATAACGCAA CAGCCCAAAC
951 TGCCCTTGCC GTAGCAGAGG CCGCAACTAC GGTTTGGGGC GGTAAAAAAG
1001 TAGAACTTAA CCCGACCAA TGGGATTGGG TTAAAAATAC CGGTATATAA
1051 ACACCTGCTG TTCGCACCAT GCATACTTG GATGGGAAA TGGCCGGTGG
1101 GAATAGACCG CCTAAATCTA TAACGTCCAA CAGCAAAGCA GATGCTTCCA
1151 CACAA

```

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

**a238.pep** (partial)

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGGKYHL
51 FGNARGSVKN RYVAVQTFDA TAVGPILPIT HERTGFEGII GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS
151 DYPPPGGARD IYSYYVKGTS TKTKSNIVPR APFSDRWLKE NAGAASGFFS
201 RADEAGKLIW ESDPNKNWWA NRMDDIRGIV QGAVNPFLMG FQGVGIGAIT
251 DSAVSPVTD TAAQOTLQGIN HLGNSPEAQ LAAATALQDS AFAVKDGIN
301 ARQWADAHPN ITATAQTALA VAEATTWVG GKKVELNPTK WDWVKNTRYK
351 TPAVRTMHTL DGEMAGGNRP PKSITSNSKA DASTQ

```

**m238/a238** 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKK
a238	MNLPIQKFMM	LFAAAISLLQ	IPISHANGLD	ARLRDDMQAK	HYEPPGGKYHL	FGNARGSVKN
	70	80	90	100	110	120
m238.pep	RVYAVQTFDA	TAVSPVLPIT	HERTGFEGV	IGYETHFSGH	GHEVHSPFD	HDHDSKSTSDFSG
a238	RVYAVQTFDA	TAVGPILPIT	HERTGFEGV	IGYETHFSGH	GHEVHSPFD	HDHDSKSTSDFSG
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYYVKGTS	TKTKTNIVPQ
a238	GVDGGFTVYQ	LHRTGSEIHP	EDGYDGPQGS	DYPPPGGARD	IYSYYVKGTS	TKTKSNIVPR
	190	200	210	220	230	240
m238.pep	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDVRGIV	QGAVNPFLMG
a238	APFSDRWLKE	NAGAASGFFS	RADEAGKLIW	ESDPNKNWWA	NRMDDIRGIV	QGAVNPFLMG
	250	260	270	280	290	300
m238.pep	FQGVGIGAIT	DSAVSPVTD	TAAQOTLQGI	NDLGKLSPEAQ	LAAASLLQDS	AFVKDGIN

[illegible]

g239.seq

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

g239.ppt

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

m239.seq

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

m239/g239

a239.seq

1	ATGCTCCACC	ATAAAGGTAT	TGCCCGAAAC	CGGCGGATGG	AGGTTTTGTT
51	TTTCTGCCGC	CGCCTGATC	TGCTTCGTGGT	TCGCCAAACG	CGCCTGTTGC
101	AGCCTCATTT	GCGCATAATC	TGCTTCCAAG	CGCATTTCTCT	GTCTTTTTCCG
151	CTTATCCAAA	CGTGTGAAGT	TGAGCCTGTA	CTGGTTTTGC	TGCATCACAA
201	CGGAAAAAGC	GGAACGCGAC	ACCGCAAGCA	GCAGAAGGAA	ATTCAATTTG
251	TTCAATTGCA	TTCAGACGTT	TTTTCTCTGT	ATTGTTCCGG	TATCGGACCG
301	GCAGTCCGCT	CGCCACACG	CAAAACCGCA	CTTCTCGCCC	TCGGATTGGC
351	GGCAATTTCC	CGCTCACCCG	GCTTTAATGC	CTGCCCCGGG	ATTTTCAGGG
401	GCGGCTCGGG	CAAAATCCGCT	TCCCTGACCG	CCGCCACGCG	CGGCAGGGGC
451	GCGTGTTGCG	AATATTTTTT	GACAACTGCC	TTCACAAATG	GGTCTTCCAA
501	CGAATGGAAA	GCAATGACCG	CCAAACGTCC	CGCCTCTTTC	AGACGACACA
551	TGACCTCGCG	CAATACTGCC	CCTACTTCTT	CAAGCTCGCG	GTTAATFAAG
601	ATGCGGATTG	CCTGGAAGGT	GCGCGTCGCA	GGATCCTGCC	CCCCTCGCG
651	AGTACGGACG	TTTTGTGCCA	CGATCTGCGC	CAGCTTGC GG	GTTGTATCGA
701	TGGGACTTTC	CGCCCGTTGC	GCAACAATGG	CGCGCGCAAT	CTGGCGGCTA
751	AACCGCTCTT	CACCATAA			

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
1  MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFLFFR
51  LIQSCEVEPV LVLLHHNGKS GNAHRKQKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

	10	20	30	40	50	60
m239.pep	MLHHK	GXARNR	XMEVLFF	CRRPDR	FVVRQT	RLLQPHLRRI
a239	MLHHK	GIARNR	RRMEVLFF	CRRPDR	FVVRQT	RLLQPHLRRI
	10	20	30	40	50	60
	70	80	90	100	110	120
m239.pep	LVLLH	HNGKSG	NAHRKQ	QKEIQF	VHCHSD	VFLCDCSG
a239	LVLLH	HNGKSG	NAHRKQ	QKEIQF	VHCHSD	VFLCDCSG
	70	80	90	100	110	120
	130	140	150	160	170	180
m239.pep	ASPGF	NALPTI	FRGSSG	KSASLT	AAQRGR	GACCEY
a239	ASPGF	NALPAI	FRGSSG	KSASLT	AAQRGR	GACCEY
	130	140	150	160	170	180
	190	200	210	220	230	240
m239.pep	RRHMT	CGNTAP	TSSSSR	LIKMR	TAWKVR	VAGSCPR
a239	RRHMT	CGNTAP	TSSSSR	LIKMR	TAWKVR	VAGSCPR
	190	200	210	220	230	240
	250					
m239.pep	ATMAR	AIIRLN	NRSSPX			
a239	ATMAR	AIWRLN	NRSSPX			
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
1  atgatagaag tcatacattt cttcggcgcc gaaacgcgca gacagtttgc
51  ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacad gggatcatc gcgcacggga gacggtccga tttataagg
151 ctgcgtattc agccgttcgt tcaaatcggg ttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcgggt
251 acggcacggg tgccgcgctg ttcgctgtct gcccgccggg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcgg gcttttgctt gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccggttttgc gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcaaaa caacttcgcg gccgtcttcg
551 ccatacagcg tgtcttcaag cgaaagtcc aaaccttctt gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
1  MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
51  LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVAPL FAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRSGFCLMVF DRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFITFA
```

550

201 VNIGKSDDVC KQVAHRVMAF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

m240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCGTG CGGCATCCA
351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCCTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATGCC CTGCCGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GGCGTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 902; ORF 240&gt;:

m240.pep

```

1 MIEVIHFFGT ETRRQFACAD VGRFLHDAH IQRGVNMGIA HRRSDFIRL
51 RIQPFVQIGF ARIQCLRNHK RFDCTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGQED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

m240/g240

	10	20	30	40	50	59
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAHIQRGVNMGIAHRRSDFIRLRIQPFVQIG					
	:     :     :     :     :     :					
g240	MIEVIHFFGAETRRQFACADVGRFLHNAHIQRGVNMGIIAHRRSDFIRLRIQPFVQIG					
	10	20	30	40	50	60
	60	70	80	90	100	119
m240.pep	FARIQCLRNHKRFDCTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGQEDFPRAGIQXH					
	:     :     :     :     :     :					
g240	FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGQEDFPRAGIQNH					
	70	80	90	100	110	120
	120	130	140	150	160	179
m240.pep	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR					
	:     :     :     :     :     :					
g240	HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRFCFIARGVQAVHNIALPVPQNNFR					
	130	140	150	160	170	180
	180	190	200	210	220	
m240.pep	AVFAMQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAFX					
	:     :     :     :     :     :					
g240	AVFAIQAVFKRKFTFLTFVAVNIGKSDDVCKQVAHRVMAF					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

a240.seq

```

1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

```

551

```

251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTCCGGCT TTTGCCTGAT GGTATTGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
1  MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RDCRTGFDH IGYGTVAPLF AVCPAGVGI
101 VGGRIQGED FPRAGIQNH RSGFCLMVD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVEFKR KFQTFLTFAV
201 NIGSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

	10	20	30	40	50	60
m240.pep	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRSDFIRLRIQPFVQIGF					
a240	MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRSDFIRLRIQPFVQIGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m240.pep	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGVGVGGRIQGEDFPRAGIQXHH					
a240	ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGVGVGGRIQGEDFPRAGIQNH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m240.pep	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFKARGVQAVHNIALPVPQNDFRA					
a240	RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFARGVQAVHNIALPVPQNDFRA					
	130	140	150	160	170	180
	190	200	210	220		
m240.pep	VFAMQAVEFKRKQTFLTFAVNIGSDDVCKQVAHRVMAFX					
a240	VFAMQAVEFKRKQTFLTFAVNIGSDDVCKQVAHRVMAFX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
1  ATGATAGAAG TCATACATT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTCCGGCT TTTGCCTGAT GGTATTGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
1  MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHPHE PASSTCAAKS

```



552

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCTC ATCGGATGCA TCGCGCACGC TTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCGA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGAACG
351 CCTCTTCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTGTG CAAAAGCTGA TTGTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KKHADFDNR EHARIFDQD LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIAHAFNC
g241						
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVGF	KKHADFDNR
g241						
	130	140	150	160	170	180
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFFGFV
g241						
	190	200	210	220	230	240
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241						
	250	260				
		IMQRNHGIFC	NSHICPFRNS	RLITGAFX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAATCA
151 GCGAACCACG GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC

```

251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGCGG
301	ACCGTGGACA	TGACCGTGTG	CGATTTCCTC	ATCGGATGCA	TCGCGCACAC
351	TTTCAACCGT	AGCCTTAAAG	CGGATTTTCA	TGCCTGCCAA	AGGATGGTTG
401	CCGTCCACCA	CCGCCTTACC	GTCGGCAACA	TCGGTTACAC	GATAGACGAC
451	AACATCGCGC	GTTTCAGGAT	CGTCGGCTTC	AAACATCATG	CCGACTTCGA
501	CTTCAACAGG	GAACACGCCC	GCATCTTAA	TACGGACCAA	CTCCGGATCC
551	TGCTCGCCGA	ACGCATCGTC	GGGGCAAGC	GCCACATCGA	CCGATTCGCC
601	GGCATCCTTA	CCGTGCAACG	CCTCTTCCAC	CAAAGGGAAA	ATGCGCTCGT
651	AACCGCCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTTGTC	CAAAGCTGA
701	TTGTATGGCAT	CATACATCTC	ATAATGCAGC	GAAACCACGG	AATTCTTCAC
751	GATAGCCATA	TTTGTCTCTT	CAGGAACAGC	AGATTAAATTA	CAGGCGCATT
801	CTAA				

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```
a241.pcp
1  MPTRPTRA AK HPTPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDFL IGCTAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDFNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLEF QRENAVTVAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPRFNS RLITGA*
```

**m241/a241 96.0% identity in 177 aa overlap**

```
m241.pep      10          20          30
                RQSVVMTVRAVDMTVCDFLIGCIAHAFNC
a241           |||||:::|||||:::|||||:::||
                QPTYLLHPSNKMPSSEMQTLFRRHQIPPCRQSVVMTVRTVDMTCDFLIGCIAHTFNFR
                   70         80         90        100        110        120

                   40         50         60         70         80         90
m241.pep      SLKADFHACQRMVAVHHRLAVGNIGYTI DDNIAGFRIVGFKHHADFDFNREHARIFD TDQ
a241           |||||:::|||||:::|||||:::||
                SLKADFHACQRMVAVHHRLTVGNIGYTI DDNIAGFRIVGFKHHADFDFNREHARIFD TDQ
                   130        140        150        160        170        180

                   100        110        120        130        140        150
m241.pep      LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
a241           |||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
                LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
                   190        200        210        220        230        240

                   160        170
m241.pep      IMQRNHGIFHDSHICPFRNSRLITGA FX
a241           |||||:::|||||:::|||||:::||
                IMQRNHGILHDSHICPFRNSRLITGA FX
                   250        260
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>>:

g241-1.seq

1	ATGATAGAAG	TCATACATT	CTTCGGCACC	GAAACGCGCA	GACAGTTTGC
51	TTGTGCCGAC	GTGGACGAT	TTCTGCATGA	TGCCGCGCAC	ATCCAAAGAG
101	GGGTAAACAT	GGGTATCGCG	CACGGGAGAC	GGTTCGATT	TATAAGGCTG
151	CGTATTACAG	CGTTCGTTC	AATCGGTTTT	GCCCGCATCC	AATCGGTTTCG
201	CAATCACAAA	CGGTTTGATT	GCCGAACCGG	GTTTCGATCAT	ATGCTTTACG
251	GCACGGTTGC	CGCGCTGTT	GCTGTCTGCC	CGCGCCGGCC	TGTTGGGATC
301	GTAGGCGGGG	GTAATTGCCA	AGGCGAGGAT	TTCCTCCGTC	CGGGCATCCA
351	ATACCACCAC	CGTTCGGGCT	TTTGCTGAT	GGTATTTCGAC	CGCCTTGTTC
401	AACCTTTCAT	AGGCCAAGGT	CTGAATCTCT	TGATCGAGGG	AAAGGATGAT
451	GCTCTTGCCG	TTTTTCCGGG	CTTTAKTTCG	CGGGGAGTCC	AAGCTGTCCA
501	CAATATTGCC	TGCGCGGTCC	CGCAAAACGA	CTTCGCGCTC	GTTCTTCGCCA
551	TGCAAGCTGT	CTTCAAGCGA	AAGTTCCAAA	CCTTCCTGAC	TTTGGCGGTC
601	AATATCGGTA	AATCCGATGA	CGTGTGCAAA	CAGGTTGCC	ATCGGGTAAT
651	GGCGTTTTAA				

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

## g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFEDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

## m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCCG GCCAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCCT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCGGTGGACA TGACCGGTG CGATTTCCTC ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCGA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAAGCTGA
701 TTGTTGGCAT CATACATCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

## m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVMTVR
101 AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHADFDNFNR EHARIFDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPYPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPYPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	70	80	90	100	110	120
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVMTVRVAVDMTVCDLIGICIAHAFNC					
	70	80	90	100	110	120
m241-1.pep	130	140	150	160	170	180
g241	SLKADFHACQRMVAVHRLAVGNIGYTIDDNIAGFRIVGFKHADFDNFREHARIFDQ					
	130	140	150	160	170	180
m241-1.pep	190	200	210	220	230	240
g241	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	250	260				
g241	IMQRNHGIFHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

## a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

101	AAACGCATAC	ACCGCATGAA	CCGGCTTCCT	CAACCTGCGC	GGCAAAATCA
151	GGCAACCGAC	GGGAAAAATT	TCATAATGCC	CAACCGACAT	ACCTTCTCCA
201	TCCGATCCAA	AAATCCCGGT	CTGAAATGGA	ACAAACCCCT	TTACGACGGC
251	ATCAGATACC	TCCAAGCTGC	CGGCAATCAG	TGGTGGTGAT	GACCGTGGGG
301	ACCGTGGACA	TGACCGTGTG	CGATTTCCT	ATCGGATGCA	TCCGGCACAC
351	TTTCAACCGT	AGCCTTAAAG	CGGATTTTCA	TGCCTGCCAA	AGGATGGTTG
401	CCGTCCACCA	CCGCCTTACC	GTCGGCAACA	TCGGTATAC	GATAGACGAC
451	AACATCGCCG	GTTCTCAGAT	CGTCGGCTCT	AAACATCATG	CCGACTTCGA
501	CTTCAACAGG	GAATCAGGCC	CGATCTTCAA	TACCGACCAA	CCCTGGATCC
551	TGCTCGCCGA	ACGCATCGTC	GGGCAGAAAG	GCCACATCGA	CTCGATGCCC
601	GGCATCTCTT	CCGTGCAACG	CCTCTTCCAC	CAAGGGGAAA	ATGCCGTCGT
651	AACCCGCGTG	CAGATACGCA	ATCGGTTCTT	CGGTTTGTG	CAAAAGCTGA
701	TGTATGGCAT	CATACATCTC	ATAATGCAGC	GAAACCAAGG	AAATTCTCAG
751	GATAGCCATA	TTTGTCTTTT	CAGGAACAGC	AGATTAATTA	CAGGCGCATT
801	CTAA				

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

**a241-1.pgp**

1	MPTRPTRAAK	HPTPTTWLQT	AYCPRPFPYR	PSVQTHTPHE	PASSTCAAKS
51	ANRRNEFNHA	QPTYLLHPSN	KLMSEMEQTL	FRRHQIIPPSC	RQSVVMVTTR
101	TVDMTVCDFL	IGCIAHTFNR	SKLADFHACQ	RMVAVHHRLT	VGNIGYTTDR
151	NIAGFPIVGF	KHHADFDENR	EHARIFNTDQ	RLVLLAEIRV	GRKHAIDRIA
201	GILTVQRQLF	QRENVAVTAV	QIRNREFGFV	QKLIVGIIHL	IMQRNHGILH
251	SHTCPFPFRNS	RLITAGF*			

m241-1/a241-1 95.1% identity in 267 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1   atgatcggcg aacttgttgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgtc gatttcgtcg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccc cggatttcgc
201 tttcgtcgcg cacgccgccc aaggccatac ggacatattt ccgccccggt
251 gctttggcga tggattcgcc caaagaggtt ttgccaccgc ccggaggggc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt tttggacgg
351 cgagggtattc caaaatccgt tctttgactt ttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgtgta cgcgggattt
451 tttcttccac ggcagtcgca gcagggtgtc gatgtagttg cgtcacgacg

```

556

```

501 tggattcggc agacatcggc ggcattcattt tgagtttttt cagttcggac
551 aggcattttt cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgctc ttcttcgccc aattctttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttggcgtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgac
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcgttcgc ccagtttcaa ctgcaaatgc
851 gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pep

```

1 MIGELVVLFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51 LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFDGF A QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LOGIQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHN
251 EFQFQLCQOE FHPFADFGNL QNLLALRQFQ LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

```

1 ATGATCGGCA AACTTGTTGT TTTGTTCCGGG ATCGAGCACT TCGAGCAACG
51 CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTGTG GATTTCGTGC
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTGCG
201 TTTGTCGCG CACGCCGCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTGCGC CAAAGAGGTT TTGCCACGC CCGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATT
451 TTTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTCTTTGT
651 GTATCGCTTT AATCTGTTTC TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGGAATTC CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pep

```

1 MIGKLVVLFV IEHFQQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51 LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGF A QRGFAHARRA
101 DQAQNRFAFEF VHTFLDGEVF QNPFFDFFQA VVVGIOHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFEFF QFGQAFFFRF FGHTRLFDIC
201 FOGQFAVFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHN
251 EFQFQLCQOE FHPFADFGNF QNLLALRQFQ LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

	10	20	30	40	50	60
m242.pep	MIGKLVVLFVIEHFQQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA					
	:          :      :  :          :       :     :					
g242	MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVS YACFCHILQNL LAGHRADIGT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242.pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGF A QRGFAHARRADQAQNRFAFEVHTFLDGEVF					
	: :                   : : :					
g242	AVPADFAFVAHAAQGHDTIFPPRCFGDGF A QRGFAHARRADQTQNRTEFELVHTFLDGEVF					
	70	80	90	100	110	120

557

	130	140	150	160	170	180
m242 . pep	QNPFDFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQLEQSVDDVVAYDGGFRRHRWHHFELF					
g242	QNPFDFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQSEQGVDDVVAYDGGFRRHRHHFEFF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m242 . pep	QFGQAFFFRFFGHTRLFDCIQGIIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS					
g242	QFGQAFFFRFFGHTRLFDCIQGIIQFAVFVFFAQFFVYRNFVQIIIFALGFFHLAFDAS					
	190	200	210	220	230	240
	250	260	270	280	290	
m242 . pep	AYAFFGLHNVEFGFQLCQEQFHPFADFGNLFQNLALRQFQLQMRCDRIGX					
g242	AYAFFGLHNVEFGFQLCQEQFHPFADFGNLFQNLALRQFQLQMRCDRIGX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 921>:

a242 . seq

1	ATGATCGGCG	AACTTGTGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAACG
51	CGCTGGCGGG	ATCGCCCCGG	AAGTCGCTAN	CCAATTTGTC	GATTTCGTG
101	AGCAGGAACA	ATGGGTTTTT	TACGCCGGCT	TTTGCCATAT	TCTGCAAAAT
151	CTTACCGGGC	ATGGAGCCGA	TATAGGTGCG	GCGGTGTCCC	CGGATTTGCG
201	TTTCGTGCGC	CACGCCGCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCACGC	CTGGAGGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATACGT	TTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCC	GATGTGGTCG
401	GTATCCAGCA	CCAATCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATT
451	TTTCTTCCAC	GGCAGTTTCA	GCAGGTGTG	GATGTAGTTG	CGTACGACGG
501	TGGATTCGGC	AGACATCGGC	GGCATCATT	TGAGCTTTT	CAGTTCGGAC
551	AGGCATTTT	CTTCCGCTTC	TTTGGTCATA	CCCGCCTTT	TGATATCTGC
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGTC	TTCTTCGCCC	AGTTCTTTGT
651	GTATCGCTTT	AATCTGTTCG	TTCAGATAAT	ATTCGCGCTG	GGATTTTTC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TGCCCATT
801	CGGGAATTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAATGC
851	GCTGCGACCG	TATCGGTTAG			

This corresponds to the amino acid sequence <SEQ ID 922; ORF 242.a>:

a242 . pep

1	MIGELVLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQQVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFDGF	QRFHAWRA
101	DQQRNFAFEF	VHTFLDGEVF	QNPFDFDFFQ	VVVGIIHQSG	FGDVFADAGF
151	FLPRQFEQGV	DVVAYDGGFG	RHRHHFELF	QFGQAFFFRF	FGHTRLFDC
201	EQGIQFAFV	FFAQFFVYR	NLEFVQIIIF	ALGFFHLAFDAS	AYAFFGLHN
251	EFQFQLCQEQ	FHPFADFGNF	QNLALRQFQ	LQMRCDRIG*	

m242/a242 95.2% identity in 289 aa overlap

	10	20	30	40	50	60
m242 . pep	MIGKLVLFGIEHFEQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTGHRADIGA					
a242	MIGELVLLGIKHFEQRAGGIAPEVAXQFVDFVEQEQQVFYAGFCHILQNLTGHGADIGA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m242 . pep	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQRFHARRADQAQNRFAEFVHTFLDGEVF					
a242	AVSPDFAFVAHAAQSHADIFPPRCFGDGFQRFHAWRADQAQNRFAEFVHTFLDGEVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m242 . pep	QNPFDFDFFQAVVVGIIHQSGFGDVFADAGFFLPRQLEQSVDDVVAYDGGFRRHRWHHFELF					

```

a2 42      QNPFDFDFQAVVVGIIHQSGFGDVFADAGFFLPRQFEQGVDDVAYDGGFGRHRRHHFELE
           130      140      150      160      170      180

           190      200      210      220      230      240
m2 42.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIFALGFFHLAFDAS
           |||||||
a2 42      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIFALGFFHLAFDAS
           190      200      210      220      230      240

           250      260      270      280      290
m2 42.pep  AYAFFGLHNVEFGFQLCQQEFHPPADFGNFQNLALRQFQLQMRCDRIGX
           |||||||
a2 42      AYAFFGLHNVEFGFQLCQQEFHPPADFGNFQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcc cgAGTTaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gatactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTGAC GCGGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATcc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTGAC GCGGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCACACAG GGGGCGAaYA GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

m243/g243

```

           10      20      30      40      50      60
m243.pep  MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60

           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```

70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGC GAATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQRFLTESKT GANKSSSSCK PAIFNISASD SSRTSTISS TVTLPM SFLF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANKSSSSCKPAIFSISASDSSRTSTISSMVILPMSFLFSSTTGAVTKSX					
a243	GANKSSSSCKPAIFNISASDSSRTSTISSTVTLPM SFLFSSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1  atgccgectg aagcccggcc ggcgggttca gacggcattg ccgctttact
51  tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcatcgcttg atggatattc
251 ggatcgagct tatcgccgcg tttaggattg atttccttga tttgctggc
301 atcaaacgcc ttctgcaact cattcaaatg catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaacttc tgtccggcga acttggtgct
451 atcggcaatt tctgctggtt ggcggcgccg caggttttgc tegtgtgcca
501 aagcgcgcag ttgttctgct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggtcggcgc gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacggtttc caccgcctcc acattttcaa
651 ccgctttctc actgttttgc tgctgtgtct gttcgctcat atcgatcccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1  MPPEARPAGS DGIAALLRSV YTQNALQEI QIIPQTPSGF LPCHRNHSRA
51  QHTVGQGITL LHHTNHGIGF LLTGHRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLLQLIQS HLHTHFQRIE ITALIQKRFH QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSFLYLT
201 VRISYCLDGF HLRHIFNRF TVLLLCLFAH IVSLKTNWKS KSGYYP SKIR
251 TFSRNFKQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

m244.seq



560

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCTT CTTTCATACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGGGCGGCG CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTCGCTTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTTCT GCACACCGTC
601 CGCATTTTCT ACTGTTTCGA CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

```

m244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQBIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPRLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCFLFAH VSLKTNWKS SYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTONALQBINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQBINQIIPQTPSGFLPCHRNHSRAQHTVGGGITL					
	10	20	30	40	50	60
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFLDLRSIKCFLQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVFLRFQL					
	130	140	150	160	170	180
m244.pep	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVFLRFQL					
	130	140	150	160	170	180
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCFLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCFLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFT VLLLCFLFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFT VLLLCFLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQEQEISHPPNTLPQKPYKRX					
	250	260	270			
m244.pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKXYRRX					
g244	KSGYYPSKIRTFSRNFKQEQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTCATCAGC CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCGCG TTTAGGATTG ATTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CCTACTGTCT CGACGGTTTC CACGCGCTCC ACATTTTCAA
651 CCGCTTCTC ACTGTTTTC TGCTGTGCT GTTCGCTCAT ATCGTATCCC
701 TTAAACAAA TTGGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1  MPSEARQAGS DGIAALLRSV YTONALQEI QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRQLILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRF TVLLCLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

m244.pep	10	20	30	40	50	60
a244	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
a244	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
a244	130	140	150	160	170	180
m244.pep	180	190	200	210	220	239
a244	190	200	210	220	230	240
m244.pep	240	250	260	270		
a244	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1  atgccgcctg aagcccgcc ggcgggttca gacggcattg ccgctttact
```

562

```

51  tgcagcgggt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatattc
251 ggatcgagct taccgcccgc tttaggattg atttcctga ttgctggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcatcgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acatttccac ggcaaaacttc tgcggcgga acttgctgct
451 atcggcaatt tctgctgggt ggcgggcgcg caggttttgc tcgtttgcca
501 aagcggcgag ttgttcgtct tcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctgtt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgcgtgtctt gttcgtcat atcgatccc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccggag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgcgcgc
801 gaatacccta ccgcaaaaac catataaacg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

g244-1.pep

```

1  MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51  QHTVQGQITL LHHTNHGIGF LLTGHRHLRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFQRIE ITALIQKRHF QIILDRQHFF GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFFVQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLCLFAH IVSLKTNWKS KSGYYPISKIR
251 TFSRNFKQRQ EISHPPNTL PQKPYKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

m244-1.seq

```

1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCCT CTTTCATACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGGTTG ATTTCCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCAGC CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAACCTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGCGCGCGC CAGGTTTTGC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTCTT ACTGTTTTCG CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAACAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCTACCG AAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTNHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRS
101 IKCFLLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFF GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPLQILISR LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLCLFAHI VSLKTNWKSK SSYYPRKIRT
251 FSRNFXQXR ISNSFSNPLP KK*

```

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLPCHRNHSRAQHTVQGQITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTNHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLLVQSHLHAHFQRIE					
g244-1	LHHTNHGIGFLLTGHRHLRLMDIRIELIARFRIDFLDLRGIKRLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

563

	130	140	150	160	170	180
m244-1.pep	IAALIQRHFQIILDRQHFHKGKLLSGELVRIRNFFLVAAQVLLVCQSAALLVFQRLRFQL					
g244-1	ITALIQRHFQIILDRQHFHKGKLLSGELVRIGNFFLVAAQVLLVCQSAQLFVFQRLRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTFSRNFXQQRISNSFSNPLPKKX					
g244-1	KSGYYPSKIRTFSRNFKQRQEISHPPNPLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

1	ATGCCGCTCG	AAGCCCGACA	GGCGGGTTCA	GACGGCATTG	CCGCTTTACT
51	TCGATCGGTT	TATACGCAAA	ACGCGCTTCA	GGAATAAAT	CAGATTATTC
101	CCCAGACGCC	TTCAGGCTTC	CTTCTGTGCC	ACCGTAACCA	TAGCCGGGCG
151	CAACACGCGG	TCGGACAGCG	TATAACCCTT	CTTCATCAGC	CCCACCACGG
201	TATTGGGTTT	CTGTTTCGCT	GCCACCGCCT	GCATCGCCTG	ATGGATATTC
251	GGATCGAGCT	TATCGCCCGC	TTTAGGATTG	ATTTCCTTGA	TTTGGGTAGC
301	ATCAAATGCT	TTCTGCAACT	CGTTCAAAGT	CATCTGCACG	CCCATTTTCA
351	GCGCATCGAA	ATTGCCGCTC	TGATCCAAAA	GCGCCATTTC	CAGATAATCC
401	TTGACCGGCA	GCATTTCAC	GGCAAATTC	TGTCCGGCGA	ACTTGTGCGT
451	ATCCGCAATT	TCCTGCTGGT	GGCGGCGGCG	CAGGTTTTC	TCGTTTGCCA
501	AAGCGCGCAG	CTGCTCGTCT	TTCAACTGCG	CTTCCAGCTC	GGCAATCCGC
551	GCCTGCAAT	CCTCATAAGC	CGGCTCTGCG	GCAGCCTGTT	CCTGCACACC
601	GTCGCGCATT	CCTACTGTCT	CGACGGTTTC	CACGCGCTCC	ACATTTTCAA
651	CCGCTTCTTC	ACTGTTTTC	TGCTGTGTCT	GTTGCTCAT	ATCGTATCCC
701	TTAAACAAA	TTGGAAATCA	AAATCCAGTT	ATTACCCGCG	CAAGATAAGG
751	ACATTTTCAA	GAAACTTCAA	GCAAAGGCAG	AGAATTTCAA	ATTCATTTTC
801	AAATCCCTTA	CCGAAAAAT	AA		

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

1	MPSEARQAGS	DGIAALLRSV	YTONALQEI	QIIPQTPSGF	LLCHRNHSRA
51	QHAVGQRITL	LHHAHHGIGF	LFACHRLHRL	MDIRIELIAR	FRIDFLDLRS
101	IKCFLQLVQS	HLHAHFQRIE	IAALIQRHF	QIILDRQHFH	GKLLSGELVR
151	IRNFFLVAA	QVLLVCQSAQ	LLVFQRLRFQ	GNPRLQILIS	RLCGSLFLHT
201	VRISYCLDGF	HRLHIFNRFF	TVLLCLFAH	IVSLKTNWKS	KSSYYPRKIR
251	TFSRNFRQ	RISNSFSNPL	PKK*		

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEIINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEIINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQRHFQIILDRQHFHKGKLLSGELVRIRNFFLVAAQVLLVCQSA-LLVFQRLRFQ					
a244-1	IAALIQRHFQIILDRQHFHKGKLLSGELVRIRNFFLVAAQVLLVCQSAQLLVFQRLRFQ					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLCLFAHIVSLKTNWKS					
	190	200	210	220	230	240

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgcc tctgtttcga
51  ccagacacag cgtgcccggt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgcgtga aatatcgcgc agggctttgc gggcgaaatcc
151 ggtcagttgt tccacgtcgt ctgtaagcgg tggtccgagg ttttggtgga
201 acagttctgt gacctgttct ttggtttat gtagtgcggg catcacgata
251 tgggtcgggt tttcgctcgc cattggacg ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 ctctcgctgac catggatttg cctttgacca tcagcttgcc gtttttggct
401 gtgatgttgc cgtggataat ttggcaggct tcggcagggg tttccgcccc
451 gtgtactttc acgccaact tagtcagggt ttcttccaac tgcctcagca
501 qcgcgggttaa
```

g246.pep

1	MYGRNGSTQA	AVAFVFDQTQ	RARFGNGEVY	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCKR	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCVF	IMVQLDFPAD	HGFAFDHQLA	VFGDDVVDN	LAGFGRGFRP
151	VYFHAOLSOV	FFOLLQQRG*			

```
m246.seq (partial)
1 ATGCACGGGC GGTACGGTGG TACTCAAGCG ACCGTTgCTT CGTTTTCCAC
51 CAGACACAGC GTACCTGTTT CAGCAACGGC AAAGTTTACG CCACTCAAAC
101 CGACATCGGC AGTGCTGTAA ATATCGCGCA GTGCTTTACG GGCGAAGCCG
151 GTCAGTTGGT CTACATCGTC TGTCAGCGGC GTACCGAGGT TTTGGTGGAA
201 CAGTTCGCTA ACCTGTTCTT TGGTTTGTG GATAGCAGGC ATCACGATAT
251 GGGTCGGTTT TTCGCCTGCC ATTTGGACGA TGAActCGCC CAAGTCGCTT
301 TCTACCGCTT TAATGcyTTT TGCTTCAAG TAATGrTTCA GCTCGATTTT
351 CTCGCCTGACC ATCGGATTTG CTTTGACCAT CAGCTTCCGG TTTTTFGGCTG
401 TGATGATGTC GTGGATAATT TTTGACGGCT CGGTCTGGGGT TTCTGCCCG...
```

```
m246.pep (partial)
1  MHGRYGGTQA TVAFVFHQIQ RTCFSNGKVY ATQTDIGSAV NIAQCFTGEA
51  GQLVYIVCQR RTEVLVEQFA NLFFGFVDSR HHDGMRFFAC HLDDELAQVA
101 FYRFNAFCFK IMXQLDFLAD HRFAFDHQLA VFGCDVVDN LAGFGRGFCP...
```

**Homology with a predicted ORF from *N. gonorrhoeae***

m246/q246

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQ	TQRTCF	SGNKVYATQTDIG	SAVNIAQCFTGEAGQLVYIV	CQR	
	:	: : :	: :	: : : : :	: : : : :	: :
g246	MYGRNGSTQA	AVAFVFDQ	TQRRARFGNGEVYAAQADIG	SAVNIAQGFAGESGQLVHV	VCKR	
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDD	ELAQVAFYR	FNAPCFKIMXQLD	FLAD		
	:	: : : : :	:	: : : : : : : : : : : : : : :	: : : : : : : : : : : :	: : :
g246	CAEVLVEQFADLFFGFMDCGHHDMGRFFACHLDD	KLAAQVAFHRLNAPCFKIMVQLD	FFAD			

565

	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFAFDHQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246.seq (partial)

```

1  ATGCACGGGC GGAACGGTGG TACTCAAGCG ACCGTGCGCT TCGTTTTCCT
51  CCAGACACAG CGTACCTGTT TCAGCAACGG CGAAGTTCAC GCCACTCAAA
101 CCGACATCGG CAGTGTCTGTA AATATCGCGC AGTGCTTTAC GGGCGAAGCC
151 GGTCAGTTGG TCTACGTCGT CCGTTAACGG TGTGCCGAGG TTTTGGTGGA
201 ACAGTTCGCT AACCTGTTCT TTGGTTTTAT GGATTGCGGG CATCACCATA
251 TGGGTCGGTT TTTCACCTGC CATTGAGCG ATGAAGTCGC CCAAGTCGCT
301 TTCCACCGCT TTAATGCCTT TTGCTTCAAG ATAATGGTTC AGCTCGATTT
351 CCTCGCTGAC CATCGATTG CCTTTGACCA TCAGCTTGCC GTTTTGGCT
401 GTGATGATGT CGTGGATGAT TTCGCAGGCT TCGGCCGGTG TTTCCGCCCA
451 GTGTACTTTT ACGCCCAACT TGGTCAGGTT TTCTCCAGC TGCTCCAGCA
501 G

```

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246.pep (partial)

```

1  MHGRNGGTQA TVAFVEHOTQ RTCFSNGEVH ATQTDIGSAV NIAQCFTGEA
51  GQLVYVVR*R CAEVLVEQFA NLFFGFMDCG HDMGRFFTC HLDDELAQVA
101 FHRFNAFCFK IMVQLDFLAD HRFAFDHQLA VFGCDDVDD FAGFGRCFRP
151 VYFYAQLGQV FFQLLQQ

```

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQTQRTCFNSNGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQTQRTCFNSNGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHDMGRFFTCCHLDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246.pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVDDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247.seq

```

1  atgaaacgta aaatgctaaa cgtaccaaag ggcgggttatg atggtatgaa
51  gggttttacc attgttgaat ttctggttgc gggcctgctc agtataattg
101 tcctgatagc ggtcgtatcg agttacttta catcccgga attaaatgat
151 gtggcaaacg agcgtcttgc cattcaacag gatttgcgga atgcggcaac
201 attaattgtc cgcgatgcaa gaatggcggg gagcttcggt tgtttcaata
251 tgtccgagca tactaaagac gatattgttg attcaagtaa tcaaactcaa
301 tctaaccctg caaaacccgg tgccaaacaa gaaaatcccc ttttttcctt
351 aaaaaggagc ggcattgata aacaactgat tcccgttgct gaatccatag
401 atattaaata tccgggtttt atccagcgcc ttaacgcatt ggtttttcaa
451 tacggtatcg atgatcttga tgcgagtgtc gagactgttg tagtcagcag
501 ctgttccaaa atagcaaac cgggtaagaa aatatctacc ttgcaagaag
551 caaagagtgc attacagatt actaatgatg ataaacaaaa tggaaatatc

```

```

601 acccgtcaga aacatgtggt caatgcctat gcggtcggca ggtttggcaa
651 taatgaggaa agtttgttcc gcttccaatt ggatgataag ggcaagtggg
701 gtaatcctca gttgctcgtg aaaaagggtta aacgtatgga tgtgcggtat
751 atttatgttt ccggttgtcc tgaagatgaa gatgccggca aagaggaaaa
801 attcagatat acgaataaat tcgacaaatc caaaaatgct gttacgcctg
851 ccggggtgga ggttttattg gatagcggcc ttaatgccaa gattgccgct
901 tcttcagaca atagtattta tgcttaccgt atcaatgcga caatacgcgg
951 gggaaatgta tgcgcaaaaca gaacactttg a

```

This corresponds to the amino acid sequence <SEQ ID 948; ORF 247.ng>:

g247.pep

```

1 MKRKMLNVPK GGYDGMKGFT IVEFLVAGLL SIIVLIAVVS SYFTSRKLND
51 VANERLAIQQ DLRNAATLIV RDARMAGSFG CFNMSEHTKD DIVDSSNQTS
101 SNLAKPGAKQ ENPLFSLKRS GMDKQLIPVA ESIDIKYPGF IQRLNALVFQ
151 YGIDDLASA ETVVSSCSK IAKPGKKIST LQEAKSALQI TNDDKQNGNI
201 TRQKHVVNAY AVGRFGNNEE SLFRFQLDDK GKWGNPQLLV KVKRMDVRY
251 IYVSGCPEDE DAGKEEKFRY TNKFDKSKNA VTPAGVEVLL DSGLNAKIAA
301 SSDNSIYAYR INATIRGGNV CANRTL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 949>:

m247.seq (partial)

```

1 ATsAGACGTA AAATGCTAAA CGTwsyArAA GGCAGTTATG ATGGTATGAA
51 AGGTTTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCGGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 GCGGCAAACG AGCGTCTTGC CGCGCAACAG GATTTCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CCGCTTCGGT TGTTTCAATA
251 TGTCCGAGCA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTT CCTTAAAAAG GAACGGTATA GATAAACTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTC AATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AAGTTTGTTC CGTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAACTCTC AGTTGC...

```

This corresponds to the amino acid sequence <SEQ ID 950; ORF 247>:

m247.pep (partial)

```

1 XRRKMLNVXX GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51 AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPTTQON
101 SPFSLKRNGI DKLIPIAESS NINYQNFFQV GSALIFQYGI DDVNASTATT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEESLF RFQLDDKGKW GNPQL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 247 shows 69.3% identity over a 238 aa overlap with a predicted ORF (ORF 247.ng) from *N. gonorrhoeae*:

m247/g247

	10	20	30	40	50	60
m247.pep	XRRKMLNVXXGSYDGMKGFTIIEFLVAGLLSMIVLMAVGSSYFTSRKLND AANERLAAQQ					
	:      :     :     :     :     :     :					
g247	MKRKMLNVPKGGYDGMKGFTIVEFLVAGLLSIIVLIAVSSYFTSRKLNDVANERLAIQQ					
	10	20	30	40	50	60
	70	80	90	100		
m247.pep	DLRNAATLIVRDARMAGGFGCFNMSEHPATDVI-----PDTTQONS PFSLKRN					
	:     :     :     :     :     :					
g247	DLRNAATLIVRDARMAGSFGCFNMSEHTKDDIVDSSNQTSNLAKPGAKQENPLFSLKRS					
	70	80	90	100	110	120
	110	120	130	140	150	160
m247.pep	GIDK-LIPIAESSNINYQNFFQVGSALIFQYGIDVDVNASTATTVVSSCAAISKPGKQIPT					
	:    :    :    :    :   :     :     :     :					





```
g247-1.seq (partial) ..
1      CCGGCTGGCCA AACAGAAAAA TCCCCTTTT TCCTTAAAAA GGAGCGGCAT
51     GGGATPAACAA CTGATCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101    GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATATG
151    CTTGATGCGA GTGCTGAGAC TGTGTAGTTC AGCAGCTGTT CCAAAATAGC
201    AAAACCGGGT AAGAAATAT TACCTTGCA AGAAGCAAA CTGGCATTAC
251    AGATTACTAA TGATGATAAA CAAATGGAA ATATCACCCG TCAGAAACAT
301    GTGGTCAATG CCTATGCGGT CGGAGGTTT GGCAATAATG AGGAAAGTTT
351    GTTCCGCTTC CAATGGGATG ATAAGGCGAA GTGGGGTAAT CCTCAGTTGC
401    TCGTGAAAAA GGTTAACGT ATGGATGTGC GGTATATTTA TGTTCGCGT
451    TGCTCTGAAG ATGAAGATGC CGGCAAGAG GAAAAATTC AATATACGAA
501    TAAATTCCGAC AAATCAAAA ATGCTGTTAC CGCTGCCGG GTGGAGGTTT
551    TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601    ATTTATGCTT ACCGTATCAA TGCGACAATA CGCGGGGAA ATGTATCGCG
651    AAACAGAACA CTTTGA
```

g247-1.pep (partial) ...

1	PGAQENPLF	SLKRSQMDKQ	LIPVAESIDI	KYPGFIQRLN	ALVFQYIGDD
51	LDAASATLV	SSKSIKAPG	KKISTLQEAQ	SALQITNDKQ	QNGNITROKH
101	VVNAYAVGRF	GNNEESLFRF	QLDDKRGKWN	PQLLVKKVKR	MDVRYIYVSG
151	CPEDEDAGKE	EKFYRTNFKD	SKKNAVTPAG	VEVLLDSGLN	AKIAASSDNS
201	IYAYRINATI	RGGRVCAKNT	L*		

```
m247-1.seq
1  ATGAGACGTA  AAATGCTAAA  CGTACCAAAA  GGCAGTTATG  ATGGTATGAA
51  AGGTTTACC  ATTATTGAAT  TTTTGGTTCG  GGGCTGCTC  AGTATGATTG
101 TCCTGATGCG  GGTGCGATCG  AGTTACTTCA  CATCCCGGAA  ATTAATGAT
151 GCGGCAACG  AGCCTCTTGC  CGCACAACAG  GATTTCGGTA  ATCGCGCAAC
201 ATTGATTGTC  CGCGATGCGA  GACATGACAG  CGGCTTCGGT  TGTTTCAATA
251 TGTCCGAGCA  TCCTGCAACT  GATGTTATTC  CCGATACGAC  GCAACAAAAT
301 TCTCCTTTT  CCTTAAAAAG  GAACGGTATA  GATAAACTTA  TTCCCATAGC
351 GGAATCTTCA  AATATCAATT  ATCAGAATTT  TTTCCAGGTT  GGTAGCGCAT
401 TGATTTTTC  ATACGGAAAT  GATGATGTTA  ATCGAAGCAC  CGGCACATCC
451 GTCGTCAGCA  GCTGTGCCGC  AATATCGAAA  CCGGGCARGC  AAATCCCTAT
501 TTTAGAAGAT  GCAAAAAAAG  AATTGAAGAT  TCCGGATCAG  GATAAGGAGC
551 AAAATGGCAA  TATAGCCGCT  CAAAGCGATG  TGGTCAATGC  CTATGCGGTC
601 GGCAGGATTG  CCGATGAGGA  AGGTTTGTTT  CGCTTCCAAT  TGGATGATAA
651 GGGCAAGTGG  GGTAACTCTC  AGTTGCTCTG  GAAAAGAGTT  AGCATATGTA
701 AAGTGCGGTA  TATCTATGTT  TCCGGCTGTC  CTGAAGATGA  AGATGCCGGA
751 AAAGAGGAAA  CATTCAAATG  TACGGATAAA  TTCGACACGC  CCCAAATGCG
801 TGTTACGCCC  GCCGGGGTGG  AGGTTTATTT  GAGTAGCGGT  ACTGATACCA
851 AGATTGCCCG  TTCTTCAGAC  AATCATATTT  ATGCTTACCG  TATCGATGCG
901 ACAATACCGG  GGGGAAATGT  ATGCCGAAAC  AGAACACTTT  GA
```

m247-1.pap

1	MRRKMLNVPK	GSYDGMKGFT	II EFLVAGLL	SMIVLMVGS	SYFTSRKLN
51	AA NERLAAQI	DLRNAATLIV	RDARMAGFG	CFNMSEHPAT	DVIDPTTQN
101	SPFSLKRNIG	DKLPIAESS	NIRNYQNFQV	GSALIFQYGI	DDVNASTAT
151	VVSSCAAISK	PGKQIPTLED	AKKELKIPDQ	DKEQNGNIAR	QRHVVNAYAV
201	GRIADEEGLF	RFQLDDKGKW	GNPQLLVKKV	RHMKVRYIYV	SGCPEDDDAG
251	KEETFKYTDK	FDSAQNAVPT	AGVEVLLSSG	TDTKIAASSD	NHIYAYRIDA
301	TRIGGNVCAN	RTL*			

m247-1 / g247-1 72.1% identity in 222 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

1	AATAATACAG	CTAAATTGAT	TCCTATTGCT	GAATCCACAG	ATATTAATA
51	TCCGGGTTTT	GCCGAGGCTC	GTCGCGCAT	GATTTTCCAA	TACGGCATCG
101	ATGACTCTGA	TCCGAGTGCT	GAGACTGTTG	TAGTCAGCAG	CTGTTCCAAA
151	ATAGCAAAAC	CGGCTAAGAA	AATAATCTACC	TGTCAAGAAG	CAAGAGGTGC
201	ATTACAGATT	ACTAATGATG	ATAAACAAAA	TGAAATATC	ACCGTCAAA
251	GGCATGTGGT	CAATGCCTTA	GCGGTGGCA	GGATTGCCGG	TGAGGAAGGT
301	TGTTCCCGTT	TCCAATTGGA	TGATAAGGGC	AAGTGGGGTA	ATCTTCAGTT
351	GCTCGTGAA	AAGATTAGAC	ATATGAAAT	CGGGTATATC	TATGTTTCCG
401	ACTGTCTCTG	AGATGACGAT	GCCGGCAAAG	AGGAAAAATT	CAAAATACG
451	GGTACATTCG	ACAGCTCCAC	AAATGCTGTT	ACGCCCCGCC	GGGTGGAGGT
501	TTTATTGAGT	AGCGGTACTG	ATACCAAGAT	TGCCGCTTCT	TCAGACAATC
551	ATATTATATG	TTACCGTATC	GATGCGACAA	TACGCGGGGG	AAATGTATGC
601	GCAACACGAA	CACCTTTGA			

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TND DKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEKFFYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIIYAYRI DATIRGGNVC
201 ANRTL*

```

[illegible]

570

```

m247-1      YAVGRIADEEGLFRFQLDDRGKWNQPLLKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            | |||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa tttcagggtt tggatttggg atatgctgcg gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaaggct tgtgtaccgc agtgaatgtg
301 cggacaaata ataattgtag tgaagaggct tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttctgacctt gcaaagtctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgctg caggcgctag caaaatgccg cgctatatta tcgaatatatt
501 aggcgtgaag aacggacaaa atgtttatcg ggttactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcaataat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNGSEEA FGNIVVQGKP AVEAVKRSCP AKSGKNSTDL CIDNKGMEYN
151 KGAAGVSKMP RYIIEYLGVK NGQNVYRVTA KAWGKNANTV VVLQSYVGN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.TyWT
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGTCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACGTGT GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCac.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGtAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISKNESDRKL AXSLAEXXXR
51  EGELQVLDLE YDTSKVTFS ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXEYKKG TRSVTKMPRY IIEYLGvXNG
151 ENVYRVTAKA WgKNANTVVV LQSYVSNND *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISKNESDRKLAXS
               | ||: |||| | |||| | |||| | |||| | |||| | |||| |

```

571

```

g248      MRKQNTLTGIPTSDGQRGSALFIVLMVMIVVAFVLTAAQSYNTEQRI SANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTDSKVTFSENCGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  |||:||||| :||||||| ||| :||||| :|||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNGSEEAFFGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA----NSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVKNGENVYRVTA
           :||||||| |||||:| |||:| :|:||||| :|:|
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYII EYLGVKNGENVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNINDEX
           |||||:|||||
g248      KAWGKNANTVVVLQSYVGNINDEX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTACAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCGG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQGFALFIVLMVMIV VAEFLVVTAAQ SYNTEQRI SA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLGVKNGENV YRVTAKAWGK NANTVVVLQS YVSNINDEX*

```

m248/a248 89.4% identity in 180 aa overlap

```

m248.pep      10      20      30      40
               GFALLIVLMVXIVVAFXXVTAAQSYNTEQRI SXNESDRKLAXS
               |||:||||| ||||| ||||| ||||| |||||
a248          MRKQNTLTGIPTSDGQGFALFIVLMVMIVVAFVLTAAQSYNTEQRI SANESDRKLALS
               10      20      30      40      50      60

               50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTDSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  |||||:||||| |||||:| |||:| :|:||||| :|:|
a248      LAEAAALREGEFQVLDLEYDTDSKVTFSENCGLCTAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100      110      120

           110      120      130      140      150      160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVKNGENVYRVTA KAWGK
           ||||| :|| ||||:| |||:| :|:||||| :|:|
a248      VEAVKRSCTAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGVKNGENVYRVTA KAWGK
           130      140      150      160      170      180

           170      180
m248.pep  NANTVVVLQSYVSNINDEX

```

a248

|||||  
NANTVVVLQSYVSNINDEX  
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCITTGTCT TTGGCCGAGG CGGCTTTGCC
201 GGAAGGCGAA CTTCAAGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAGAGTTC TGTGTGCCG AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCACCC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLVTTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEA VRSCPA NSTDL CIDKK GMEYKKGTRS
151 VSKMPRIIE YLGVKNGENV YRVTAKAWGK NANTVVVLQS YVSNNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQKPT					
g248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQKPT					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA----NSTDL CIDKKGMEYKKGTRSVSKMPRIIEYLGVKNGENVYRVTA					
	:					
g248	AVEAVKRSCPAKSGKNSTDL CIDNKGMEYNKGAAGVSKMPRIIEYLGVKNGENVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNINDEX					
g248	KAWGKNANTVVVLQSYVGNINDEX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLVTTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQKPT					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQKPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDL CIDKKGMEYKKGTRSVSKMPRIIEYLGVKNGENVYRVTA					
	:					
a248	VEAVKRSCPAKSTGL CIDNKGMEYKKGTRSVSKMPRIIEYLGVKNGENVYRVTA					
	130	140	150	160	170	180

```

                190
m248-1 . pep  NANTVVVLQSYVSNNDEX
                |||||
a248          NANTVVVLQSYVSNNDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249 . seq
1   atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtattttgg
101 cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151 acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201 gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251 acatgggaaa acagacacta tcagctgtgg atggtgagtt tatgcttgat
301 gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351 tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401 tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcggtgct
451 ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501 attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551 ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcggg
601 ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249 . pep
1   MKNNDCLRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  TQTIVSQITO NLMEGMLMNP TIDLSNKKY YSLYMGKQTL SAVDGEFMLD
101 AEKSKAQLAE EQLKRFSHEL KNALPDVAI HYAVCKDSSG DAPTLSDSGA
151 PSSNCDNKAN GDTLIKVLWV NDSAGDSDIS RTNLEVSGDN IVYTYQARVG
201 GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249 . seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTACAGTTG CCGACAGTCN NNNNNNNNNN NNNNNNNNNN
151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301 GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351 TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401 TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451 TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501 GTGGGTAAAT GATTCGGCAG GGGATTCCGA TATTTCCCGT ACCAATCTTG
551 AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCCGAGGT
601 CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249 . pep
1   MKNNDCFRLK DSQSGMALIE VLVAMLVLTIGILALLSVQL RTVXXXXXXXX
51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKKY YNLYMGNHTL SAVDGDFAID
101 AMKTKGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151 SSNCDNKANG DTLIKVLWVN DSAGDSDISR TNLEVSGDNI VYTYQARVGG
201 RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

                10      20      30      40      50      60
m249 . pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
                |||||:||||: |||||||||||||||||||||||||||||: : :

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249 . pep XLMEGMLMNPTIDSDSNKKNYNLYMGNHTLSAVDGDFAIDAMKTGQLAEQALKRFSYEL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      NLMEGMLMNPTIDLDSNKKNYSLYMGKQTL SAVDGEFMLDAEKSQAQLAEQALKRFSHEL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249 . pep KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLTKVLWVND SAGDS DIS
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      KNALPDAAAIHYAVCKDSDGAPTLSGAFSSNCDNKANGDTLTKVLWVND SAGDS DIS
           130     140     150     160     170     180

           180     190     200
m249 . pep RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGGTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCAGTTG CCGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AACTAAGAC GCAGTTGGCA GAGGCACAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGCGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTCTGCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1  MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  QTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND SAGDS DI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249 . pep MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAEQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249 . pep XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEQALKRFSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNHHSVVDGDFQVDAIKTKTQLAEQALKRFSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249 . pep LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND SAGDS DI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND SAGDS DI
           130     140     150     160     170     180

```





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D + M G A + T L + A + L ++ ++KN LP A  
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAFPTAPSSCTPLPDAIKDRLGCVAEQVKNELEFGAG 126  
 Query: 130 AI---HYAVCKDSSGVAPTLASGSTFSSNCDGSANGDTL-IKVLWVNDASAGSDIARTNL 185  
 + Y +C+ S +CDG G L I++ W + A ++  
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLLEIRLAWRGKQACVNAADSSA 172  
 Query: 186 ETN 188  
 +T+  
 Sbjct: 173 DTS 175  
 m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	DSQSG	MALIE	VLVAM	LVLTIG
	10	20	30	40	50	60
m249-1.pep	NLM	EGMLM	NPTID	SDSNK	KNYNLY	MGNH-TL
a249	NLM	EGMLM	NPTID	SDSNK	KNYNLY	MGNH-TL
	70	80	90	100	110	119
m249-1.pep	SAVDG	DFAID	AMKTG	QQLAE	AQLKR	FSYE
a249	SAVDG	DFAID	AMKTG	QQLAE	AQLKR	FSYE
	70	80	90	100	110	120
m249-1.pep	LKNAL	PDAAAI	HYAVCK	DSSGN	APTLS-	GNAFSS
a249	LKNAL	PDAAAI	HYAVCK	DSSGN	APTLS-	GNAFSS
	120	130	140	150	160	170
m249-1.pep	CDNKAN	GDTLIK	VLWVN	DASAG	DSDI	
a249	CDNKAN	GDTLIK	VLWVN	DASAG	DSDI	
	130	140	150	160	170	180
m249-1.pep	SRTN	LEVSG	DNIVY	TYQAR	VGGREX	
a249	SRTN	LEVSG	DNIVY	TYQAR	VGGREX	
	180	190	200			
m249-1.pep	ARTN	LETNG	NNIVY	TYQAR	VGGREX	
a249	ARTN	LETNG	NNIVY	TYQAR	VGGREX	
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1  atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51  aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggta
101 tgcagggcgg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacgtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataacctt atgattaatt
251 cgcgccatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1  MHTASPRDE FIRIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51  GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1  ATGCACACCT TCCCCGCATA ACGAATTAT ACGCGGCATC AAAGAAAGTT
51  CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GCGCGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCGAAGC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1  MHTSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51  MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

              10      20      30      40      50      59
m250.pep    MHTPSPHNEFIRGIKESSPMLIGLLPWALIILGMGGQKGMWLEMLLMTSMNFAGGSEF
              ||::|||||||||||||||||||||||||||:|||||:|||||
g250        MHTTASPRDEFIRGIKESSPMLIGLLPWALIILGMGGQKGMGRLEMLLMTGMNFAGGSEF
              10      20      30      40      50      60

              60      70      80      90      100     110
m250.pep    ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVFYVX
              |||||||||||||||||||:|||||
g250        ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRARAVFYV
              70      80      90      100     110

```

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGCG	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGGCGG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACCTCTG	CCGATACTCG	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CCGTATGGGG	G. CGGCACCT	GCCCCGCACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

1 MTHISSPRNE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MSWLEMLLMT  
51 GMNFAGGSEF ATVNLAEP L PILLIATVTF MINSRHILMG XGTC PAPERN  
101 TAEKSRA RTV FYV\*

```

59          10          20          30          40          50
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTSMNFAGGSEF
|
|:|||||||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGSWLEMLLMTGMNFAGGSEF
          10          20          30          40          50
60

60          70          80          90          100          110
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRARTVIFYVX
|:|||||||||||||||||||||:|||||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCAPAPERNTAEKSRARTVIFYVX
          70          80          90          100          110

```

```

1  atgcctgacc caatagggat tcttttcgct gccgtcgagg ttgatttttt
51  tgcgcttggt ttgagggggc gttttcaacg aataggcgcg gttggcatgt
101 tgataataat aatcctgatg gcggagggtc gaaccaaacc ggtcgtaacc

```

578

```

151 gaggttgacg ctcaggttgt ggcggatttt ggcggatcgc aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaa at cagcggctgc
251 gatttgtagt aggaagacgg cttgtcggca ctcgggcggc aatatttgtc
301 cgaaccgtcg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgccc aagtgtctta
401 tcggcattgg tatagacata ttccaaaccg tagcggcttt tgggtgctgt
451 ctcgtcgtaa aacacgccc gaccgtattc cgcgcccacc tccgcaccgt
501 tttcaccgtt ggtaatcagc ccgctgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta ttttcatcaa aaaccgcctt
601 ggtcaggaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgtcg
651 tgcgttcgag tatgccgccc atgtagtgcc gtttgttttc aaaacgaaaa
701 cccggcgga acagccacga cgggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1 MPDPGILFA AVGVDFFAV LRGRFORIGA VGMLIIIIIM AEVGTKTVVT
51 EVDAQVADF GGIEGFFECR LQEPVAFVNV HAVGFVVGRR LVGTRAAIFV
101 RTVGGTVRL KMIQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFVVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYS VFFIFIKNRL
201 GQECRNHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1 ATGCGTGCTG CCGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCACCC
51 TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTC CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTCACTGCCG GTTGGGGCTG ATTTTTTTGC CGTGTGTTTG AGGGGGCGTG
251 TCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTCACGCTC AGGTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTTGA ATGCGCGCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTTGTCCGA ACCGTCGGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTGCCGGTC GTAAGAGAGG
551 CGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAAC ACGCCGTAC
651 CGTATTCGCG GCCCACCAGC GCACCGTTTT CGCCGTTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCCCCG GTATTGCGG TTACCGGGCA AAGAACCCGC
751 CTGTTTTTTA TTTGCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGCGAA GTTTGTTGCG TGTGTTGAG TATGCCGCCG
851 ATGTAGTGCC GCTTATCTC AAAACGAAAA CCCGGCGGGA ACAGCCACGA
901 CCGGCTTTTC TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1 MRAAVVVAQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51 LPRNDISPAY GDPGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIIIILMA
101 EIRAKAVKPE IHAQVADFG GIEGFFECRL QEPVAFVNVH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFVRL VVKHARTVFR AHQRTVFAVG QSAVFVVAR VFAVTGQTR
251 LFFICIKNRL GQECRNHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40          50          60          70          80          90
m251.pep  TVDAARRAVRISIVAQAADLPRNDISPAYGDPGAGFTA VGADFFAVVL RGRVRRIGAVG
          |||| |::||:||||||| |::|||
g251      MPDPGILFAAVGVDFFAVVL RGRFORIGA
          10          20          30

```



580

a251	ADPIGLVLAAVGVGGF----RGRFRRI	70	80	90	100	110
m251.pep	GIEGFFECRLQEPVAFPNHAIGFVIGKRLVGTAAIFVRTVGRTVRLKMIQTALPV	130	140	150	160	170
a251	GIEGFFECRLQEPVAFPNHAGFVVGKRLVGTAAIFVRTVGRTVRLKMIQTALPV	120	130	140	150	160
m251.pep	VREAGIIRPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR	190	200	210	220	230
a251	VREAGIIHPSVFIGIGIDIFQTVAAFGVRLVVKHARTVFRAHQRTVFAVGKQSAVFVVAR	180	190	200	210	220
m251.pep	VFAVTGQTRLFFICIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR	250	260	270	280	290
a251	VFAVASYSR-VFSIFIKNRLGQECRNRIARVESLLRVFEYAADVPLILKTKTRAEQPR	240	250	260	270	280
m251.pep	PAFVX					
a251	SAFVX					
	300					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 987>:

g253.seq

```

1  atgatcgaca gggaccgtat gttgcgggac acgttgaac gtgtgcgtgc
51  ggggtcgttc tggttatggg tgggtggtggc atcgatgatg tttaccgcgc
101 gattttcagg cacttatctt ctgatggaca atcaggggct gaatttcttt
151 ttagttttgg cgggagtgtt gggcatgaat acgctgatgc tggcagtatg
201 gttggcaacg ttgttcctgc gcgtgaaagt gggacggttt ttcagcagtc
251 cggcgacgtg gtttcggggc aaaggccctg taaatcaggc ggtgttgagg
301 ctgtatgcgg accagtggcg gcaaccttcg gtacgatgga aaataggcgc
351 aacggcgcac agcttgtggc tctgcacgct gctcggatg ctggtgtcgg
401 tattgctgct gcttttggtg cggcaatata cggtcaactg ggaaagcacg
451 ctgttgagca atgccgcttc ggtacgcgcg gtggaaatgt tggcatggct
501 gccgtcgaaa ctgcggttcc ctgtccccga tgcgcgggag gtcacgaag
551 gtcgtctgaa cggcaatatt gccgatgcgc gggcttggtc ggggctgctg
601 gtcggcagta tcgtctgcta cggcatcctg ccgcgcctct tggcttggtg
651 agtgtgtaaa atccttttga aaacaagcga aaacggattg gatttgaaa
701 aaacctatta tcaggcggtc atccgcgcgt ggcagaacaa aatcaccgat
751 gcggatacgc gtcgggaaac cgtgtccgcc gtttcgccga aaatcgtctt
801 gaacgatgcg ccgaaatggg cgctcatgct ggagaccgag tggcaggacg
851 gccaatgggt cgagggcagg ctggcgaggc aatggctgga taaggcgctt
901 gccgccaatc gggaacaggt tgccgcgctg gagacagagc tgaagcagaa
951 accggcgcaa ctgcttatcg gcgtacgcgc ccaaactgtg ccggaccggg
1001 gcgtgctgcg gcagattgtg cggctttcgg aagcggcgca gggcggcgcg
1051 gtggtgcagc ttttggcgga acaggggctt tcagacgacc tttcggaaaa
1101 gctggaacat tggcgtaacg cgctgaccga atgcggcgcg gcgtggcttg
1151 agcctgacag ggtggcgagc gaaggccgtt tgaagacca ataa

```

This corresponds to the amino acid sequence <SEQ ID 988; ORF 253.ng>:

g253.pep

```

1  MIDRDRMLRD TLERVAGSF WLWVVASMM FTAGFSGTYL LMDNQGLNFF
51  LVLAVGLGMN TLMLAVLAT LFLRVKGRF FSSPATWFRG KGPVNQAVLR
101 LYADQWRQPS VRWKIGATAH SLWLCTLLGM LVSVLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRLNGNI ADARAWSGLL
201 VGSIVCYGIL PRLLAWVCK ILLKTSENGL DLEKTYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIVLND PKWALMLETE WQDGQWFEGR LAQEWLDKGV

```

301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGG  
 351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRVAQ EGRLKDQ\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 989>:

m253.seq

```

1 ATGATTGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51 GGGGTCGTTC TGGTTGTGGG TGGTGGCGGC GACGTTTGCA TTTTITACCG
101 GTTTTTCAGT CACTTATCTT CTAATGGACA ATCAGGGTCT GAATTTCTTT
151 TTGGTTTGG CGGCGGTGTT GGGCATGAAT ACGCTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTGTC GTGTGAAAGT GGGGCGTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCCTG TAAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGTGTGCGG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAGACACG
451 CTGTTGAGCA ATGCCGCTTC GGTACGCGCG GTGGAAATGT TGGCATGGCT
501 GCCGTCGAAA CTCGGTTTCC CTGTCCCGA TCGCGGGCGG GTCATCGAAG
551 GCCGTCTGAA CGGCAATATT GCCGATGCGG GGGCTTGGTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTGC TGGCTTGGGT
651 AGTGTGTAAA ATCCTTTTGA AAACAAGCGA AAACGGATTG GATTTGGAAA
701 AGCCCTATTA TCAGGCGGTC ATCCGCGCTG GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCCGCC GTTTCACCGA AAATCATCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAG TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCACCAATC GGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGCAGCG CCAAAGTGTG CCGGACCGCG
1001 GCGTGTGCG GCAGATTGTC CGACTCTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGACGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTGCGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGGCCGA ATGCGGCGCG GCGTGGCTTG
1151 AGCCTGACAG GCGGCGCAG GAAGGGCGTT TGAAAGACCA ATAA
  
```

This corresponds to the amino acid sequence <SEQ ID 990; ORF 253>:

m253.pep

```

1 MIDRNRMLRE TLERVRAGSF WLWVVAATFA FFTGFSVTYL LMDNQGLNFF
51 LVLAVGLGMN TLMLAVWLAM LFLRVKVGFR FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLSNAASVRA VEMLAWLPSK LGFPVPDARA VIEGRNLNGI ADARAWSGLL
201 VGSIAICYGIL PRLLAWVCK ILLKTSENGL DLEKPYQAV IRRWQNKITD
251 ADTRRETUSA VSPKIIILDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 ATNREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGG
351 VVQLLAEQGL SDDLSEKLEH WRNALAECGA AWLEPDRAAQ EGRLKDQ*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 253 shows 94.7% identity over a 397 aa overlap with a predicted ORF (ORF 253.ng) from *N. gonorrhoeae*:

m253/g253

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETTLERVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAVGLGMN					
g253	MIDRDRMLRDTLERVRAGSFWLWVVASMMFTAGFSGTYLLMDNQGLNFFLVLAVGLGMN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m253.pep	TLMLAVWLAMLFLRVKVGFRFFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
g253	TLMLAVWLATLFLRVKVGFRFFSSPATWFRGKGPVNQAVLRLYADQWRQPSVRWKIGATAH					
	70	80	90	100	110	120
	130	140	150	160	170	180
m253.pep	SLWLCTLLGMLVSVLLLLLVRYTFNWESTLLSNAASVRVEMLAWLPSKLGFPVPDARA					
g253	SLWLCTLLGMLVSVLLLLLVRYTFNWESTLLSNAASVRVEMLAWLPSKLGFPVPDARA					
	130	140	150	160	170	180

582

	190	200	210	220	230	240
m2 53 . pep	VIEGR	LNGNIADAR	AWSGLLVGS	IACYGILP	RLLA	VVCKILLKTS
g2 53	VIEGR	LNGNIADAR	AWSGLLVGS	IVCYGILP	RLLA	VVCKILLKTS
	190	200	210	220	230	240
	250	260	270	280	290	300
m2 53 . pep	IRRWQ	NKITDAD	TRRET	VS	SAVSPKI	ILNDAPK
g2 53	IRRWQ	NKITDAD	TRRET	VS	SAVSPKIV	LNDAPK
	250	260	270	280	290	300
	310	320	330	340	350	360
m2 53 . pep	ATNRE	QVA	ALET	ELKQK	PAQL	LLIGVRA
g2 53	AANRE	QVA	ALET	ELKQK	PAQL	LLIGVRA
	310	320	330	340	350	360
	370	380	390			
m2 53 . pep	SDDL	SEK	LEHWR	NALAE	CGAAW	LEPDRAA
g2 53	SDDL	SEK	LEHWR	NALTE	CGAAW	LEPDRAA
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

```

a2 53 . seq
1  ATGATCGACA GGAACCGTAT GCTGCGGGAG ACGTTGGAAC GTGTGCGTGC
51  GGGGTCGTC TGGTTGTGGG TGGCGGCGGC GACGTTTGCG TTTTTCACCG
101 GTTTTTCAGT TACTTATCTT CTAATGGACA ATCAGGCTCT GAATTTCTTT
151 TTGGTTTTGG CGGGCGTGTT GGGCATGAAT ACGTGATGC TGGCAGTATG
201 GTTGGCAATG TTGTTCTGCG GCGTGAAAGT GGGGCGTTTT TTCAGCAGTC
251 CGGCGACGTG GTTTCGGGGC AAAGACCCCTG TCAATCAGGC GGTGTTGCGG
301 CTGTATGCGG ACGAGTGGCG GCAACCTTCG GTACGTTGGA AAATAGGCGC
351 AACGTCGCAC AGCCTGTGGC TCTGCACGCT GCTCGGAATG CTGGTGTGCG
401 TATTGTTGCT GCTTTTGGTG CGGCAATATA CGTTCAACTG GGAAAGCAGC
451 CTGTTGGGCG ATTCTGCTTC GGTACGGCTG GTGGAATGT TGGCATGGCT
501 GCCTGCGAAA CTGGGTTTTT CCGTGCCCTGA TGC GCGGGCG GTCATCGAAG
551 GTCGTCTGAA CGGCAATATT GCCGATGCGC GGGCTTGCTC GGGGCTGCTG
601 GTCGGCAGTA TCGCCTGCTA CGGCATCCTG CCGCGCCTCT TGGCTTGCGC
651 GGTATGCAAA ATCCTTTTGA AAACAAGCGA AAACGGCTTG GATTTGGAAA
701 AGCCCTATTA TCAGGCGGTC ATCCGCCGCT GGCAGAACAA AATCACCAGT
751 GCGGATACGC GTCGGGAAAC CGTGTCGCCG GTTTCGCCGA AAATCGTCTT
801 GAACGATGCG CCGAAATGGG CGGTCATGCT GGAGACCGAA TGGCAGGACG
851 GCGAATGGTT CGAGGGCAGG CTGGCGCAGG AATGGCTGGA TAAGGGCGTT
901 GCCGCCAATC GGGAACAGGT TGCCGCGCTG GAGACAGAGC TGAAGCAGAA
951 ACCGGCGCAA CTGCTTATCG GCGTGCGCGC CCAAACTGTG CCCGACCGCG
1001 GCGTGTGCG GCAGATCGTC CGACTTTCGG AAGCGGCGCA GGGCGGCGCG
1051 GTGGTGCAGC TTTTGGCGGA ACAGGGGCTT TCAGACGACC TTTTCGAAAA
1101 GCTGGAACAT TGGCGTAACG CGCTGACCGA ATGCGGCGCG GCGTGGCTGG
1151 AACCCGACAG AGCGGCGCAG GAAGGCCGTC TGAAAACCAA CGACCGCACT
1201 TGA

```

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

```

a2 53 . pep
1  MIDNRNRLRE TLERVRAGSF WLWVAAATFA FFTGFSVTYL LMDNQGLNFF
51  LVLAGVLGMN TLMLAVWLAM LFLRVKVGRF FSSPATWFRG KDPVNQAVLR
101 LYADEWRQPS VRWKIGATSH SLWLCTLLGM LVSLLLLLV RQYTFNWEST
151 LLGDSSSVRL VEMLAWLPAK LGFPVPDARA VIEGR LNGNI ADARAWSGLL
201 VGS IACYGIL PRLLA VAVCK ILLKTS ENGL DLEKPYQAV IRRWQNKITD
251 ADTRRET VSA VSPKIVL NDA PKWAVMLETE WQDGEWFEGR LAQEWLDKGV
301 AANREQVAAL ETELKQKPAQ LLIGVRAQTV PDRGVLRQIV RLSEAAQGGG
351 VVQLLAEQGL SDDLSEKLEH WRNALTECGA AWLEPDRAAQ EGRLKTNDR
401 *

```

## m253/a253 97.2% identity in 395 aa overlap

m253.pep	10	20	30	40	50	60
	MIDRNRMLRETLEVRAGSFWLVVAAATFAFFTGFSTVYLLMDNQGLNFFLVLAGVLGMN					
a253						
	10	20	30	40	50	60
	MIDRNRMLRETLEVRAGSFWLVVAAATFAFFTGFSTVYLLMDNQGLNFFLVLAGVLGMN					
m253.pep	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253						
	70	80	90	100	110	120
	TLMLAVWLAMFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
m253.pep	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLSNAASVRAVEMLAWLPSKLGFPVPDARA					
a253						
	130	140	150	160	170	180
	SLWLCTLLGMLVSVLLLLLVQRQYTFNWESTLLGDSSSVRLVEMLAWLPAKLGFPVPDARA					
m253.pep	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVCKILLKTSENGLDLEKPYQAV					
a253						
	190	200	210	220	230	240
	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLAWVCKILLKTSENGLDLEKPYQAV					
m253.pep	250	260	270	280	290	300
	IRRWNQKITDADTRRETSAVSPKIIINDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
a253						
	250	260	270	280	290	300
	IRRWNQKITDADTRRETSAVSPKIVLNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
m253.pep	310	320	330	340	350	360
	ATNREQVALETELKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253						
	310	320	330	340	350	360
	AANREQVALETELKQKPAQLLIGVRAQTVPDGRVLRQIVRLSEAAQGGAVVQLLAEQGL					
m253.pep	370	380	390			
	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGRLKDQX					
a253						
	370	380	390	400		
	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGRLKTDNRTX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcagggttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg tttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaaaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcactgggtt ctttgagaaa cgggccgggc
301 tggacgggat tttcactgtc ctggctgctg gcggtgcgag gaatcgacac
351 agaactcacc atcggacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacacgctc ggcatttact ggtttgtaa cgatgaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aaccgaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLLLKT IGHGDGYRIF SVSVYGISLL

```



584

51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG  
 101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLS SIAIYVMGW MVLAVMKSLT  
 151 ASLPPAGLAW LAAGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF  
 201 VSVYGYVI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

m254.seq (partial)  
 1 ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTTGA GTTCCTGGCT  
 51 GTACCACGGA ATTGCAGCCG GAAAACGTAA AAGCATTTTG AAAAAACCG  
 101 ACCACTGCAT GATTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA  
 151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG  
 201 GCTGCTGGCG GCTGCAGGAA TCGACAAGA ACTCACCATC GGACGGAAAA  
 251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG  
 301 GTCTTGCGCG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT  
 351 GGCTTGCGTG GCGGCAGGCG GTATGCTGTA CAGTGTGGGC ATTTACTGGT  
 401 TTGTAAACGA TGAAAAATC CGACACGGGC ACGGAATCTG GCATCTGTTC  
 451 GTATTGGGCG GCAGCATCAC CCAATTTGTC AGCGTGTACG GTTACGTAAT  
 501 CTGA

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

m254.pep (partial)  
 1 ..VSVYGISLLL LYLSSWLYHG IAAGKLKSL KKTDHCMYV LIAGSYTPFA  
 51 LVSLRNGPW TVFSLSWLLA AAGIAQELTI GRKSEKRLS IYIYVMGWM  
 101 VLAVMKSLTA SLPSAGLAWL AAGMLYSVG IYWFVNDEKI RHGHGIWHLF  
 151 VLGGSITQFV SVYGYVI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

m254/g254

m254.pep				10	20	30
				VSVYGISLLL	LYLSSWLYHGIAAGKLKSL	
g254	HLSGLILAAAGLMMLLKTIGHGDGYRIFSVSVYGISLLL	LYLSSWLYHGIAAGKLKSL				
	20	30	40	50	60	70
m254.pep		40	50	60	70	80
		KKTDHCMYVLIAGSYTPF	LVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLS			
g254		KKTDHCMYVLIAGSYTPF	LVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLS			
	80	90	100	110	120	130
m254.pep		100	110	120	130	140
		IVIYVMGWMVLAVMKSLTASLPSAGLAWLAAGMLYSVG	IYWFVNDEKIRHGHGIWHLF			
g254		IAIYIVMGWMVLAVMKSLTASLPPAGLAWLAAGMLYSVG	IYWFVNDEKIRHGHGIWHLF			
	140	150	160	170	180	190
m254.pep		160				
		VLGGSITQFVSVYGYVIX				
g254		VLGGSITQFVSVYGYVIX				
		200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

a254.seq  
 1 ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTTGA GCGGTTTGAT  
 51 TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG  
 101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT  
 151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAACCT  
 201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTAT GTGCTGATTG  
 251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGC

585

```

301 TGGACGGTAT TTTCACTGTC CTGGCTGCTG GCGGCTGCAG GAATCGCACA
351 AGAACTCACC ATTGGACGGA AAAGCGAAAA ACGACTGCTG TCTATTGCGA
401 TTTATATCGT AATGGGCTGG ATGGTCTTGG CCGTAATGAA ATCCCTGACA
451 GCCTCACTCC CGCCGGCAGG ACTGGCTTGG CTGGCGGCAG GCGGTATGCT
501 GTACAGCGTC GGCATTACT GGTTCGTAAA CGATGAAAAA ATCCGACACG
551 GGCACGGAAT CTGGCATCTG TTCGTATTGG GCGGCAGCAT CACCCAATTT
601 GTCAGCGTGT ACGGTTACGT AATCTGA

```

This corresponds to the amino acid sequence <SEQ ID 998; ORF 254.a>:

a254.pep

```

1 MYTGERFNTY SHLSGLILAA AGLALMLLKT IGHGDGYRIF SVSVYGISLL
51 LLYLSSSLYH GIAAGKLKSI LKKTDHCMYI VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLI SIAIYIVMGW MVLAVMKSIL
151 ASLPPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

m254/a254 97.6% identity in 167 aa overlap

```

30 10 20
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL
|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
20 30 40 50 60
70 40 50 60 70 80
90
m254.pep
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMYIVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80 90 100 110 120
130 100 110 120 130 140
150
m254.pep
IVIYVVMGWMVLAVMKSILTASLPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
|:|:|
a254
IAIYIVMGWMVLAVMKSILTASLPAGLAWLAAGGMLYSVGIYWFVNDEKIRHGHGIWHLF
140 150 160 170 180
190
160
m254.pep
VLGGSITQFVSVYGYVIX
|||||
a254
VLGGSITQFVSVYGYVIX
200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

**g255.seq**

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

**g255.ppt**

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pcp

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

	10	20	30	40	50	60
m255.pep	VVGQ	EALR	GQFV	AVFA	AALRY	AVKTCAD
	:	:	:	:	:	:
g255	MVGQ	EALR	GQFV	AVFA	AALRY	AVKTCAD
	:	:	:	:	:	:
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GC	FDMQ	LRA	DGIQ	GFAH	AVHIVF
	:	:	:	:	:	:
g255	GG	FDMQ	FR	ADGI	QGF	AHTV
	:	:	:	:	:	:
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FR	AEFF	QPF	FG	NGS	GSNAG
	:	:	:	:	:	:
q255	FR	AEFF	QPF	FG	NGS	GGNAG
	:	:	:	:	:	:

587

	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
	:					
g255	AALVGVADX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCGG TGTTTCGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GCGCGTCGAA
151 TACGGGTTTCG CCCAAGCCGA CGGGGACGTT GCGGGCTTCA ATATGCAAGT
201 TCGCGCGGAC GGAATCCAAG GATTTGCGCA CGCTGTCCAT ATAGTTTTCC
251 AGCTCCGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTTCCGAC CTTCAAACC GGATTTCTTT TTCGCGCACT TGGGTAACTG
351 AGGCGGTGAT TTCGTGCCG AATTTTCTT TCAACCAATT TTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GCGGTTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTGTG CCAATAGTA TAGTCGGCGT
501 GCCCCGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTCGCGTGG
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

a255.pap

1	VVGQ <b>EALRGE</b>	FVA <b>VF</b> AAALR	YAVKTCADFH	AFDGVDAHHG	VGDFGIEAVE
51	YGFAQADGDV	GGFN <b>Q</b> LRAD	GIQGF <b>A</b> HAVH	IVFQLGNL <b>A</b> M	VGGKKRILGN
101	VFAAFK <b>P</b> DEF	FADLGN <b>V</b> GGD	FRAEFFFQ <b>P</b> F	FGNGSGGN <b>A</b> G	GGFAGGT <b>P</b> AA
151	AP <b>V</b> VARAV <b>F</b> V	PIGIVGV <b>A</b> G	EAGGDVAV <b>V</b> F	AALVG <b>I</b> AD*	

**m255/a255 93.1% identity in 188 aa overlap**

```

10      20      30      40      50      60
m255.pep VVGQEALRGQFVAVFAALRYAVKTCADFHAFDGVDAHHRVVGDFGIEAVKNRFAQADRDI
|||||:|||||:|||||:|||||:|||||:
a255     VVGQEALRGEFVAVFAALRYAVKTCADFHAFDGVDAHHGVVGDFGIEAVEYGFAQADGDV
10      20      30      40      50      60

70      80      90      100     110     120
m255.pep GCFDMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD
|:|||||:|||||:|||||:|||||:|||||:
a255     GGFNMQLRADGIQGFAHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFFADLGNVGGD
70      80      90      100     110     120

130     140     150     160     170     180
m255.pep FRAEFFFQPFNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF
|||||:|||||:|||||:|||||:|||||:
a255     FRAEFFFQPFNGSGGNAGGGFAGGT PAAAPVVARAVFVPIGIVGVAGAEAGGDVAVVF
130     140     150     160     170     180

189
m255.pep AALVGIADX
|||||
a255     AALVGIADX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

g256.seq

```
1 atgctcgcgg tacgcaatcg ggggttggcac ggcgcagtcg tccatttccg
51 cagctcgggc ggcgtagcga acaccgcccc ggtgtttctac cacttgggtg
101 ataccgccga aatcgccctt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttggcgcaa caggggcaaa aggcattgcc gcaagcctcg gccgcgcat
251 ccgcccccg tgaatgcagag gcggcaggca gcgcgttcga cagcgccatc
301 acgcggctgc tctacacgcg ctacttcctc cgcacactga taccaaaag
```

g256.pcp

```

1  MLAVNRNRGWH  GAVVHFRSCG  GVANTAPVVFY  HLGDTAEIAF  ALDTLTARYR
51  EIYAVGVSLG  GNAPAKYLGE  QGKKALPHAS  AAVSVPVDAE  AAGSRFDSGI
101  TRLLYTRYFL  RTLLPKARSL  QGGQTAFAGA  CKTLGFEDDR  FTAPLHGFDL
151  RHDDYRQTSC  KPLLKHVAKP  LLLLNANDP  FLPPLEALPRA  DEASEAVTLF
201  QADYGGHAGC  VSSVTGRLHL  QWLPGTVLSY  FDSFRNRR*

```

m256.seq

1	ATGCTTGCGG	TACGCGATCG	GGGTGGGCAC	GGCGTAGTCG	TCCATTTCGG
51	CAGCTGCGGC	GGCATTGCCA	ACACCGCTCC	GGTGTCTAC	CA.CTtGGCG
101	ATACCGCCGA	AATCGCCTTT	ACTTTGGACA	CGTTGCGCGC	GCGTTACCGT
151	GAAATATACG	CCGTGCGCGT	ATCGCTGGGC	GGCAACGCGC	TGGCAAAATA
201	TTTGGGCGAA	CAGGGCAAAA	AGGCATTGCC	GCAAGCCGCT	GCGGTCATCT
251	CCGCCCCCGT	CGATGCAGAG	CGCGGAGGCA	GACGCTTCGA	CAGCGGCATC
301	ACGCGGCTGC	TCTACACGCG	CTACTTCTCT	CGCACCTTGA	TACCCAAAGC
351	AAAATCGCTC	CAAGGTTTTT	AGACGGCATT	TGCCCGAGGG	TGCAAAACAC
401	TGGGCGAGTT	TGACGACCGC	TTCACCGCAC	CGCTGCACGG	CTTTGCCGAC
451	CGGCACGACT	ACTACCGCCA	AACTTCTGTC	AAACCGCTGC	TCAAAACAGT
501	TGCCAAACCG	CTGCTCTGTC	TCAATGCCGT	CAACGACCCC	TTCCTGCCGC
551	CCGAAGCCCT	GCCCCGCGCA	GACGAAGTAT	CCGAAGCCGT	TACCCTGTTC
601	CAGCCGGCTA	ATGTTGGTCA	TGTCGGCTTT	GTCAGCAGCA	CCGGCGGCGAG
651	GCTGCACCTG	CAATGCTGTC	CGCAGACCGT	CCTGTCTAT	TTCGACAGCT
701	TCCGCACAAA	CAGGCGTTAA			

m256.pcp

```

1  MLAVRDRGWH  GVVVHFRSCG  GIANTAPVVFY  XLGDTAEIAF  TLDTFAARYR
51  EIIYAVGVS LG  GNALAKYLGE  QGKKALPQAA  AVISAPVDAE  AAGRRFRDSGI
101  TRLLYTRYFL  RTLLPKAKSL  QGQQTAFQAA  CKTLGFEDDR  FTAPLHGFD
151  RHDDYRQTSC  KPLLKHAVAK  LLLLNVAADF  LPPEALPRA  DEVSEAVTLF
201  QPAYGGHVGF  VSSGTGRLHL  QWLPQTVLSY  FDSFRTRNR*

```

**Homology with a predicted ORF from *N. gonorrhoeae***

m256/g256

	10	20	30	40	50	60
m256.pep	MLAVRDRGWGHGVVHFRSCGGIANTAPVFFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG					
g256	MLAVRNRGWGHGAVVHFRSCGGVANTAPVFFYHLGDTAEIAFALDTLTARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAAVISAPVDAAAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
g256	GNAPAKYLGEQGKKALPHASAAVSAPVDAAAGSRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFTAFAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNVAVNDP					
g256	QGFTAFAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCPKLLKHVAKPLLLLNAAVNDP					

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVG FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
g256	FLPPEALPRADEVSEAVTLFQPAHGGHAG FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

a256.seq	1	ATGCTCGCGG	TACGCGATCG	GGGTTGGAAC	GGCGTAGTCG	TCCATTTCCG
	51	CAGCTGCGGC	GGCGTAGCGA	ACACCGCCCC	GGTGTCTAC	CACTTGGGCG
	101	ATACCGCCGA	AATTGCCTTT	ACTTTGGACA	CGCTCGCCGC	GGGTTACCGT
	151	GAAATATACG	CCGTCGGCGT	ATCGCTGGGC	GGCAACGCGC	TGGCAAATA
	201	TTTGGGCGAA	CAGGGCGAAA	ACGCGCTGCC	GCAAGCCGCC	GCGTCATCT
	251	CCGCACCCGT	CGATGCAGAG	GCGGCAGGCA	ACCGCTTCGA	CAGCGGCATC
	301	ACACGGCTGC	TCTACACGCG	CTACTTCCTC	CGCACACTGA	TACCCAAAGC
	351	ACGGTCGCTC	CAAGGTTTTC	AGACGGCATT	TGCCGCAGGG	TGCAAAACAC
	401	TGGGCGAGTT	TGACGACCGT	TTCACCGCAC	CGTCGCACGG	CTTTGCCGAT
	451	CGGCACGACT	ACTACGCGCA	AACCTCCTGC	AAACCGCTGC	TCAAACACGT
	501	TGCCAAACCG	CTGCTCCTGC	TCAATGCCGT	CAACGACCCC	TTCCTGCCGC
	551	CCGAAGCGCT	GCCCCGCGCA	GACGAAGTGT	CCGAAGCCGT	TACCCTGTTT
	601	CAGCCGACAC	ACGGTGGTCA	TGTCGGCTTT	GTCGGCAGCA	CCGGCGGCAG
	651	GCTGCACCTG	CAATGGTTGC	CGCAGACCGT	CCTGTCCTAT	TTGCACAGCT
	701	TCCGCACAAA	CAGGCGTTAA			

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

a256.pep	1	MLAVRDRGWN	GVVHFRSCG	GVANTAPVY	HLGDTAEIAF	TLDTLAARYR
	51	EIYAVGVSLG	GNALAKYLGE	QGENALPQAA	AVISAPVDAE	AAGNRFDSGI
	101	TRLLYTRYFL	RTLIPKARSL	QGFQTAFAAG	CKTLGEFDDR	FTAPLHGFD
	151	RHDYYRQTS	KPLLKHVAKP	LLLLNAVNDP	FLPPEALPRA	DEVSEAVTLF
	201	QPTHGGHVG	VGSTGGRLHL	QWLPQTVLSY	FDSFRTNRR*	

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGW HGVVHFRSCGGIANTAPVFYX L GDTAEIAFTLDTFAARYREIYAVGVSLG					
	:     :     :     :     :					
a256	MLAVRDRGWNGVVHFRSCGGVANTAPVFYH L GDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQ GKALPQAAVISAPVDAE AAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	:     :     :     :     :					
a256	GNALAKYLGEQ GENALPQAAVISAPVDAE AAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFA DRH DYYRQTSCKP L LKHVAKP L L L L NAVNDP					
	:     :     :     :     :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFA DRH DYYRQTSCKP L LKHVAKP L L L L NAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVG FVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	:     :     :     :     :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVG FVGSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

g256-1.seq	1	ATGATTTTGA	CACCGCCGGA	CACGCCCTTT	TTCTCCGCA	ACGGCAATGC
	51	CGACACGATT	GCCGCCAAT	TCTGCAACA	CCCCGCACCC	GCATACCGCC

590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CAAAACCGC CTACGACTTT
151 TCAGCAGGCG GCATTTCGCC CGATGCGCGG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTCGAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GCGCGAGTCG TCCATTTCGG CAGCTGCGGC
301 GCGGTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCCTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCTCGC GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTC AGACGGCATT TGCCGCGAGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGGCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCTGCGCGC CCGAAGCCCT
801 GCCCGGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGGTGC CGCAGACCGT CCTGTCTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVVLFHGLEG SSRSHYAVEL MLAVNRNGWH GAVVHFRSCG
101 GVANTAPVYF HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLG
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFA DHDYRQTSC KPLLKHVAKP
251 LLLNNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSTGGRHLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCTCCGCA ACGGCAATGC
51 CGACACGATT GCCGCCAAAT TCCTGCAACG CCCGCGCCCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CAAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCCGCCGA TCGCCGCTGT GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGACGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCGCGAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCA CTTGGCGGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCACG CGGCTGCTCT
551 ACACGCCTTA CTCCTCCGCG ACCCTGATAC CCAAAGCAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTGCG CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCCGTTT ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGCTCA ATGCCGTCAG CGACCCCTTC CTGCCGCCCG AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTTAC CCTGTTCAG CCGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCCT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLFHGLEGS SRSHYAVELM LAVDRGWHG VVHFRSCGG
101 IANTAPVYFH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFA DR HDYRQTSC KPLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVG FV SSTGGRHLHL
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

          10      20      30      40      50      59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
          |||||
g256-1      MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
          10      20      30      40      50      60

          60      70      80      90     100     110     119
m256-1.pep LVVLFHGLEGSSSRSHYAVELMLAVDRGWHG VVHFRSCGGIANTAPVYFHLGDTAEIAF

```

591

```

|||||
g256-1  LVVLFHGLEGSSRSYHAVELMLAVNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
          70      80      90      100     110     120

          120     130     140     150     160     170     179
m256-1.pep TLDTFARYREIYAVGVSLGGNALAKYLGEQKKALPQAAVISAPVDAEAAGRFRDSGI
          :|||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAGRFRDSGI
          130     140     150     160     170     180

          180     190     200     210     220     230     239
m256-1.pep TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRTAPLHGFADRHDDYRQTSC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRTAPLHGFADRHDDYRQTSC
          190     200     210     220     230     240

          240     250     260     270     280     290     299
m256-1.pep KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSTGGRLHL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||
g256-1  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHL
          250     260     270     280     290     300

          300     310     319
m256-1.pep QWLPQTVLSYFDSFRTNRRX
          |||||:|||||:|||||
g256-1  QWLPQTVLSYFDSFRTNRRX
          310     320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA CACCGCCGGA CACACCCCTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACG CTCGCCACCT GCATACCGCC
101 GCGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAACCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TCGCGCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAGGGCGGC AGTGGCAGCC ATTACGCGGT CGAACTGATG CTCGCGGTAC
251 GCGATCGGGG TTGGAACGGC GTAGTCGTCC ATTTCCGCAG CTGCGCGGGC
301 GTAGCGAACA CCGCCCGGT GTTCTACCAC TTGGCGGATA CCGCCGAAAT
351 TGCCTTTACT TTGGACACGC TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGCGCGC AACCGCGCTG CAAATATTT GGGCGAACAG
451 GCGGAAAACG CGCTGCCGCA AGCCGCCGCC GTCATCTCCG CACCCGTCGA
501 TGCAAGGCG GCAGGCAACC GCTTCGACAG CGGCATCACA CGGCTGCTCT
551 ACACGCGCTA CTTCCTCCGC AACTGATAC CAAAGCACG GTCGCTCCAA
601 GGTTTTCAGA CGGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGTTT ACCGCACCGC TGCACGGCTT TGCCGATCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGCTGCTCA AACACGTTGC CAAACCGCTG
751 CTCTGCTCA ATGCCGTCAG CGACCCCTTC CTGCCGCCCG AAGCGGTGCC
801 CCGCGCAGAC GAAGTGTCAG AAGCCGTTAC CCTGTTCCAG CCGACACAG
851 GTGGTCATGT CGGCTTTGTC GGCAGCACCG GCGGCAGGCT GCACCTGCAA
901 TGGTTGCCGC AGACCGTCCT GTCCTATTT CACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF FLRNGNADTI AAKFLQRSAP AYRRELLPDS TGKTKTAYDF
51  SDGISPDAPL VVLFHGLEGG SGSHYAVELM LAVDRGWNG VVHFRSCGG
101 VANTAPVFYH LGDTAEIAFT LDTLAARYRE IYAVGVSLGG NALAKYLGEQ
151 GENALPQAAA VISAPVDAEA AGNRFDSGIT RLLYTRYFLR TLIPKARSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFADR HDYYRQTSCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PTHGGHGVFV GSTGGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep MILTPPDTPFFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1  MILTPPDTPFFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

          70      80      90      100     110     120
a256-1.pep VVLFHGLEGGSGSHYAVELMLAVDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1  VVLFHGLEGSSRSYHAVELMLAVDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```



592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAAGNRFDSGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQGGKALPQAAAVISAPVDAEAAAGRRFDSGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLQGFQTAFAGCKTLGEFDDRFTAPLHGFADRHDYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGFGVSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGFGVSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgcccgttc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgcg atgaaaatgt gtttttctgg
151 aaagggtgctc cgctgggttc cggcgcgag ctgcgcctgt tcggcggtgga
201 cgacagacag gcggcggatt tggccaataa ggttttggcg gaagtggcgc
251 gtttggaaaa aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgcg acggttatct gacttcgcct ccggcggtt ttttggaaat
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIPT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTTCCGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GCGGGGgAc. GCGGcGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAATGT GTTTTTCTGG
151 AAAGGTGTCT CACTGGGTTC CCGTGCGGgA. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTTCAGC CTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNGD EKRNEVFFW
51  KGVALGSGAX LRLFGVDDRR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIPTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10

20

30

40

50

60

593

```

m257.pep  MGRHFGRRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAD
          |||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      MGRHFGRRRFLTAAAVAVAGAAVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVALGSGAE
          10      20      30      40      50      60

          70      80      90      100     110     120
m257.pep  LRLFGVDDRRADLVNKKVLAELVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:
g257      LRLFGVDDRQAADLVNKKVLAELVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110     120

m257.pep  AAIFTXX
          |||||
g257      AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC ATTTCTGGGCG CAGGCGTTTT TTGACAGTTG CCGCCGTTGC
51  GCGGCGGGC GCGGCGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAACG CAATAAAGAT GAAAAACGCA ATGAAAATGT GTTTTTCTGG
151 AAAGGTGTCG CACTGGGTTC CGGTGCGGAG CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA AATGTTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGT
301 CTGAACCGTG ACGGTTATTT GACTTCGCCG CCGCGGATT TTTTGGAACT
351 GTTGAGCCTG GCCGTGATAT TCACGCGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF LTVAAVAAG AAVSFLPNPF AADDEKRNKD EKRNVFFW
51  KGVALGSGAE LRLFGVDDRR AADLVNKKVLA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

          10      20      30      40      50
60
m257.pep  MGRHFGXQRF LTVAAVAAGXAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAX
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:
a257      MGRHFGRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVALGSGAE
          10      20      30      40      50
60

          70      80      90      100     110
120
m257.pep  LRLFGVDDRRADLVNKKVLAELVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
          |||||:||||:||||:|||||:|||||:|||||:|||||:|||||:
a257      LRLFGVDDRRADLVNKKVLAELVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
          70      80      90      100     110
120

m257.pep  AAIFTXX
          |||||
a257      AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

g258.seq

```

1  atgcgccgct tcctaccgat cgcagccata tgcgccgtcg tcctgtgtga
51  cggattgacg gcggcgaccg gcagaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtgtt gtccgccgtt
151 ttggcacggt atgtcatatt gctgttgaaa gacaggcgca acggcggtgtt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggccgcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatc
551 cgcaccaatt cgaccagccg cttcccagca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgaaa agcataggcg gcgtattgta
651 cgcgcaggga tggttgtcgg caggtacgca caacggggcg gattacgcgc
701 tgttcttcgg ccagccgatt cccgaaaatg tggcacagga tgcctgtctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaagg
801 tttgcagacc tttttctggt taacctgtct gattgcctcg ctgctgtcga
851 ttttctctgc gctgtaattg gactgtatt ttgcccgcg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag cgggtggcg agggtgattt
951 cagccagacg cgccccgtat tgcgcaacga cgagttcgga cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgcaa agaagcagac
1051 gaacgcaacc ccggcgcgga ggaagccgcc cgtcactacc tcgaagtcgt
1101 gttggatggg ttgactaccg gtgtggtggt ctctacccc ctctctgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctcccctct ttcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

g258.pep

```

1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWIVSFS AMLLLVLSAV
51  IARYVILLLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVPOV IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLQT FFLVTLIIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTGTVVVSYP LSCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

m258.seq

```

1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TCGGTCAGC GCAATGCTGC TGCTGGTGTG GTCCGCCGTT
151 TTGGCACGTT ATGTCAATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGCG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTCCTG TTCGGCGTTT CCGCAGATT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCCTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGCT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCGG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAAGG
801 TTTGCGAGCC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCGCGCG TTTCGTCGAA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG CCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TCGCAACGA CGAGTTCGGA CGCTTGACCA

```

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAACsTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGtGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CCGCGCAGCA
1251 GTCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAaGT GGCGaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCAGG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAAA TCCTGACCGG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATCGG
1651 CGTCCCCCTT CGCTCAAATT GGAAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGCTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

m258.pep

```

1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51 LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAVVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLOT FFLATLLIAS LLSIFLALVM ALYFARFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQSSL AEFVFAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERKA XKLGGKLDEQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

m258/g258

```

          10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLSAVLARYVILLK
          |||
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVSFSAM L VLSAVLARYVILLK
          10      20      30      40      50      60

          70      80      90      100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          |||
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGLFLFGISAQFINGTINSWFGNDTHEALERSLNL
          70      80      90      100     110     120

          130     140     150     160     170     180
m258.pep SKSALNLAADNALGNAVVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||
g258      SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGVLEHYAGSGFAQLALYNAASGKIEK
          130     140     150     160     170     180

          190     200     210     220     230     240
m258.pep SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGR DYALFFRQPV
          |||
g258      SINPHQFDQPLPDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGR DYALFFRQPI
          190     200     210     220     230     240

```

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	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFPLATLLIASLLSIFLALVMALYFARRFVE					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFPLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDPSQTRPVLNRNDEFGRLLTKLFNHMTQLSIAKEADERNRRREEAA					
g258	PILSLAEGAKAVAQGDPSQTRPVLNRNDEFGRLLTKLFNHMTQLSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKAEEQILGMPLTPLWGSRRHGWHGVSQAQQLL					
g258	RHYLECVDGLTTGVVVSYPSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1027>:

a258.seq

1	ATGCGCCGTT	TTCTACCGAT	CGCAGCCATA	TGCGCCGTCG	TCCTGTTGTA
51	CGGACTGACG	GCGGCAACCG	GCAGCACCAG	TTGCTGGCG	GATTATTTCT
101	GGTGGATTGT	TGCGTTCAGC	GCAATGCTGC	TGCTGGTGTT	GTCCGCCGTT
151	TTGGCACGTT	ATGTCATATT	GCTGTTGAAA	GACAGGCGCG	ACGGCGTATT
201	CGGTTGCGAG	ATTGCCAAAC	GCCTTTCCGG	GATGTTTACG	CTGGTTGCCG
251	TACTGCCCGG	CGTGTTCCTG	TTGCGCGTTT	CCGCACAGTT	TATCAACGGC
301	ACGATTAATT	CGTGGTTCGG	CAACGATACC	CACGAGGCGC	TTGAACGCAG
351	CCTCAATTG	AGCAAGTCCG	CATTGAATCT	GGCGGCAGAC	AACGCCCTTG
401	GCAACGCCAT	CCCCGTGCAG	ATAGACCTCA	TCGGCGCGGC	TTCCCTGCCC
451	GGGGATATGG	GCAGGGTGCT	GGAACATTAC	GCCGGCAGCG	GTTTTGCCCA
501	GCTTGCCCTG	TACAATGCCG	CAAGCGGCAA	AATCGAAAAA	AGCATCAACC
551	CGCACAAAGCT	CGATCAGCCG	TTTCCAGGTA	AGGCGCGTTG	GGAAAAATC
601	CAACAGGCGG	GTTGCGTCAG	GGATTGGAA	AGCATAGGCG	GCCTATTGTA
651	CGCGCAGGGC	TGGCTGTCGG	CAGGTACGCA	CAACGGGCGC	GATTACGCCT
701	TGTTTTTCCG	TCAGCCGGTT	CCCAAAGGCG	TGGCAGAGGA	TGCCGCTCTA
751	ATCGAAAAGG	CAAGGGCGAA	ATATGCTGAG	TTGAGTTACA	GCAAAAAAGG
801	TTTGCAGACC	TTTTTCTGG	CAACCCTGCT	GATTGCCTCG	CTGCTGTCGA
851	TTTTTCTTGC	ACTGGTCATG	GCACTGTATT	TCGCCGCGCG	TTTCGTGCAA
901	CCCGTCTTAT	CGCTTGCCGA	GGGGCGGAAG	GCGGTGGCGC	AAGGCGATTT
951	CAGCCAGACG	CGCCCCGTGT	TGCGCAACGA	CGAGTTCGGA	CGCTTGACCA
1001	AGTTGTTCAA	CCACATGACC	GAGCAGCTTT	CCATCGCCAA	AGAAGCAGAC
1051	GAGCGCAACC	GCCGGCGCGA	GGAAGCCGCC	AGACATTATC	TCGAATGCGT
1101	GTTGGAGGGG	CTGACCACGG	GCGTGGTGGT	GTTTGACGAA	CAAGGCTGTC
1151	TGAAAACCTT	CAACAAAGCG	GCGGAACAGA	TTTTGGGGAT	GCCGCTTACC
1201	CCCCTGTGGG	GCAGCAGCCG	GCACGGTTGG	CACGGCGTTT	CGGCGCAGCA
1251	GTCCCTGCTT	GCCGAAGTGT	TTGCCGCCAT	CGGCGCGGCG	GCAGGTACGG
1301	ACAAACCGGT	CCATGTGAAA	TATGCCGCGC	CGGACGATGC	CAAAATCCTG
1351	CTGGGCAAGG	CAACCGTCCT	GCCCCAAGAC	AACGGCAACG	GCGTGGTAAAT
1401	GGTGATTGAC	GACATCACCG	TTTTGATACA	CGCGCAAAAA	GAAGCCGCGT
1451	GGGGCGAAGT	GGCAAAACGG	CTGGCACACG	AAATCCGCAA	TCCGCTCAGC
1501	CCCATCCAGC	TTTCTGCCGA	ACGGCTGGCG	TGGAAATTGG	GCGGGAAGCT
1551	GGACGAGCAG	GACGCGCAAA	TCCTGACACG	TTGACCGAC	ACCATCATCA
1601	AACAAGTGGC	GGCATTAAAA	GAAATGGTCG	AGGCATTCCG	CAATTACCGC
1651	CGTTCCCCCT	CGCTCAAATT	GGAAATCAG	GATTTGAACG	CCTTAATCGG
1701	CGATGTGTTG	GCATTGTACG	AAGCTGGTCC	GTGCCGGTTT	GCGGCGGAAC
1751	TTGCCGGCGA	ACCGCTGATG	ATGGCGGCGG	ATACGACCGC	CATGCGGACG
1801	GTGCTGCACA	ATATTTTCAA	AAATGCCGCC	GAAGCGGCGG	AAGAAGCCGA
1851	TGTGCCCAGG	GTCAGGTAA	AATCGGAAGC	GGGCGAGGAC	GGACGGATTG
1901	TCCTGACAGT	TTGCGACAAC	GGCAAGGGGT	TCGGCAGGGA	AATGCTGCAC
1951	AATGCCTTCG	AGCCGTATGT	AACGGACAAA	CCGGCTGGAA	CGGGATTGGG
2001	ACTGCCCGTG	GTGAAAAAAA	TCATTGAAGA	ACACGGCGGC	CGCATCAGCC
2051	TGAGCAATCA	GGATGCGGGC	GGCGCGTGTG	TCAGAATCAT	CTTGCCAAAA
2101	ACGGTAGAAA	CTTATGCGTA	G		

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```
a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TTIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIFKNAA EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*
```

m258/a258 99.0% identity in 584 aa overlap

```
m258.pep      10      20      30      40      50      60
MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLLVLSAVLARYVILLK
|||||
a258          10      20      30      40      50      60
MRRFLPIAAICAVVLLYGLTAATGSTSSLDYFWWIVAFSAML VLLVLSAVLARYVILLK

m258.pep      70      80      90     100     110     120
DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
|||||
a258          70      80      90     100     110     120
DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL

m258.pep     130     140     150     160     170     180
SKSALNLAADNALGNAVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK
|||||
a258         130     140     150     160     170     180
SKSALNLAADNALGNAIPVQIDLIGAASLPDGMGRVLEHYAGSGFAQLALYNAASGKIEK

m258.pep     190     200     210     220     230     240
SINPHKLDQPFPGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
|||||
a258         190     200     210     220     230     240
SINPHKLDQPFPGKARWEKIQQAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV

m258.pep     250     260     270     280     290     300
PKGVAEDAVLIEKARAKYAE LSYSKKGLQTF FLATLLIASLLSIFLALVMALYFARRFVE
|||||
a258         250     260     270     280     290     300
PKGVAEDAVLIEKARAKYAE LSYSKKGLQTF FLATLLIASLLSIFLALVMALYFARRFVE

m258.pep     310     320     330     340     350     360
PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA
|||||
a258         310     320     330     340     350     360
PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA

m258.pep     370     380     390     400     410     420
RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL
|||||
a258         370     380     390     400     410     420
RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLT PLWGSSRHGW HGVSAQQSLL

m258.pep     430     440     450     460     470     480
AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
|||||
a258         430     440     450     460     470     480
AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK
```

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	430	440	450	460	470	480
m258.pep	490	500	510	520	530	540
	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIHKQVAALK					
	490	500	510	520	530	540
m258.pep	550	560	570	580	589	
	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNI FKNAAEAAEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1  atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tactttatgt
51  tttgattttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgcgcgatt gtccgccgtc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgcgtt caaaggctaa
201 ggcagaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatatcacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaatgtct
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccc acgacgaaga cgcgcgacg attgccgccc
401 agttggcaaa aatggatatg ttgcgattgg ggacggacgc ggtcgccctg
451 ggcgaaacct atggcgcggt gttcgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcggtca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccc gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAELAKMDM PALGTD AVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKHLRRC LPFGNGVGF
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GGCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACKGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGMGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGMGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGGCGTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAELAKMDM PALGTD AVAS

```

151 GETYGRVFAD IFELSXALEG RAFKGLMLKT AEYKXHLRRC LPFGNGVGVG  
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGMAEQVRFKAE					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSXALEGRAFKGLMLKT					
g259	VLPDDEDARTIAAELAKMDMFALGTD AVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRC LPFGNGVGVGR TQSGVAGDF KNIR					
g259	AEYKXHLRRC LPFGNGVGVG GRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTGACCGC	GCAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGT CAGGTT
351	CAAGCGCGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCAATTG	GGACGGACGC	GGT CGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCCGCCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAAGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTC	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQI	WFNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHKGK	MAEQVREKAE	VLPDDEDART	IAAELAKMDM	FALGTD AVAS
151	GETYGRVFAD	IFELSAALEG	RAFKGLMLKT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIF FAGFLTAQIWFNQKAYTEELPPLLSALSAVALVWLAWAFV					



600

	10	20	30	40	50	60
m259. pep	70	80	90	100	110	120
a259	70	80	90	100	110	120
m259. pep	130	140	150	160	170	180
a259	130	140	150	160	170	180
m259. pep	190	200	210			
a259	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1. seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1. pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1. seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCCTGCA CGCCTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTGCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTCA AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1. pep

```

1  MMHASVQSR FAPILYVLIF FAGFLTAQIW FNQAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGLMLLT AEYKNIFGDA CRSETALELG
201 ALNQLAQEIS KTSEKSKRIF Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLHKPQMLALLVKNHKGKMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLHKPQILALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALE					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGTTT TTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGTTCGTG TCGGCGCGTT CAAAGGCTAA
201 GCGCGAAAG TTCTACCGCG AAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCCGCTCG
451 GCGGAACCT ATGGACCGGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGCGGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGELTAQIW FNQAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDVAS
151 GETYGRVFAD IFELSAALEG RAFRGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
m259-1	MMMHASVQSRFAPILYVLIF FAGELTAQIWFNQAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLHKPQMLALLVKNHKGKMAEQVRFKAE					
m259-1	SARSKAKAEKFYREKMIQNESIHPVLHASLQHLHKPQILALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFGMLKLT					
m259-1	VLPDDEDARTIAAELAKMDMFALGTDVASGETYGRVFADIFELSAALEGRAFGMLKLT					
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALELGALNQALQEISKTSEKSRIFYX					
m259-1	AEYKNIFGDACRSETALELGALNQALQEISKTSEKSRIFYX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

q260.pep

1 MGAGVVFVVF QPFSLFRAL FEGGVGIVEG AHDAECDFL SEEFTRI RIG  
51 DVFIDSVGQI TARFFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL  
101 RVLHKDAVEV DIDGGNTVSG HFLIRTD FDD GDAVCLFQAE ARFAANVAQH  
151 QYLARINQVG IVDLIPVRAP OGGTIATGCT GICPKYPTGC RPV\*

m260.seq

1	ATGGGTGCGG	GTATGGTATT	CGTTGTCTTT	CGGCCGTCT	CCAGCCTGTT
51	TCGAGCGTTG	TTCGAGGACA	GAGTCGGTAT	AGTCGAGGGA	GCGCACGATG
101	CCGCTGAATG	CGACTTCCTG	CCCAGGAAT	TTACCCGTAT	CCGGATCGGT
151	GATGTTTTTA	TTGATTCCGT	AGGTCAGGTA	GCGGCCCGGC	TCTTTCAAGC
201	CTTTGGTGTA	AACCTCGGTG	CCTTTGGTGT	ACAGCAGCCT	GCCTTCCGGG
251	CCCAGwrcA	sgCGCGgyGC	GGCAGCGGTT	TCTTTGCGGG	AAACGATTTG
301	CGGATGCCGC	ATAAAGATGC	GGTAGAAGTT	GACATCGATG	GCGGGAATAC
351	CGTATCCCGA	CAC TTCCTTA	TCCGGACTCA	TTTTGACGAC	GGGGATGCCG
401	CTGTCTGT	CCAAGCCGAG	GCGCGGTTTC	CCGTCAACGT	GGCGCAACAC
451	CAATACCTGG	TCCGGATAAA	TCAGGTCGGG	ATTGTGGATT	TGATCCCGGT
501	TCGCGTCCCA	CAG			

m260.pep

1 MGAGMVFVVV RPFSSLFRAL FEDRVGIVEG AHDAEACDFL PEEFTRIRIG  
5 DVFIDSVGQV AARLQAFGV NPGAQVQQP AFRARXXARX GSGFFAGNDL  
101 RMPHKDAVEV DIDGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH  
151 QYLVRINOVG IVDLIPVRVP Q

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260.pep	MGAGMVFVVFRRPFSSLFRALFEDRVGIVEGAHDAAECDLPEEFTRIRIGDVFIDSVGQV					
g260	:     :   :					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARKSGSFFAGNDLRMPHKDAVEVDIDGGNTVSG					
g260	:   :  :					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHDDGDVCLFQAEARFAVNVAQHGYLVRLINQVGIVDLIPVRVPQ					
g260	:       :       :       :       :					
	130	140	150	160	170	180
	HFLIRTDFDGDVCLFQAEARFAANVAQHGYLARINQVGIVDLIPVRAPQGGTIATGCT					

g260

GICPKYPTGCRPV

190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq

```

1  ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51  TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGCGCGC GGCAGCGGTT TCTTTCGCGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGACTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTCT CCGTCAACGT GCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC. CCATTGCCAC GGGCTGTACA GGTATTGTCC
551 CGAAATGCCC CACAGGGTGT CGCCCTGTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep

```

1  MGAGMVVVVF RPFSSLFRL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51  DVFIDSVGVQ AARLFQAFGV NPGAFGVQQP AFRAREQARR GSGFFAGNDL
101 RVPKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*

```

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVVVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
a260	MGAGMVVVVFRPFSSLFRLFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGVQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAFGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAFGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVPQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq

```

1  atggagcttg ggcataatcgt attccttggtg ctttgcgcg gttcagacgg
51  cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacag
101 ctcgggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctggtcgcg atgtagtcca acacgcccatt ttcgtccgcc aacgcccacg
201 tttgcgccctt ggtcaggtac atcagcgggc tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatg gatttgacga acacgcgcg
301 gcagtcggga tagcccgaaa aatcggtttc gcacacgccc gcgatgatgt
351 gccggatacc ctgcccttgg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgcccgttg cggcggtttc
451 gatggcgggg gtttcgatgg cggcggtttc gtccatcagg gcgttggtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttccagc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgcccgtag gtttggtattg

```

604

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag  
701 gcttttttgt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG  
51 LFADVVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA  
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF  
151 DGGGFDGGG VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP  
201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGLV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTCGCGCT GTTCAGACGG  
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTCCGCG CAAGATACAG  
101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT  
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCACG  
201 TTTGCGCCTT GGTACAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG  
251 TCCATCGCCA AATTAAGGT AACGTTATC GATTTGACAA ACACGTGCGG  
301 GCAGTCGGGA TAGCCGAGA AGTCGGTTC GCACACGCC GCGATGATGT  
351 GCCGTATCCC CTGCCCTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC  
401 gCGTTGCGGC CGTCTACAAA GGTATTGCGA ACGCCGTTT CGGCAGTTTC  
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA  
501 GgCTcAAGTC GAGTACGGT TGTTCGACG CCAAATCCTG CGCAATCCAG  
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT  
601 GGCTTGACG TTTTCGCGCC CGTAGGTTG GATTGCCTGA ATCAGGCAGG  
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG  
51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA  
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRAAVYK GIRNAVFGSF  
151 DGGGVVHGGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN  
201 GLDVFPVGL DCLNQAGGRI LTARKDDQGL LV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	::					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVVQHAH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAA AVGIARKIGF AHARDDVPDT					
	70	80	90	100	110	120
	130	140	150	160	170	
m261.pep	LPFGVNRGIEQEKRAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVQVEYGLF					
	::        :        :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
	180	190	200	210	220	230
m261.pep	DAQILRNPAFTFQLDGMALPVLESNGLDVFPVGLDCLNQAGGRILTARKDDQGLLVX					
	:   ::  :					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFVFPVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1  ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCCCAAG
201 TTTGCGCCTT GGTCAAGTAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAAGGT AACGTTTCATG GATTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGAGGA AGTCGGTTTC GCACACGCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTTCGGA ACGCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GGCTCAAGTC GAGTACGGTT TGTGTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1  MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFOLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

m261.pep	10	20	30	40	50	60
	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
a261	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQRAH					
	10	20	30	40	50	60
m261.pep	70	80	90	100	110	120
	FVRQRPRRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVAAVGIAGEVGFHAARDDVPYP					
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHGFDKHVTAVGIAGEVGFHAARDDVPYP					
	70	80	90	100	110	120
m261.pep	130	140	150	160	170	180
	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAVQVEYGLFDAQIL					
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAVQVEYGLFDAQIL					
	130	140	150	160	170	180
m261.pep	190	200	210	220	230	
	RNPAGTFOLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI LTARKDDQGLLVX					
a261	RNPAGTFOLDGMALPVLESNGLDVFAFVGLDCLNQAGGRI LTARKDDQGLLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1  atggcacgtt taaccgtaca caccctcgaa accgcccccg aagccgccaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggttttata cccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgccgcca cagcctgacc gccggcggaag tcgaagtgat
201 ccggtatcat gccgtccgca ccaaccaatg cagcttctgc gtggcagggc
251 acaccaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgccccgc ctttgccggc aggtaaatct gacgatgcc aactcggcgc
351 gcttgccgcc ttcacccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctggaagcgg gctacaaccg gcagcaggca
```

451 gtcgagtcg taatgggcgt agccttgcca actttgtgca actacgcca  
 501 caacctcgcc caaacgaaa tcaaccccaa attgcaggca tacgcctaa

This corresponds to the amino acid sequence <SEQ ID 1054; ORF 263.ng>:

g263.pep

1 MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV  
 51 GKLNANSLT AGEVEVIRII AVRTNQCSFC VAGHTKLATL KKLLSEQSLN  
 101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDEELNAF LEAGYNRQQA  
 151 VEVVMGVALA TLCNYANNLA QTEINPKLOA YA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1055>:

m263.seq (partial)

1 ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC  
 51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG  
 101 CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG  
 151 GCGGT.AsyC TgGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC  
 201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

This corresponds to the amino acid sequence <SEQ ID 1056; ORF 263>:

m263.pep (partial)

1 ..GCAGCAGGCG AATTTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC  
 51 CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG  
 101 CATTTTTCGA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG  
 151 GCGGT.AsyC TgGCAACCCT GTGCAACTAC GTCAACAACC TCGGACAAAC  
 201 CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

				10	20	30
m263.pep				AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
				:		
g263	QCSFCVAGHTKLATLKKLLSEQSLNAARALAAGKSDDAKLGALAAFTQAVMAKKGAVSDD					
	80	90	100	110	120	130

	40	50	60	70	
m263.pep	ELKAFFDAGYNQQQAVEVVMGVXLATLTCNYVNNLGQTEINPELQAYAX				
	:   :    :				
g263	ELNAFLEAGYNRQQAVEVVMGVALATLTCNYANNLAQTEINPKLOAYAX				
	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1057>:

a263.seq

1 ATGGCACGTT TAACCGTACA CACCCTCGAA ACCGCCCCCG AAGCCGCCAA  
 51 AGCGCGCGTC GAGGCGGTAC TTCAAACAA CGGCTTTATC CCCAACCTTA  
 101 TCGGCGTATT ATCAAACGCC CCGAAGCCT TGGCGTTTTC CCAAGAAGTC  
 151 GGCAAGCTCA ACGCCGCCAA CAGCCTGACC GCCGGCGAAG TCGAAGTAAT  
 201 CCAGATTATT GCCGCCCGCA CCAACCAATG CGGCTTCTGC GTGGCAGGGC  
 251 ACACCAAACG CGCAACCCTG AAAAAACTCC TTCCGAACA ATCCGTCAAA  
 301 GCCGCGCGCG CTTTGGCGGC AGGCGAATTT GACGATGCTA AACTCGGCGC  
 351 GCTCGCCGCC TTTACCCAAG CCGTAATGGC AAAAAAGGC GCGGTATCCG  
 401 ACGAGGAACG CAAAGCATT TTTGATGCGG GCTACAACCA GCAGCAGGCA  
 451 GTCGAAGTCG TGATGGGCGT AGCCTTGGCA ACTTTGTGCA ACTACGTCAA  
 501 CAACCTCGGA CAAACGAAA TCAACCCGA ATTGCAGGCT TACGCCTGA

This corresponds to the amino acid sequence <SEQ ID 1058; ORF 263.a>:

a263.pep

1 MARLTVHTLE TAPEAAKARV EAVLQNNNGFI PNLIGVLSNA PEALAFYQEV  
 51 GKLNANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KKLLSEQSVK  
 101 AARALAAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA  
 151 VEVVMGVALA TLCNYVNNLG QTEINPELQA YA\*

607

m263/a263 97.4% identity in 77 aa overlap

				10	20	30
m263.pep				AAGEFDDAKLGALAAFTQAVMAKKGAVSDE		
a263	QCGFCVAGHTKLATLKKLLSEQSVKAAARALAA	GEFDDAKLGALAAFTQAVMAKKGAVSDE				
	80	90	100	110	120	130

	40	50	60	70
m263.pep	ELKAFFDAGYNQQQAVEVVMGXLLATLCNYVNNLGQTEINPELQAYAX			
a263	ELKAFFDAGYNQQQAVEVVMGVALATLCNYVNNLGQTEINPELQAYAX			
	140	150	160	170

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

g264.seq

```

1   ttgactttaa cccgaaaaac ccttttcttc ctcaccgccg cgttcggcac
51  acactccctt cagacggcat ccgccgacgc agtgggtcaag ccgaaaaaac
101 tgcacgcctc cgccaaccgc agctacaaag tcgccgaatt caccgaaacc
151 ggcaacgcct cgtggtacgg cggcagggtt caccggcgca aaacttccgg
201 cggagaccgc tacgatatga acgcctttac cgccgcccac aaaaccctgc
251 ccattccccag ccatgtgcgc gtaaccaaca ccaaaaacgg caaaagcgctc
301 atcgtccgcg tcaacgaccg cggccccttc caccggcaacc gcatcatcga
351 cgtatccaaa gccgccgcgc aaaaattggg ctttgtcagc caagggacgg
401 cacacgtcaa aatcgaacaa atcgtcccgc gccaatccgc accggttgcc
451 gaaaaacaaag acatctttat cgacttgaaa tctttcggta cggaacacga
501 agcacaagcc tatctgaacc aagccgccca aaatttcgcc gtttcgtcat
551 caagcccgaa cctctcgggt gaaaaacgcc gttacgaata cgttgtaaaa
601 atggggccgt ttgcctcgca ggaacgcgcc gccgaagccg aagcgcaggg
651 acgcggtatg gttcgggcgg tactgacctc cggttga

```

This corresponds to the amino acid sequence &lt;SEQ ID 1060; ORF 264.ng&gt;:

g264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK PEKLHASANR SYKVAEFTQT
51  GNASWYGGRF HGRKTSGGDR YDMNAFTA AH KTLPIPSHVR VTNTKNGKSV
101 IVRVNDRGPF HGNRIIDVSK AAAQKLG FVS QGTAHV KIEQ IVPQGSAPVA
151 ENKDIFIDLK SFGTEHEAQA YLNQAAQ NFA ASSSSPNLSV EKRRYEYVVK
201 MGPFFASQERA AEAEQAQARG VRAVLTS G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

m264.seq

```

1   TTGACTTTAA CCCGAAAAAC CCTTTTCCTT CTCACCGCCG CATTCCGGCAG
51  ACACCTCCCTT CAGACGGCAT CCGCCGACGC AGTGGTCAAG GCAGAAAAAC
101 TGCACGCCTC CGCCAACCGC AGCTACAAAG TCGCCGGA AA ACGCTACACG
151 CCGAAAAACC AAGTCGCCGA ATTCACGCAA ACCGGCAACG CCTCGTGGTA
201 CGGCGGCAGG TTTCACGGGC GCAAACTTC CGCGGAGAA CGATACGATA
251 TGAACGCCTT TACCGCGGCC CACAAAACCC TGCCCATCCC CAGCTATGTG
301 CGCGTAACCA ATACCAAAAA CGGCAAAAGC GTCATCGTCC GCGTCAACGA
351 CCGCGGCCCC TTCCACGGCA ACCGCATCAT CGACGTATCC AAAGCCGCCG
401 CGCAAAAATT GGGCTTTGTC AACCAAGGGA CGGCACACGT CAAAATCGAA
451 CAAATCGTCC CGGGCCAATC CGCACCGGTT GCCGAAAACA AAGACATCTT
501 TATCGACTTG AAATCTTTCG GTACGGAACA CGAAGCACAA GCCTATCTGA
551 ACCAAGCCGC CCAAACTTC GCCGTTTCGT CATCGGTAC GAACCTCTCG
601 GTTGAAAAAC GCCGTTACGA ATACGTCGTC AAAATGGGAC CGTTACCTC
651 GCAGGAACGC GCCGCCGAAG CCGAAGCTCA GGCGCGCGGT ATGGTTCGGG
701 CGGTATTGAC CGCCGGCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1062; ORF 264&gt;:

m264.pep

```

1   LTLTRKTLFL LTAAFGTHSL QTASADAVVK AEKLHASANR SYKVAGKRYT
51  PKNQVAEFTQ TGNASWYGGF FHGRKTS GGE RYDMNAFTA HKTLPISYV
101 RVTNTKNGKS VIVRVNDRGP FHGNRIIDVS KAAQKLG FV NQTAHV KIE
151 QIVPGQSAPV AENKDIFIDL KSFGEHEAQ AYLNQAAQNF AVSSSGTNLS
201 VEKRRYEYVV KMGPFTSQER AAEAEQAARG MVRAVLTAG*

```



Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHFGRKTS GGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHFGRKTS GGDYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
g264	FHGNRIIDVSKAAQKLG FVSQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPFPSQERAAEAEQA RGMVRAVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPFASQERAAEAEQA RGMVRAVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCCGAAAAAC	CCTTTTCCTC	CTCACC GCCG	CATTCCGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGAAA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTCACGCAA	ACCGGCAACG	CCTCGTGGTA
201	CGCGCGCAGG	TTTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	CGGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCCG
401	CGCAAAAT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAATCGTCC	CGGGCCAATC	CGCACC GGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTAAFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA	AHKTLPIPSYV
101	RVNTNKGKS	VIVRVNDRGP	FHGNRIIDVS	KAAQKLG FV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNP NLS
201	VEKRRYEYV	KMGPFASQER	AAEAEQA RQ	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

609

	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQTAHV KIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQTAHV KIEQIVPGQSAPVAENKDIFIDLKSFGTEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF T SQERAAEAE AQARGMVRVLTAGX					
a264	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF T SQERAAEAE AQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGCGCGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151 ATGCTCAGCA GTGCGGTGTC GCGCGAGGTC AAGAGAAGGT GTTTGATGTT
201 CATAT.TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251 AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301 CGCGCCTGAG CTTCCGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351 CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MLSSAVAAEV KRRCLMFI XFVNVRGLENV DINKVSNNRQ PAVNTARTIP
101 RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNVRGLENVDINKVSNNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

## a265 . seq

```

1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GGC GCGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... ..GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGTTCC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

## a265 . pep

```

1   MSVILPPTRA NAAFAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*

```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265 . pep	MSVILPPTRANAFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSAVAAEV					
a265	MSVILPPTRANAFAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMPISAVAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFIXFAFVNRGLENVINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
	: : :     : :     : :     : :     : :     : :     : :					
a265	KRRRLKFI---FAPAKYLXXCLKDVKAGHQPAVNTARTIPRAXASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

## g266 . seq

```

1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcttc acgaccagac tggtcgcggt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgac gagctggcgg caggtttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccgtagc ggagcggtac acaatcaggg
251 ttgggagttt tacgccaccg tegtctgcct gtacctcatt ttcgccttcc
301 cgtgttcgt gcggcggtat ttttggcaca cgcgcaacag ggaataa

```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

## g266 . pep

```

1   MQFRRHRRRO CPNRKPIMTA SMYILLVLAL IFANAPFLT RLFGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILES RAGA VHNQGWEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

## m266 . seq

```

1   ATGCCGTTCC GCAACGCGTt cAGACGCGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTsGAATCC CGTGCAAGAT
251 CCGTACACGA TCAGGGTTGG GAGTTTTATG CCACAGTCGT CTGCCTGTAC
301 CTGATTTTGG CGTTCCATG TTTGTGTGG CCGTATTTT GGCACACGCG
351 CAACAGGGAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

m266.pep

```

1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101 LIAFPFCFVW RYFWHTRNRE *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

m266/g266

```

              10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      MQFRHRRRQCPNRKPMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
              10      20      30      40      50

              70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNRE
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW EFYATVVCLYLI FAFPCFVRRYFWHTRNRE
              60      70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

a266.seq

```

1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCC
101 TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151 CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201 TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251 CGGTACACGA TCAGGGTTGG GAGTTTACG CCACCGTCGT CTGCCTGTAC
301 CTGATTTTTC GGTTCCTGTT TTTCTGTGG CGGTATTTT GGCACACGCG
351 CAACAGGGAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

a266.pep

```

1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101 LIAFPFCFVW RYFWHTRNRE *

```

m266/a266 91.7% identity in 120 aa overlap

```

              10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||  |||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      MPFRNAFRRHRRRQCPNRKPAMTASMYILLLLALIFANAPFLTTKLFGIVPLKRKHFGHH
              10      20      30      40      50      60

              70      80      90      100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNRE
          :|||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW EFYATVVCLYLI FAFPCFVWRYFWHTRNRE
              70      80      90      100     110     120

```

```

m266.pep  X
          |
a266      X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

g267.seq

g267.pcp

m267.seq

m267.pcp

m267/g267

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	GGTCGGGCAG	GCTTCTTCGC	AGAAACCGCA	GAAGATCGAC
101	TGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTGC	CGTCTTCGCG
151	TTCTTCCGAT	TCGATGTTGA	TGCCCATATG	GGGGCAACG	GGTTACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	CGGTTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATTTCGGC	GTTTTCTCTT	CGGGAAAATA
301	AATCGTGTCT	TTCGCGGGCA	AAAAGTTTTT	GAGCGTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101 NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVFTFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPPLFAVRIP	PLRVQTAETHGLRRFLFG	INCVFAGEKVFERYAHTFYQF			
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFG	KINRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
1  atgaaaaaaa atttaccgcg actggcattg gcaagtatgc tgattttgtc
51  gggctgcgac cgtttgggaa taggcaaccc gttttccgga aaggaaattt
101 cctgcggaag cgaagagact aaagagattt tggtaaact ggtccgcgac
151 aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaga
201 ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251 gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301 tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagcga
351 tgttgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401 agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451 tatgtcaaaa ctatttctta cagcgtccag ccgacagacg acaaaagcaa
501 aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551 agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaacaaa
601 aggaacgaaa aactgaagc ggcagaagcc accgcgcagg aagcgagggg
651 ggcagaagaa gcggcgggcg aggaggcatt gggtcgggag caggaaagccg
701 cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751 gagcagtttt ggaaggattt gcctcaact gtacagaata agctgcaagc
801 ctgcgagaaa acatggaaaa gcggtatgga caagatctgt gccacaatg
851 cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901 tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951 aaaagccctt atcgacgaaa tggtcaggga agaggacaag aaagaactgc
1001 caaagcggt ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVDR
51  NVEGETVKTF DDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101 SSKLKCEAL KLDVPDDVVD YAVANQSIG NSHKTPDFF EPYRKEGAY
151 YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201 RNEKLEAAEA TAQEAREAE AAAQEALGRE QEAARVSEWE ERYKLSRSEF
251 EQFWKGLPQT VQNKLOASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301 CKTAETEAREL EBLHNRRKAL IDEMVEEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
1  ..ATGGCACTGA TTAAAGAGCC GTTGGACAAA GTGAAACAAA GGAACGAAGA
```

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```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGGCGC
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCN TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCTGAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGYCAGGGAA GCGGACAMGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   ..MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||||:||||:||||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQKARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  --EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLPQSQTWKSMD
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g268      AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLPQSQTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAEKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCTGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCTGGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCTGAGC
301 GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLQA SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
a268      MALIKEPLDKAKQRNEELEAAEEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```

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	10	20	30	40	50	60
	70	80	90	100	110	120
m268.p ep	PQTVQNKLPQSQKTKWSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	:    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :					
a268	PQTVQNKLPQSQKTKWSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK					
	70	80	90	100	110	120
	130	140				
m268.p ep	KALIDEMKREADKKELSKRLX					
	:    :    :    :    :    :    :    :    :    :    :    :    :    :    :					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCGCGGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1.p ep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30
m268-1.p ep		VQSRDGLHKFKHICSAAMALIKEPLDKVKORNE		
		:  :  :    :  :    :    :    :    :    :    :    :    :    :		
g268	KEGAYYVKTISYSVQPTDDKSKIFAELSOAHDIHPLSELVS--MALIKEPLDKAKORNE			
	150 160 170 180 190 200			
	40 50 60 70 80			
m268-1.p ep	ELEAAE-----EAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
	:    :    :    :    :    :    :    :    :    :    :    :    :    :    :			
g268	KLEAAEATAQEAREAEAAAEALGREQEAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
	210 220 230 240 250 260			
	90 100 110 120 130 140			
m268-1.p ep	KLOASQKTKWSGMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE			
	:    :    :    :    :    :    :    :    :    :    :    :    :    :			
g268	KLOASQKTKWSGMDKICANNAKAEGKTPNGIKVSELACKTAKTEARLEELHNRKKALIDE			
	270 280 290 300 310 320			
	150 159			
m268-1.p ep	MAREADKKELSKRLX			
	:    :    :    :    :    :    :    :    :    :    :    :    :    :			
g268	MVREEDKKELPKRLX			
	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1.seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```



401 TGCACAACCG TAAAAAGCC CTTCTCGACG AATGGCCAG GGAAGCGGAC  
451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep  
1 VQSRDGLHK FKHCSAAMA LIKEPLDKAK QRNEELEAAE EAAAEALGR  
51 EQEVDVRVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLOASQ KTWKSGMDKI  
101 CANNAKAEGE TPNGIKFSEL ACKTAETEAR LEEHNRKKA LLEDEMAREAD  
151 KKELPKRL\*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHCSAAMALIKEPLDKAKQRNEELEAAEAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHCSAAMALIKEPLDKVQRNEELEAAEAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLOASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
	70	80	90	100	110	120
a268-1.pep	ACKTAETEARLEELHNRKKA LLEDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKA LLEDEMAREADKKELSKRLX					
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKA LLEDEMAREADKKELPKRLX					
m268-1	ACKTAETEARLEELHNRKKA LLEDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq  
1 atggttttggc gtgtgaattg gcgggcaacg gcggcgctga ttttttcgct  
51 cagcccttgg atttgggagg tggtgtgggt gtggtcgagg tcggtctttt  
101 cctgcaaacc ttgcccagc cttgacgcgt ccagtgcgcc ggcgttggcg  
151 gtttcgccgt gggactttat ccggaacacg gcttcgcca aggtgtcggc  
201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc  
251 cgcccggtgc cattttgctg tccaatcgcg gggttaaaaa accgttgcg  
301 ttaagtgcg cgtccgtcca agtcgatacg agcgcgcttc tttgccttcc  
351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep  
1 MVWRVNCAAT AALIFSSSPW IWAUVVWSR SAFSCKPCAS LDASSAPALA  
51 VSPWDFIRNT ASPKVSAAALM HSPKTRALGR FSAPPVAILL SNRGVKKPLS  
101 FKSPSVQVDT SALLCLSLRS S\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq  
1 ATGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC  
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGTCTCGG TCGGCTTGT  
101 CTTGCAAACC TTGCGCCaCG TGCCCGCGTC CAGCGCCTGC GTTGATGGTT  
151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTGCGCGGC  
201 TTTGATGCAC AGTTTAAAAA CCAGGGCTTT GGGGCGGTTT TCGTCCCGC  
251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCTGTT  
301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT  
351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep  
1 MVWRVNCAAT AVLIFSSSPW IWAUVVWSR SALSCKPCAT CPRPAPALMV  
51 SPWDFIONTA SPKVSAAALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF  
101 KFSSVQVDT SALLCLSLRSS \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269            MVWRVNCAATAALIFSSSPWIWAVVWVWSRSAPFCKPCASLDASSAPALAVSPWDFIRNT  60

m269 . pep      ASPKVSAAALMHFSKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS 119
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g269            ASPKVSAAALMHFSKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT SALLCLSLRS 120

m269 . pep      SX 121
                ||
g269            SX 122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269 . seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCCGCGT CCAGCGCGCC GGC GTTGACG
151 GTTTCGCCGT GGGACTTTAT CCAGAACACG GCTTCGCCCA AGGTGTCCGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGGCGG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269 . pep
1  MVWRVNCAAT AVLIFSSSPW IWA AVVWVAR SALSWRFCAS VPASSAPALT
51 VSPWDFIQNT ASPKVSAAAL HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

                10      20      30      40      50      59
m269 . pep      MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269            MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSWRFCASVPASSAPALT VSPWDFIQNT
                10      20      30      40      50      60

                60      70      80      90      100     110     119
m269 . pep      ASPKVSAAALMHFSKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a269            ASPKVSAAALMHFSKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDT SALLCLSLWS
                70      80      90      100     110     120

m269 . pep      120
                SX
                ||
a269            SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270 . seq
1  atgaataaaa accgcaaatt actgcttgcc gcactgctgc tgactgcctt
51 tgccgccttc aagctcgctt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg agggttgcac gctgccggac
151 ggaagccgtg tccgcgccgc cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccg ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcata cgctgcccg tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

## g270.pep

1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ  
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

## m270.seq

1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca.CAGCCGC  
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCgGTTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTTCaACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTGCA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

## m270.pep

1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ  
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

## m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
g270	MNKNRKLLLAALLLTAFAAFKLVLLQWWQAQQPQAVAAQCDLTEGCTLPDGSRVRAAAVS					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAVRIRLPICVEGRR					
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQPSGTWQAARIRLPVCVEGRR					
	70	80	90	100	110	120
	130 140					
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

## a270.seq

1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT  
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC  
 101 AAGCTGTGGC GCGCAATGC GATTGACCG AGGGTTGCAC GCTGCCGGAC  
 151 GGAAGCCGCG TCCGCGCCGC CGCgGTTTCA ACCAAAAAAC CGTTTGATAT  
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA  
 251 GTATGAAAAA TATGGATATG GGTTTCAACC GCTATATGTT CGAGCGGCAA  
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTGCA  
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC  
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

## a270.pep

1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD  
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE \*

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALLIAFAAVKL	VLLQWQAQ	QPQAVAAQC	DLTEGCTLP	DGSRVRAAAVS
a270	MNKNRKL	LLAALLIAFAAVKL	VLLQWQAQ	QPQAVAAQC	DLTEGCTLP	DGSRVRAAAVS
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPFDI	YIEHAPAGTEQ	VSISFSMKN	MDMGFNRYM	FERQPSGTW	QAVRIRLPICVEGRR
a270	TKKPFDI	YIEHAPAGTEQ	VSISFSMKN	MDMGFNRYM	FERQPSGTW	QAVRIRLPICVEGRR
	70	80	90	100	110	120
	130	140				
m270.pep	DFTADITIGS	RTFQTAFTAE	X			
a270	DFTADITIGS	RTFQTAFTAE	X			
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1  atgttcagtt cgcggatggc gaggatttgg gcgacggggg taacgttggtg
51  tatggtcagt ccgtgtccgg cggtgacgac caagcccaa tccgccgga
101  aatgcgcgcc gttttggatg cgctcgaact gcctgatttg ttcggcggtgg
151  ctttgtgctg cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201  gacatcacgg gcggcttgga ttgacctgtc gtcggcatcg ataaacaagg
251  acacgcgtat gcccgcgtcg gtcaggattt tggcgaattc ggcgattttt
301  tcctgttgct ccaatacgtc caaaccgcct tcggtcgtga tttcctgcgc
351  tttttcaggc acgatgcaca cgtcttccgg catcacttta agcgcgtttt
401  cgagcatttc ttccgtcaac gccatttcaa ggttcaggcg cgtgcggatg
451  gcgtttttga cggcaatac atccgcgtct ttgatgtggc ggcggtcttc
501  gcgcaggtgc atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551  ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1  MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSAIF
101  SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRRVRM
151  AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1  AwGTTcagTt CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCCGG CGTTGACGAC CAAGCCCAA TCGCCGCGCA
101  AATGCGCGCC GTTTTGATG CGCTCGAAct GCCTGATTtG TTCGGCGTGG
151  CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201  GACATCACGG GCGGCTTGGA TTGcCTGTc GTCGGCATCG ATAAACAAAG
251  ACACGCGTAT GCCTGCGTGC GTCAGGATTt TGGTGAACCC GGCGATTtTT
301  TCCTGTtGCG CCAATACGTC CAAACCGCCT TCGGTcGTGA TtTCCTGACG
351  TTTtTCAGGC ACGATGCACA CGTCTTCCGG CATCACTtTC AAAGCGTtTT
401  CCAACATTTC TTCCGTCAAC GCCATTtCAA GGTTCAGGCG CGTGCcGATG
451  GCGTtTTTGA CGGCAACAC GTCCGCGTCT TTGATGTGGC GGCcGTCTTC
501  GCGCAGGTGC ATGgTAATCA AATCCGCACC GTGCgtTTcG GCAACCAGTG
551  CCGCCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1  XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101  SCCANTSKPP SVVISXRFSG TMHTSSGITF KAFSNISSVN AISRFRRVRM
151  AFLTANTSAS LMWRRSSRRC MVIKSAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTCA GTT  CGCGGATGGC  GAGGATTTGG  GCGATGGGGG  TAACGTTGTG
51  TATGGTCA GTT  CCGTGTCCGG  CGTTGACGAC  CAAGCCCAAA  TCGCTGGCAA
101 AATGCGCGCC  GTTTTGGATG  CGCTCGAACT  GCCTGATTTG  TTCGGCGTGG
151 CTGCGCGCGT  CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201 GACATCACGG  GCGGCTTGGA  TTTGCCGTGC  GTCGGCATCG  ATAAACAAGG
251 ACACGCGTAT  GCGGCGGTGC  GTCAGGATTT  TGGTGAATTC  GGCAATTTTG
301 TCTTGTTGCG  CCAATACGTC  CAAGCCGCTT  TCGGTCGTGA  TTTCTGACG
351 TTTTTCGGGC  ACGATGCACA  CGTCTCCGG  CATCACTTTA  AGCGCGTTTT
401 CGAGCATTTT  TTCCGTCAAC  GCCATTCAA  GGTTCAGGCG  CGTGCGGATG
451 GCGTTTTTGA  CAGCAAACAC  GTCCGCGTCT  TTGATGTGGC  GCGGGTCTTC
501 GCGCAGGTGC  ATGGTAATCA  GGTCGGCACC  GTGCGTTTCG  GCAACCAAGT
551 CCGCCTCCAC  GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW AMGVTLCMVS PCPALTTKPK SLAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNSAIL
101 SCCANTSKPP SVVIS*RFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRSAPCVS ATSAASTGLG *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPALFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

621

	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVKSAPCVS					
a271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
a271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1109>:

g272.seq

```

1  atgactgcaa aggaagaact gttcgcatgg ctgcgccata tgaacaaaaa
51  caaagggtcc gacctgtttg tgacgacca tttccgccc gctatgaagc
101 tggacggcaa aatcacccgc atcacggacg aaccgctgac ggcggaaaaa
151 tgtatgaaa tcgcttttc gattatgagt gcgaagcagg cggaagaatt
201 ttcacgcacc aacgagtgcg atttcgccat cagcctgccg gacaccagcc
251 gcttcgcgct caatgcgatg atacagcgcg gtgcgacggc gttggtattc
301 cgcgcgatta ccagcaagat tcccaagttt gaaagcctga acctgcgcgc
351 ggccctgaag gatgttgcgc tgaaaaaacg cgggctgggt atttttgtcg
401 gcggcaccgg ctccggcaaa tcgacttcgc tcgctcgct tatcgactac
451 cgcaatgaaa attcgttcgg acacatcatc accatcgaag atccgatcga
501 gtttgtccac gaacacaaaa actgcatcat taccagcgc gaggtcggcg
551 tggacacgga aaactggatg cgggcgttga aaaatacgtc gcgtcaggcg
601 cggatgtgta tccttatcgg cgaaatccgc gaccgtgaaa caatggacta
651 cgccatcgcc ttgcccgaag cggggcattt gtgtatggcg acgctgcacg
701 ccaacagcac caatcaggcg ctgcacgcga tcatcaactt cttccccgag
751 gagcgcgcg aacaattgct gacggatttg tcgtcaacc ttcaggcggt
801 tatttcgcaa cgcctcgttc cgcgagacgg cggcaagggc aggggtggcg
851 cagtcgaggt gctgctcaat tcgcccctga tttcggaggt gattcacaac
901 ggcaacatcc atgaaatcaa agaagtgatg aaaaaatcca ctaccctggg
951 tatgcagacc ttcgaccaac acctttacca attgtatgaa aaaggcgaga
1001 tttccttgca ggatgccttg aaaaatgccg attccgcaca tgatttgctg
1051 ttggcggtac agttgcgcag ccgcagggca caaagtccg accccgattt
1101 ggaactgctc tga

```

This corresponds to the amino acid sequence <SEQ ID 1110; ORF 272.ng>:

g272.pep

```

1  MTAKEELFAW LRHMNKNKGS DLFVTTTFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAPSIMS AKQAEFSST NECNFAISLP DTSRFRVNM IORGATALVF
101 RAITSKIPKF ESLNLPPALK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYIA FAETGHL CMA TLHANSTNQA LDRIINFPPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHL YQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRRA QSSDPDELL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1111>:

m272.seq

```

1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAwCCAAAA
51  CAAAGGTTCC GACCTGTTG TGACAACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGAAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCAATCGACC AACGAGTGCA ACTTCGCCAT CAGCCTGCCG GACACCAGCC
251 GCTTCGCGCT CAATGCGATG ATACAGCgCG GCGCGACGGC GTTGGTATTC
301 CGTACGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCGGCC
351 AGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 CGGCACCCG CTCGGGTAAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTGCGCG

```

```

551 TGGATACGGA AACTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTcGA TTTCGGAGTT GATTACAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCGGATT
1101 GGNACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMxQNKGs DLfVtTHfPP AMKLdGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVnam IQRGATALVF
101 RTITSKIPKF ESLNLPpVLK DVALKKRGLV IFVGGTGSgK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENwM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLcMA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPdGGKG RvAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQhLYQLYE KGDISLQeAL KNADSAHDLR
351 LAVQLRSRRA QsXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLRHMxQNKGsDLfVtTHfPPAMKLdGKITRITDEPLTAEK					
g272	MTAKEELFAWLRHMKNKGsDLfVtTHfPPAMKLdGKITRITDEPLTAEK					
m272.pep	70	80	90	100	110	120
	AKQAEFFSSTNECNFAISLPDTSRFRVnamIQRGATALVFRTITSKIPKFESLNLPpVLK					
g272	AKQAEFFSSTNECNFAISLPDTSRFRVnamIQRGATALVFRAITSKIPKFESLNLPpALK					
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTGSgKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTGSgKSTSLASLIDYRNENSFGHIIITIEDPIEFVHEHKNCIITQR					
m272.pep	190	200	210	220	230	240
	EVGVDTENwMAALKNTLRQAPDVILIGEIRdRETMDYAIAFAETGHLcMATLHANSTNQA					
g272	EVGVDTENwMAALKNTLRQAPDVILIGEIRdRETMDYAIAFAETGHLcMATLHANSTNQA					
m272.pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTdLSNLQAFISQRLVPdGGKG RvAAVEVLLNSPLISELIHN					
g272	LDRIINFFPEERREQLLTdLSNLQAFISQRLVPdGGKG RvAAVEVLLNSPLISELIHN					
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQhLYQLYEKGDISLQeALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQhLYQLYEKGEISLQdALKNADSAHDLRLAVQLRSRRA					

623

```

          370
m272 . pep  QSXSPDLXLLX
            || :||| |||
g272       QSSDPDLELLX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272 . seq
1  ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACC CGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAA TCGCCTTTTC GATTATGAGT GCGAAGCAGG CCGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCATTGA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 GCGGCACCGG CTCGGGCAA TCGACTTCGC TTGCCTCGCT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAATGGATG GCGGCGTTGA AAAACACGCT CGCTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACCTGTCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CCGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCTGA TTTCGGAGTT GATTCAACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGCA GGATGCCTTG AAAAAATGCC ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTTCCG GTCCCGATTT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272 . pep
1  MTAKEELFAW LRHMNKNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFSST NECNFAISLP DTSRFRV NAM IQRGATALVF
101 RAITSKIPKF ESLNLPVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLMA TLHANSTNQA LDRIINFFPE
251 ERREQLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

          10      20      30      40      50      60
m272 . pep  MTAKEELFAWLRHMKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
            ||||| :||| ||||| ||||| ||||| ||||| ||||| |||||
a272       MTAKEELFAWLRHMKNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
          10      20      30      40      50      60

          70      80      90     100     110     120
m272 . pep  AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPVLK
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a272       AKQAEFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPVLK
          70      80      90     100     110     120

          130     140     150     160     170     180
m272 . pep  DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
            ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a272       DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHIITIEDPIEFVHEHKNCIITQR
          130     140     150     160     170     180

```



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	190	200	210	220	230	240
m272.pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETM DY A I A F A E T G H L C M A T L H A N S T N Q A					
	190	200	210	220	230	240
m272.pep	LDRIINFFPEERREQLLTDSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLTDSLNLQAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272.pep	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G D I S L Q E A L K N A D S A H D L R L A V Q L R S R R A					
a272	GNIHEIKEVMKKSTTLGMQTFDQHL Y Q L Y E K G E I S L Q D A L K N A D S A H D L R L A V Q L R S R Q A					
	310	320	330	340	350	360
m272.pep	Q S X S P D L X L L X					
a272	Q S S G P D L E L L X					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

```

g273.seq
1  atgagtccttc aggcgggtatt tatatacccc ccaagccgta cgcacacaata
51  caacgaaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccgggaact
151 ccattcaccg ttttctgcc gtttctgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggcgc gtgccgctga aatcaaggcg
351 gtttgagaag tgttccnac gcgccgccg tatgtgccga aatattattt
401 gtcgctcacc tgcaaatcg ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccctg ctttttgttt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

```

g273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHTDRR QDIGVFEAGT
51  PFTVFLPLV AFEIKDDAGK QRGSRRHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRRPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

```

m273.seq
1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCGG TTTTCTGCC GCTTCTTGTG GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTCATT
251 GTTGTTCCTT AATGCTTAA AACC CGCCTG TCCGTGCAAC CGTTTAAAGG
301 CGGCAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCTGAC GCGCCGCCCT GTGTGCCGGA GTTATTGTG
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CATA CGGCGT TTACCTGCCT TTTGkTwTC AAGCAGTTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

```

m273.pep
1  MSLQAVFIYP PSRTAQYNEN QENGGAHKQ GQSGKHADRC QDIGVFKAGT
51  PFPVFLPLV AFEIKDDAGK QRGSRRH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRAALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 273 shows 86.0% identity over a 171 aa overlap with a predicted ORF (ORF 273.ng) from *N. gonorrhoeae*:

m273/g273

	10	20	30	40	50	60
m273 . pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQSGKHADRCQDIGVFKAGTPFPVFLPLL					
g273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQSGKHTDRRQDIGVFEAGTPFTVFLPFLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m273 . pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
g273	AFEIKDDAGKQGRSRARHWHCVHCCSLTVKNPPGRATVLRREIAKFVCGRVPLKSRRFEK					
	70	80	90	100	110	120
	130	140	150	160	170	
m273 . pep	CSRRRA-ALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
g273	CFXRARPMCRNIICRSPAKSPRTRFAEFPRCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

a273 . seq

1	ATGAGTCTTC	AGGCGGTATT	TGTATACCCC	CCAAGCCGTA	CCGCACAATA
51	CAACGAAAAT	CAGGAAAACG	GCGGTAAAGC	TCATAAACAG	GGACAAAGCG
101	GCAAACACGC	CGACCGCCGT	CAGGATATAG	GCGTATTCCA	GACCGGAAC
151	CCATTACCG	TTTCTCTGCC	GCTTTTGTG	GCTTTTGAA	TAAAGGATGA
201	TGCCGGCAAG	CAGCGCGGCA	GCCGCGCCCG	ACATTAGCAT	AATGTTTATT
251	GTTGTTCTTT	AACGGTTAAA	AACCGGCCCG	TCCGTGCAAC	CGTTTTTAA
301	AGGCGGTAAA	TCACAAAGTT	TGTTGGCGGA	CGTGCTCTCT	TACAATCAGG
351	GCGGTTTAA	GGGCATGATG	CACTGCCCGG	TGTGCCGGAT	ATTATTTGTC
401	GCTCACCTGC	AAAATTGCCA	AGAACGCGCT	TTGCGGGATT	TCCACATTGC
451	CCACTTGTTT	CATACGGCGT	TTGCCTGCTT	TTTGTTTTTC	AAGCAGTTTT
501	TTCTTACGCG	TAA			

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

a273 . pep

1	MSLQAVFVYP	PSRTAQYNEN	QENGGAHKQ	QSGKHADRR	QDIGVFQGT
51	PFTVFLPLFV	AFEIKDDAGK	QGRSRARH*H	NVHCCSLTVK	NPPVRATVFK
101	RR*ITKFVGG	RALLQSGRFK	GHDALPRVPD	IICRSPAKLP	RTRFAGFPHC
151	PLVSYGVCLL	FVEQAVFSYA	*		

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273 . pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGSQSGKHADRCQDIGVFKAGTPFPVFLPLL					
a273	MSLQAVFVYPPSRTAQYNENQENGGAHKQGSQSGKHADRRQDIGVFTGTFTVFLPLFV					
	10	20	30	40	50	60
	70	80	90	100	110	119
m273 . pep	AFEIKDDAGKQGRSRARHXHCVHCCSLMLKNPPVRATVLRRIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRARHXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRRALLQSGRFK					
	70	80	90	100	110	120
	120	130	140	150	160	170
m273 . pep	GCSRRRAALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPRTFRFAGFPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTCTCCCC GATATGAATG CCGCAAAAGT
201 GTTTGTCTGGC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTgt tcaaAACCCT
351 TCCGCCGGCC AACCACTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGCAGCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTCTCCCC GATATGAATG CCGCAAAAGT
201 GTTGTCTGGC GCGGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCCTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAAACCCT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCAGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEY EAVFKTLPPA					
m274	DMNAAKVFVGGEFDGKQPLNLLMHPTRKADDQTVALKPVGSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNATESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

a274 .seq

```

1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGACG
101 GCAAGCATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCC GATATGAATG CCGCAAAAGT
201 GTTTGTCTGGC GGCAGAGTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GCGGAATAT GAGGCGGTGT TCAAACCCCT
351 TTCGCCGACC AACCACTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTGT
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

a274 .pep

```

1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFEV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*

```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274 .pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m274 .pep	DMNAAKVFEV GEFDGKQPLN LLLMHPTRKADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFEV GEFDGKQPLN LLLMHPTRKADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
m274 .pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

g276 .seq

```

1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgcggt
51  ggtcaggcgg tggcgacga tgatgccggt gcggttttcc atcaggcggt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgctcaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgctc ttcaaatgg cgcggcgat
201 ggcgacgcgt tgcgctgtc cgccggataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcgcgag ggggatgcgt cgatcaggct ttgcagggtg
301 gcggcttggg gggcgacag gacttcggct tcgcccgct cgggacggct
351 gtatcgagc ttttcaaaca ggggtgctgc aaacaggaat acgtcttggg
401 agacgagggc gaattgggag cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaaggttg acgacggtg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctgt atgtcgaggt tgaagttgtc gagggctttg
601 atgccgtctg aacggtattc gacatcgacg ttgcggaagc tgatgcgccc
651 ttcgacacgc tgcggcgaga gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcgcgga ggaacatcgt ctgcataagg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag

```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276 .pep

1 MILPPSMTMM RSADSTVRR WATMPVRF S IRRSSACWTR RSDSLSNALV  
 51 ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL  
 101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLSMSAM  
 151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL  
 201 MPSEYSTST LRLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG  
 251 MLMLARLLMG AYICSIATMN AINSPMVV\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq  
 1 ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT  
 51 GGTGAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT  
 101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG  
 151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATAGG CGCGGGCAAT  
 201 GGCAGACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA  
 251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG  
 301 GCGGTTTGGG GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT  
 351 GTATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG  
 401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG  
 451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGTTTCGA CAAAGCGGGG  
 501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG  
 551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG  
 601 ATGCCGTCTG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC  
 651 TTCGACACGC TCGGGTGCGA GCGTGCCCTT GTCCTGTTCG GCGGGGGTGT  
 701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG  
 751 ATGCTGATGT TGGCAAGGCT TTGATGGGG GCGTACATTT GCAGCATCGC  
 801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep  
 1 MILPSSITMM RSAPSMVRR WATMPVRF S IRRSSACWTR RSDSLSNALV  
 51 ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GELSIRLCRL  
 101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLSMSAM  
 151 SIPSMQMLPA DGSTKRGRRL TTVDLPLPER PTRATRSPLC MSRLKLSRAL  
 201 MPSEYSTST LRLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG  
 251 MLMLARLLMG AYICSIATMN AINSPMVV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVRRWATMPVRF S IRRSSACWTRRSDSLSNALVASSNNNIGAS					
g276	MILPSSITMMRSADSTVRRWATMPVRF S IRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLSMSAMSI PSMQMLPADGSTKRGRRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLSMSAMSI PSMQMLPADGSTKRGRRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLCMSRLKLSRALMPSEYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPLCMSRLKLSRALMPSEYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

a276.seq

1	ATGATTTTGC	CGTCGTCCAT	TACGATGATG	CGGTCGGCCC	CTTCGATGGT
51	GGTCAGGCGG	TGGGCGACGA	TGATGCCGGT	GCGGTTTTC	ATCAGGCGTT
101	CGAGCGCCTG	TTGGACGAGG	CGTTCGGATT	CGTTGTCCAA	TGCGCTGGTG
151	GCTTCGTCCA	ATAATAATAT	CGGCGCGTCT	TTCAAATGG	CGCGGGCAAT
201	GGCAACGCGT	TGCCGCTGTC	CGCCGGATAA	GTTGCTGCCG	TTGCATCCGA
251	TGGGCTGGTG	CAGTCCGAGC	GGTGATGCGT	CGATCAGGCT	TTGCAGGTTA
301	GCGGCTTGGA	GGGCGGATAG	GACTTCGGCT	TCGCCC GCGT	CGGGACGGCT
351	ATATCGGACG	TTTTCAAACA	GGGTGTCGTC	AAACAGGAAT	ACGTCTTGGG
401	AGACGAGGGC	AAATTGGGCG	CGCAGGCAGT	CGAGTTTGAT	GTCGGCGATG
451	TCGATACCGT	CTATGCAGAT	GTTGCCGGCA	GACGGTTCGA	CAAAGCGGGG
501	CAGCAGGTTG	ACGACGGTGG	ATTGCGCGCT	GCCGGAACGT	CCGACCAAGG
551	CGACGCGTTC	GCCTTGCTG	ATGTCGAGGT	TGAAGCCGTC	GAGGGCTTTG
601	ATGCCGTCCG	AACGGTATTC	GACATCGACG	TTGCCGAAGC	TGATGCGCCC
651	TTGCACACGC	TGCGGTGCGA	GCGTGCCTTT	GTCCTGTTTC	GGCGGGGTGT
701	CGAGAAATGC	ACATACGCCG	TCGGCGGCGA	GGAACATCGT	CTGCATAGGG
751	ATGCTAATGT	TGGCAAGGCT	TTTGATGGGG	GCGTACATTT	GCAGCATCGC
801	GACGATGAAT	GCCATAAATT	CGCCGATGGT	GGTGTAG	

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

a276.pep

1	MILPSSITMM	RSAPSMVVR	WATMMPVRF	IRRSSACWTR	RSDSLSNALV
51	ASSNNNIGAS	FKMARAMATR	CRCPPDKLLP	FDPMGWCSPS	GDASIRLCRL
101	AAWRADRTSA	SPASGRLYRT	FSNRVSSNRN	TSWETRANWA	RRQSSILMSAM
151	SIPSMQMLPA	DGSTKRGSRL	TTVDLPLPER	PTRATRSPL	MSRLKPSRAL
201	MPSEYSTST	LRKLRPSTR	CGASVPLSCS	GGVSRNAHTP	SAARNIVCIG
251	MLMLARLLMG	AYICSIATMN	AINSPMVV*		

m276/a276 : 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRWATMMPVRFIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRWATMMPVRFIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPPDKLLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSILMSAMSIPSMQMLPADGSTKRGSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPLMSRLKLSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPLMSRLKPSRALMPSEYSTSTLRKLRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

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250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
1  ..atggtacacg tcgccgtagc ttacggtatt gccgtccggc gtttttgccc
51  aaacgaggtc atagacgttt tccacgcctt gcaggtagat cgccaagcgt
101 tcgatgccgt aggtaatctt gccgagtagc gccgtgcaat cgataccgcc
151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
201 cttcccagcc caaaccacac gcaccgaggg tggggttttc ccagtcgtct
251 tcgacaaagc ggatgtcgtg gactttggga tcgatgccca attcgcgcag
301 ggagtcgaga tagaggtcct ggatattggc gggggcgggt ttgagggcga
351 cttggaattg gtaatagtgt tgcaggcggg tggggttgtc gccgtagcgg
401 ccgtctttgg ggcggcggct gggttggaag taggcggcaa accaaggctc
451 gggggcgcagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
501 cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
551 gtttgcagtt tgaagatgat ttggtggaag gtaagcatgg cttattgttc
601 gataaaataa aggttttatt ttactgtttc catagccgct tgaatagatt
651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
1  ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
51  DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
101 GVEIEVL D I GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPR L
151 GAERAQAGGG MGCAGTDFHV EGLDDGA AFV CPEGLQFEDD LLEGKHGLLF
201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
1  ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTCGTAGTC GTTGAAC TGG
101 CGCAGCAGCC AGTCGGCATC GCTGTATTCT AAGTTGTAGG TGGATTGCTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
301 GTCGATGCCG CCGACTTGTT GGAATAGGT AAAGTGGGT ACTTCCATGC
351 CGTTGAGCCA GACTTCCAG CCCAAACCCC ACGCGCCGAG GGTGGGTTT
401 TCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGACGGCG GTTGGGGTTG
551 TCGCCGTAGC GGGCGTCTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTGTCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
1  MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG I AVFEVVGGLL
51  DFLVHVHVA V GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
101 VDAADLLEIG KLG Y FHAVEP DFPAQT PRAE GGVFPVVDK ADVVDFGIDA
151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAAVF GAAAGLDVGG
201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCECLQ FEDDLLEGKH
251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30  
MVHVAVAYGI AVRRFCPNEV IDVFHALQVH

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```

m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVG DGVAVERFCPNEVVDFYTLQVH
           30      40      50      60      70      80
g277 . pep      40      50      60      70      80      90
      RQAFDAVGNEFAEYGRAIDTADLLEIGKLYFHAVEPDFPAQTPRTEGGVFPVVFDKADVV
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLYFHAVEPDFPAQTPRAEGGVFPVVFDKADVV
           90      100     110     120     130     140
g277 . pep      100     110     120     130     140     150
      DFGIDAQFAQGVEIEVLDIGGGGFEGLDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      DFGIDAQFAQRVEIEVLDIGGSGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPRL
           150     160     170     180     190     200
g277 . pep      160     170     180     190     200
      GAERAQAGGGMGCAGTDFHVEGLDDGAAFVCPEGLQFEDDLLEGKHGLL
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPECLQFEDDLLEGKHGLX
           210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277 . seq
1   ATGCCCCGCT TTAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAACTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTC
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 GTCGATGCCG CCGACTTGTT GGAAATAGGT GAACTGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GTGGGGTTT
401 TCCCAGTCGT CTTCGACAAA GCGGATGTCG TGCACTTTGG GGTCGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTGCGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGTT GGATGACGGT GCAGCCTTTG
701 TCTGCCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277 . pep
1   MPRFEDKLVG RQEGGVVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVEPVVFDK ADVVHFGVDA
151 QFAQGVEIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

m277 . pep      10      20      30      40      50      60
      MPRFEDKLVRQEGGVVFFGKQAFGLRFVVVELAQQPIGIAVFEVVGGLLDFVLVVHVAV
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      MPRFEDKLVRQEGGVVFFGKQAFGLRFVVVELAQQPIGIAVFEVVGGLDFVLVVHVAV
           10      20      30      40      50      60
m277 . pep      70      80      90      100     110     120
      GDGVAVERFCPNEVVDFYTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLYFHAVEP
      : :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a277      SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
           70      80      90      100     110     120
           130     140     150     160     170     180

```



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```

m277.pep  DFFAQT PRAEGGVFPVVDKADVVDFGIDAQFAQRVEIEVLIDIGGSGLEGDLVLVLQA
          |||||||
a277      DFFAQT PRAEGGVFPVVDKADVVHFGVDAQFAQGVIEVLIDIGGSGLEGDLVLVLQA
          130      140      150      160      170      180

          190      200      210      220      230      240
m277.pep  VGVVAVAAVFGAAAGLDVGGKPRPGAECAGAGGMGCAGTDFHVEGLDDGAAFVCPCECLQ
          |||||||
a277      VGVVAVATVFGAAAGLDVGGKPRPGAECAGTGGGMGCAGTDFHVEGLDDGAAFVCPCECLQ
          190      200      210      220      230      240

          250
m277.pep  FEDDLLEGKHGLX
          |||||||
a277      FEDDLLEGKHGLX
          250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1  ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cggtaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaaat acggccggta
151 caggtaaccg tgtcgccctc ttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtgcgcgt ccaggttcac cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcatttaca gacagatttt cgatcttggc ttaatacaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1  LRAITPGAIF STGAVKVLI GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFNF...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1  TTGCGCGCAA TCACGCCCGG TGCATTTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CCGGTCCGAC CAGTTGCGGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTGCGCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GCGCGCGACG GAGTCGCGCT CCAGGTTTCAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGCC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTT GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTGC GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1  LRAITPGAIF SIGAVKVLI GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPOVRTSAFT DRFSILALIK SLISAGLSM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDG DRDFQLAVET LIQHLHQLAD
201 LFGQIRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278 . pep	LRAITPGAIFSTGAVKVVLIIGPLPSIGRPNASTTRPTNSRPTGTSGKIRPVQVTVSPSLIC					
m278	LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSGKIRPVQVTVSPSLMC					
	10	20	30	40	50	60
	70	80	90	100	110	120
g278 . pep	SYSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVLTSAFT					
m278	SYSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVLTSAFT					
	70	80	90	100	110	120
	130	140	150	160	170	
g278 . pep	DRFSILALIRSLISAGLSCKMTLLIRHSRVQSTQFALYRQIQNLITHFNF					
m278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQSTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFVGQRIGTVNDGRFDMVE*					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278 . seq

```

1   TTGCGCGCAA TCACGCCCGG TGCGATTTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATATGT TCGTGCTCGC CCAACACTAC
201 GCGGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGATTG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATCACC GTACCACGGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTTGCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTGAGC ATTTGCGCCA ACTCGCCGAC
601 CTGTTGTGCG GTCAACGGAT AGGCACTGTA AATGACGGCA GATTTGATAT
651 GGTGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278 . pep

```

1   LRAITPGAIF SIGAVKVVLI GPLPSIGRPN ASTTRPTSSR PTGTSGKIRPV
51  QTVSPSLIC SCSPTTAPT ESRSRFIAPK KVLPGNSSIS PCIASDKPMM
101 RTIPSVTEIT VPRVRTSAFT DRFSILALIK SLISAGLSCK KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDF DRDFQLAVET LIQHLRQLAD
201 LFVGQRIGTV NDGRFDMVE*

```

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278 . pep	LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSGKIRPVQVTVSPSLMC					
a278	LRAITPGAIFSIGAVKVVLIIGPLPSIGRPNASTTRPTSSRPTGTSGKIRPVQVTVSPSLIC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m278 . pep	SYSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVLTSAFT					
a278	SCSPNTTAPTESRSRFIAPKVLPGNSSISPCIASDKPMMRTIPSVTEITVPRVLTSAFT					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLS	CKMTLLIRHSRVQGTQ	FALYRQIQNLITHFN	FYAANQLRFDF		
a278	DRFSILALIKSLISAGLS	CKMTLLIRHSRVQGTQ	FALYRQIQNLITHFN	FYAANQLRFDF		
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHL	QLADLFVQGRIGTVND	GRFDMVEX			
a278	DRDFQLAVETLIQHL	QLADLFVQGRIGTVND	GRFDMVEX			
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggtctg cttgatttca acggttttga gtgtttcggc
51  aagtttgctg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 cgggcagcgg cagggcgcggt ttggtccggt cttctttggc ggcagccatg
151 gtgctgctga cggcgcggtt gttgcctgca atcacgactt gtccggcgga
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggcggc cattgctcct
301 acgccttgct gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcgcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTSS SKPKMAAIAP
101 TPCGTADCIS SARRRTSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTTC ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGGCAGCGG CAGGCGCGGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGGCGGC GTTGCTGCA ATCACGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACTTCGCT TTGGGCGGCT TCGGCACAAA
251 TGCTTTTAAC CTGCTCATCT TCCAAGCGA GAATCGCCGC CATTGCGCCC
301 ACGCCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGGGTGT
401 ATTCGCGGAG GCTGTGTCCG GCAACGGCGG CAGGCGTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTSS SKPRIAAIAP
101 TPCGTADCIS SARRRTSLTA SAKFNAPAA SAVYSPRLCP ATAAGVLPAP
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:	:	:	:	:	:
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

```

m279.pep      ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTTCGTADCISSARRRSLTA
||| ||||| ||||| ||| : ||||| ||| : ||||| ||||| ||||| ||||| |||||
g279          ITTCPGELKLTASTTSPCADSAQICLTSSSKPKMAAIAPTTCGTADCISSARRRSLTA
              70          80          90          100          110          120

              130          140          150
m279.pep      SAKFNAPAATSAVYSPRLCPATAAGVLPASKX
||| ||| ||||| ||||| ||| : |||
g279          SAKSNSAATSAVYSPRLCPATAAGVLPPTSKX
              130          140          150

```

a279.seq

1	ATGACNCNGA	TTTGC	GGCTG	CTTGATT	TCA	ACGGTTT	NNNA	GGGCTT	CGGC
51	GAGTTTGT	CG	GCGGCGGGT	TCATGAGG	CT	GCAATGGG	AA	GGTACN	GACA
101	CNNGCAGC	CGG	CAGGGCGCGT	TTGGCGCCG	G	CTTCTTT	TGGC	GGCAAG	CATA
151	GCGGCTCT	CGA	CGGCGGCGGC	ATTGCTCTG	CA	ATCACGACT	T	GTCCGG	GCGA
201	GTTGAAGTT	G	ACGGCTTCAA	CCACTTCAT	C	CTGTGCGG	AT	TCGGCG	CAAA
251	TTTGTTTT	AC	CTGTTCATCT	TCCAAGCCG	A	GAATCGCCG	C	CATTGC	CCCC
301	ACGCCTTG	CG	GTACGGCGGA	CTGCATCAG	T	TCGGCGCG	CA	NGCGCA	CAGAG
351	TTTGACCCG	G	TCGGCAAAAT	CCAATGCG	CC	GGCGGCAAC	N	AGTGCCG	TGT
401	ATTCGCCG	CAN	GCTGTGTCCG	GCAACGGCG	G	CAGGCGTTT	T	GCGCCC	CGCT
451	TCCGAATAG								

a279.pep

1	<u>MTXICGCLIS</u>	<u>TVXRASASLS</u>	<u>AAGFMRLQWE</u>	<u>GTDTGSGRAR</u>	<u>LAPASLAASI</u>
51	<u>ARSTAAALPA</u>	<u>ITTCGELKL</u>	<u>TASTTSSCAD</u>	<u>SAQICFTCSS</u>	<u>SKPRIAAIAP</u>
101	<u>TPCGTADCIS</u>	<u>SARXRTSLTA</u>	<u>SAKSNAPEAT</u>	<u>SAVYSPXLCP</u>	<u>ATAAGVLPPA</u>
151	SE*				

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAMARPTAAALPA :          :          :          :          :          :					
a279	MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
	10	20	30	40	50	60
m279.pep	70	80	90	100	110	120
	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA           :          :          :          :          :					
a279	ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
	70	80	90	100	110	120
m279.pep	130	140	150			
	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX					
a279	SAKSNAAPAATSAVYSPXLCPATAAGVLPPASEX					
	130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttcagcatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcgga
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 cgcacatcca acgcgcgcgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgacccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccaca acgtcgctga aacctgata aaggccgac cgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaatgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtcctga ccgggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgcccgc aaggcgtag cagcgaagcc gagccgtccg
701 ccaacaagtc cgcgcgcatc atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtt accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcggca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLFVVTFSFI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADIQRAV KQSKVSYAEA
101 TKGIQPLKAE EEGGHHHDH HDHDHDHGH HDHGEYDPH VWNDFVMSD
151 YAQNVAETLI KADPEGKVYY QRLGNYQMQ LKKLHSDAQA AFNAVPAKR
201 KVLTHGDAFS YMGNRYNISF IAPQVSSEA EPSAKQVAI IRQIKREGIK
251 AVFTENIKDT RMDRIAKET GNVVSGKLYS DALGNAPADT YIGMYRHNVE
301 ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCG TTGTAACCAG CTTAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGCTCAA CCGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCAG AAGGACACCA CCATGACCAC GGCGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTA TGCCCAAAAC
451 GTTGCCAAAG CCTTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GGCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCAACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLFVVTFSFI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNLGL LEAADVQRAV KQSKVSYTEA
101 TKGIQPLKAE EEGGHHHDH HDHGEHHDH GEYDPHVND PVLMSAYAQN
151 VAKALIKADP EGKVYYQRL GNYQMQLKKL HSDAQAAFNA VPAKRKVL

```

637

201 GHDAFSYMGK RYHIEFIAPQ GVSSEAEPSA KQVAIIIRQI KREGIKAVFT  
 251 ENIKDTRMVD RIAKETGVNV SGKLYSDALG NAPADTYIGM YRHNKALTN  
 301 AMKQ\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 280 shows 93.8% identity over a 308 aa overlap with a predicted ORF (ORF 280.ng) from *N. gonorrhoeae*:

m280/g280

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVTFSILGDVAKQIGGERVSIQSLVGANQDTHAYHM					
	::					
g280	MKHLKLTIAALLATAATAAPLPVVTFSILGDVAKQIGGERVAVQSLVGANQDTHAYHM					
	10	20	30	40	50	60
	70	80	90	100	110	119
m280.pep	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAEEEGGHHHDH-					
	::					
g280	TSGDIKKIRSAKLVLNGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAEEEGGHHHDH					
	70	80	90	100	110	120
	120	130	140	150	160	170
m280.pep	---DHDHEGHHHDHGEYDPHVWNDPVLMSAYAQNVAKALIKADPEGKVYYQORLGNYQMQ					
	::					
g280	HDHDHDHEGHHHDHGEYDPHVWNDPVLMSDYAQNVAEALIKADPEGKVYYQORLGNYQMQ					
	130	140	150	160	170	180
	180	190	200	210	220	230
m280.pep	LKKLHSDAQAAAFNAVPAAKRKVLTGHDAFSYMGKRYHIEFIAPQGVSSAEPSAKQVAAI					
	::					
g280	LKKLHSDAQAAAFNAVPAAKRKVLTGHDAFSYMGNRYNISFIAPQGVSSAEPSAKQVAAI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m280.pep	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNK					
	::					
g280	IRQIKREGIKAVFTENIKDTRMVDRIAKETGVNVSGKLYSDALGNAPADTYIGMYRHNVE					
	250	260	270	280	290	300
	300					
m280.pep	ALTNAMKQX					
g280	ALTNAMKQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq

```

1  ATGAAACACC CCAAACAC CTTATCGCC GCATTGCTGA CCACTGCCGC
51  AACTGCCGCC CCCCTGCCG TTGTAACCAG CTTACAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGCGGCG ACATTAAAAA
201 AATCCGCAGT GCAAACTCG TCCTGATTAA CGGCTTAGGA CTTGAAGCTG
251 CCGACATCCA ACGTGCCGTC AAACAGAGCA AAGTATCCTA TGCCGAAGCG
301 ACCAAAGGCA TCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG ACCATGACCA CGAAGGACAC CACCACGACC
401 ACGGCGAATA TGACCCCCAC GTCTGGAACG ACCCGTCCT TATGTCGCC
451 TATGCCCAAA ACGTCGCCGA AGCCCTGATA AAGGCCGACC CCGAAGGCAA
501 AGTTTATTAT CAACAACGCT TGGGCAACTA CCAATGCAG CTCAAAAAAC
551 TGACAGTGA CGCACAGCC GCATTTAATG CCGTCCCTGC CGCCAAACGC
601 AAAGTCCTGA CCGGGCACGA TGCCTTTTCC TATATGGGCA AACGTTACCA
651 TATCGAATTC ATCGCCCCAC AAGGTGTGAG CAGCGAAGCC GAGCCTTCAG
701 CCAAACAAGT CGCCGCCATC ATCCGACAAA TCAAACGCGA AGGCATCAAA
751 GCCGTATTTA CCGAAAATAT CAAAGACACC CGCATGGTTG ACCGCATCGC

```

638

801 CAAAGAAACC GGTGTCAACG TCAGCGGCAA ACTGTATTCC GACGCACTCG  
 851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA  
 901 GCCTTAACCA ACGCGATGAA GCAATAA

This corresponds to the amino acid sequence <SEQ ID 1156; ORF 280.a>:

a280.pep  
 1 MKHPKLTLIA ALLTTAATAA PLPVVTSFSI LGDVAQIGG ERVSIQSLVG  
 51 ANQDTHAYHM TSGDIKKIRS AKLVLLINGLG LEAADIQRAV KQSKVSYAEA  
 101 TKGIQPLKAE EEGGHHHDHD HDHDHDHEGH HHDHGEYDPH VWNDFVLMSA  
 151 YAQNVAEALI KADPEGKVYY QQRLGNYQMQ LKKLHSDAQA AFNAVPAKR  
 201 KVLTHGDAFS YMGKRYHIEF IAPQGSSEA EPSAKQVAI IRQIKREGIK  
 251 AVFTENIKDT RMVDRIKET GVNVSGLYS DALGNAPADT YIGMYRHNK  
 301 ALTNAMKQ\*

m280/a280 96.4% identity in 308 aa overlap

	10	20	30	40	50	60
m280.pep	MKHLKLTIAALLTASATAAPLPVVT	SFSILGDVAQIGGERVSIQSLVG	ANQDTHAYHM			
a280	MKHPKLTLIAALLTTAATAAPLPVVT	SFSILGDVAQIGGERVSIQSLVG	ANQDTHAYHM			
	70	80	90	100	110	120
m280.pep	TSGDIKKIRS	AKLVLLINGLGLEAADVQRAVKQSKVSYTEATKGIQPLKAE	EEGGHHHDHD			
a280	TSGDIKKIRS	AKLVLLINGLGLEAADVQRAVKQSKVSYAEATKGIQPLKAE	EEGGHHHDHD			
	130	140	150	160	170	
m280.pep	HDH----	EGHHHDHGEYDPHVWNPVLM	SAYAQNVAKLIKADPEGKVYYQQRLGNYQMQ			
a280	HDHDHDHEGHHHDHGEYDPHVWNPVLM	SAYAQNVAKLIKADPEGKVYYQQRLGNYQMQ				
	180	190	200	210	220	230
m280.pep	LKKLHSDAQA	AFNAVPAKRKVLTHGDAFSYMGKRYHIEFIAPQGSSEA	EPSAKQVAI			
a280	LKKLHSDAQA	AFNAVPAKRKVLTHGDAFSYMGKRYHIEFIAPQGSSEA	EPSAKQVAI			
	240	250	260	270	280	290
m280.pep	IRQIKREGIK	AVFTENIKDTRMVDRIKETGVNVSGLYS	DALGNAPADTYIGMYRHNK			
a280	IRQIKREGIK	AVFTENIKDTRMVDRIKETGVNVSGLYS	DALGNAPADTYIGMYRHNK			
	300					
m280.pep	ALTNAMKQX					
a280	ALTNAMKQX					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1157>:

g281.seq  
 1 atgcactacg ccctcgcatc cgtctctctgc ctgtccctca ggcgcgcacc  
 51 cgtcggcgta ttccctcgta tgcgcgcgtat gagcctgata ggcgacgcat  
 101 tgagccacgc cgtcctgccc ggtgccgcgc tcggctacat gtttgccggc  
 151 ttgagcctgc ccgctatggg tgtgggcggg tttgccgcgc gtatgctgat  
 201 ggcgctgctt gccggactcg tcagccgctt taccaccctg aaagaagatg  
 251 ccaactttgc cgccttttac ctgagcagcc tcgccatcgg cgtaatcctc  
 301 atcagcaaaa acggcagcag cgtcgattta ctccacctcc ttttcggatc  
 351 tgtgcttgcc gtcgatattc ccgcactgca actcatcgcc gccgtctccg  
 401 gcctcacgct cattaccctt gccgtcatct accgccccct ggtgctagaa  
 451 agcatagacc cccttttctt caagtccgct aacggcaaa gcggtctttg

```

501 gcacgtcatt ttcctcatcc tcgtcggtat gaacctcgta tccggcttcc
551 aagctctcgg catcctgatg tcggtcggaa ttatgatgct gcccgccatt
601 accgcccggt tatgggcaag aaatatgggg acgctcattc tgttgccgt
651 cctcatcgcc cttttttgcg gtttgatcgg gctgctcatt tcctaccaca
701 tcgaaatccc ttccggcccc gccatcatcc tctgttgag cgctctttat
751 cttttttccg tcatactcgg caaagaaggc ggcattctgc ccaaatggtt
801 caaaaaccac cgccaccaca ccacctga

```

This corresponds to the amino acid sequence <SEQ ID 1158; ORF 281.ng>:

g281.pep

```

1  MHYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51 LSLPAMGLGG FAAGMLMALL AGLVSRTTTL KEDANFAAFY LSSLAIGVIL
101 ISKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSGLTLITL AVIYRPLVLE
151 SIDPLFLKSV NGKGGWLWHVI FLVLVVMNLV SGFQALGILM SVGIMMLPAI
201 TARLWARNMG TLILLSVLIA LFCGLIGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILPKWFKNH RHHTT*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

m281.seq (partial)

```

1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCTCTGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCCC GGTGCCGCGG TCGGCTACAT GTTTGCCGGC
151 TTGAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGAG GCATGCTGAT
201 GGCAGTCTT GCCCGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG CGTAGTCCTC
301 GTCAGCAAAA ACGGGAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 TGTACTTGCC GTCGATATTC CTGCCCTGCA GCTCATCGCC GCCGTCTCCA
401 GCCTCACGCT CATTACCCTT GCCGTACATC ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCCGTC GCGGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TCATGATGCT GCCAGCCATT
601 ACCGCCCCGC TGTGGGCGAA GCATATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCGGTCCC GCCATCATCC TCTGTTGCAG CGTCTTTTAT
751 CTCCTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CC..

```

This corresponds to the amino acid sequence <SEQ ID 1160; ORF 281>:

m281.pep (partial)

```

1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51 LSLPAMGLGG VAAGMLMALL AGLVSRTTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSSLTLITL AVIYRPLVLE
151 SIDPLFLKSV GGKGGWLWHVL FLVLVVMNLV SGFQALGILM SVGLMMLPAI
201 TARLWAKHMG ALILSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILT..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

m281/g281

```

          10      20      30      40      50      60
m281.pep  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGLGG
          |:|||||
g281      MHYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPAAVGYMFAGLSLPAMGLGG
          10      20      30      40      50      60

          70      80      90     100     110     120
m281.pep  VAAGMLMALLAGLVSRTTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
          |||
g281      FAAGMLMALLAGLVSRTTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA
          70      80      90     100     110     120

          130     140     150     160     170     180
m281.pep  VDIPALQLIAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGWLWHVLFLVLVVMNLV

```



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```

g281      |||||:|||||:|||||:|||||:|||||:|||||:
          VDIPALQLIAAVSGLTLITLAVIYRPLVLESIDPLFLKSVNGKGLWHVIFLILVVMNLV
          130      140      150      160      170      180

          190      200      210      220      230      240
m281.pep  SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTAALLCGLSGLLISYHIEIPSGP
          |||||:|||||:|||||:|||||:|||||:|||||:
g281      SGFQALGILMSVGIMMLPAITARLWARNMGTLLLSVLIALFCGLIGLLISYHIEIPSGP
          190      200      210      220      230      240

          250      260
m281.pep  AIILCCSVLYLFSVILGKEGGILT
          |||||:|||||:|||||:|||||:
g281      AIILCCSVLYLFSVILGKEGGILPKWFKNHRHHTTX
          250      260      270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1161>:

```

a281.seq
1  ATGCGCTACG CCCTCGCATC CGTCTTCTGC CTGTCCCTCA GTGCCGCACC
51  CGTCGGCGTA TTCCTCGTCA TGCGCCGTAT GAGCCTGATA GGCGACGCAT
101 TGAGCCACGC CGTCTGCCC GGTGCCGCCG TCGGCTACAT GTTTGCCGGC
151 TTAAGCCTGC CCGCCATGGG TTTGGGCGGC GTAGCCGCAG GTATGCTGAT
201 GGCACTGCTT GCCGGACTCG TCAGCCGCTT CACCACCCTG AAAGAAGATG
251 CCAACTTTGC CGCCTTTTAT CTCAGCAGCC TCGCCATCGG TGTAGTCCTC
301 GTCAGCAAAA ACGGCAGCAG CGTCGATTG CTCCACCTCC TTTTCGGCTC
351 CGTACTTGCC GTCGATATTC CTGCCCTGCA ACTCATCGCC GCCGTATCCA
401 CCCTCACACT GCTTACCCTT GCCGTCATCT ACCGCCCGCT CGTACTCGAA
451 AGCATCGACC CCCTGTTTCT CAAATCTGTC GGCGGCAAAG GCGGGCTTTG
501 GCACGTCCTC TTTCTCGTCC TGGTCGTCAT GAACCTCGTA TCCGGCTTTC
551 AAGCCCTCGG CACACTCATG TCCGTCGGAC TTATGATGCT GCCAGCCATT
601 ACCGCCCGCC TATGGGCGAA GCACATGGGC GCACTCATCC TCCTATCCGT
651 TCTGACAGCC CTGCTGTGCG GCTTGAGCGG ACTGCTCATT TCCTACCACA
701 TCGAAATTCC TTCCGGTCCC GCCATCATCC TCTGTTGCAG CGTCCTTTAT
751 TCCTTTTCCG TCATACTCGG CAAAGAAGGC GGCATTCTGA CCAAATGGCT
801 CAAAACCAC CGCCACCACA CCACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1162; ORF 281.a>:

```

a281.pep
1  MRYALASVFC LSLSAAPVGV FLVMRRMSLI GDALSHAVLP GAAVGYMFAG
51  LSLPAMGLGG VAAGMLMALL AGLVSRFTTL KEDANFAAFY LSSLAIGVVL
101 VSKNGSSVDL LHLLFGSVLA VDIPALQLIA AVSTLTLLTL AVIYRPLVLE
151 SIDPLFLKSV GKGGLWHVL FLVLVVMNLV SGFQALGTLM SVGLMMLPAI
201 TARLWAKHMG ALILLSVLTA LLCGLSGLLI SYHIEIPSGP AIILCCSVLY
251 LFSVILGKEG GILTKWLKNH RHHTT*

```

m281/a281 99.2% identity in 264 aa overlap

```

          10      20      30      40      50      60
m281.pep  MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAGVGYMFAGLSLPAMGLGG
          |||||:|||||:|||||:|||||:|||||:|||||:
a281      MRYALASVFCLSLSAAPVGVFLVMRRMSLIGDALSHAVLPGAAGVGYMFAGLSLPAMGLGG
          10      20      30      40      50      60

          70      80      90      100     110     120
m281.pep  VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
          |||||:|||||:|||||:|||||:|||||:|||||:
a281      VAAGMLMALLAGLVSRFTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA
          70      80      90      100     110     120

          130     140     150     160     170     180
m281.pep  VDIPALQLIAAVSSLTTLITLAVIYRPLVLESIDPLFLKSVGGKGLWHVFLVLVVMNLV
          |||||:|||||:|||||:|||||:|||||:|||||:
a281      VDIPALQLIAAVSTLTLLTLAVIYRPLVLESIDPLFLKSVGGKGLWHVFLVLVVMNLV
          130     140     150     160     170     180

```

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	190	200	210	220	230	240
m281.p	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.p	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttgggtgct
51  gatcaatccg tttagcgcgt tgtcgcttta ccttgacctg accaacggac
101 a cagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 t ttgccgtga ttgcggtatt tgcgctgac ggcggtgcgc tattgaaggt
201 t ttgggcatc agcgtcgggt cgttcagggt cggcgccggg attttgggtgc
251 t gctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 a atctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 a ggggcgatt gccgtcgtgc ccatcgccat accgatcacc atcgggtccgg
401 g cgggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 g atatcgcgc tgattatcgc ggccgggttg gtggtcagtg cgatttggtta
501 t gccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 g gctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 g tggagatta ttgtgtcggg actgaaaacg atattccgc aactggcagg
651 t tga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALVLINP FSALSLYLDL TNGHSTKERR KVARTAATAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMLAAYS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAT CCGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGT CGTTTCAGGT CCGCGCGCGG ATTTTGGTGC
251 TGCTGATCGC CATTTTCATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CCGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGCGCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTGGG ACTGAAAACG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSLYLDL TNGHSTKERR KVARTAATAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLI GATGLTILNR IMGMMLAAYS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	:					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	:					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	:					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRLI					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

1	ATGGGATTGG	GCATGGAAAT	CGGCAAGCTG	ATTGTGGCTT	TTTTGGTGCT
51	GATTAAATCCG	TTTAGCGCGT	TGTCGCTTTA	CCTTGACCTG	ACCAACGGGC
101	ACAGCACGAA	GGAGCGCAGG	AAGGTCGCGC	GGACGGCCGC	CGTTGCCGTG
151	TTTGCCGTGA	TTGCGGTATT	TGCGCTGATC	GGCGGTACGC	TGCTGAAGGT
201	TTTGGGCATC	AGCGTCGGTT	CGTTTCAGGT	CGGCGCGGGA	ATTTTGGTGT
251	TGCTGATTGC	CATTTTCGATG	ATGAACGGCA	ACGACAATCC	CGCCAAGCAG
301	AATCTCGCGG	CGCAGCCGGA	AACGGGGCAG	GTGCGCCCCG	CCCGCAATGC
351	CGGAGCGATT	GCCGTCGTGC	CCATCGCCAT	ACCGATCACC	ATCGGCCCGG
401	GCGGTATTTT	GACCGTGATT	ATTTACGCTT	CGGCGGCTAA	AACATACGGC
451	GACATCGCGT	TGATTATCGC	GGCCGGTTTG	GTGGTCAGTG	CGATTTGTTA
501	TGCCATTTTA	ATCGTTGCCG	GGAAGGTCAG	CCGCCTGCTG	GGTGCGACGG
551	GGCTGACGAT	TTTAAACCGT	ATCATGGGTA	TGATGCTGGC	GGCGGTATCG
601	GTGGAGATTA	TTGTGTCGGG	ACTGAAAATG	ATATTCCTCG	AACTGGCAGG
651	TTGA				

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

1	MGLGMEIGKL	IVAFVLINP	FSALSPLYLDL	TNGHSTKERR	KVARTAAVAV
51	FAVIAVFALI	GGTLLKVLGI	SVGSFQVGGG	ILVLLIAISM	MNGNDNPAKQ
101	NLGAQPETGQ	VRPARNAGAI	AVVPIAIPIT	IGPGGISTVI	IYASAAKTYG
151	DIALIIAAGL	VVSAICYAIL	IVAGKVSRLI	GATGLTILNR	IMGMLAAVS
201	VEIIVSGLKM	IFPQLAG*			

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARFARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282.pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

g283.seq

1	atgaactttg	ctttatccgt	catcacattt	accctcgcct	ctttcctgcc
51	cgtcccgccct	gccggaaccg	ccgtctttac	ttggaaagac	ggcggcgcca
101	acagctattc	ggatgtgccg	aaacagcttc	atcccgacca	gagccaaatc
151	ctcaacctgc	ggacgctcca	aaccaaacccg	gcggtcaagc	ccaaacctgc
201	cgtcgatacg	aatgcggaca	gtgcgaagga	aaacgaaaag	gatatcgccg
251	agaaaaacgg	gcagcttgag	gaagaaaaga	aaaaaattgc	cgaaaccgaa
301	cggcagaaca	aagaagaaaa	ctgccggatt	tcaaaaatga	acctgaaggc
351	ggtgggaaac	tcaaatgcga	aaaacaagga	tgatttgatc	cgtaaataca
401	ataacgccgt	aaacaaatac	tgccgttaa		

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

g283.pep

1	MNFALSVITF	TLASFLPVPP	AGTAVFTWKD	GGGNSYSVDP	KQLHPDQSQI
51	LNLRTLQTKP	AVKPKPAVDT	NADSAKENEK	DIAEKNGQLE	EEKKKIAETE
101	RQNKEENCRI	SKMNLKAVGN	SNAKNKDDLI	RKYNNVAVNKY	CR*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

m283.seq

1	ATGAACCTTG	CTTTATCCGT	CATTATGTTG	ACCCTCGCCT	CTTTCCTGCC
51	CGTCCCGCCT	GCCGGAGCCG	CCGTCTTTAC	TTGGAAGGAC	GGCGGCGGCA
101	ACAGCTATTC	GGATGTACCG	AAACAGCTTC	ATCCCGACCA	AAGCCAAATC
151	TTAAACCTGC	GGACGCGCCA	AACCAAACCG	GCGGTCAAAC	CCGCCCAAGC
201	CGACGCAGGG	AAGCGCACAG	ACGGCGCGGC	ACAGGAAAAC	AATCCCGACA
251	CTGCCGAGAA	AAACCGGCAG	CTTGAGGAAG	AAAAGAAAAG	AATTGCCGAA
301	ACCGAACGGC	AGAACAAAGA	AGAAACTGTC	CGGATTTCAA	AAATGAACCT
351	GAAGGCGGTG	GGAAATTCAA	ATGCAAAAAA	CAAGGATGAT	TTGATTCGGA
401	AATACAATAA	CGCCGTAAAC	AAATACTGCC	GTAA	

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

m283.pep

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGNSYSVDP	KQLHPDQSQI
51	LNLRTROTKE	AVKPAQADAG	KRTDGAAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKEENC	RISKMNLKAV	GNSNAKNKDD	LIRKYNNVAVN	KYCR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRTLQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSVDPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

```

              70      80      90      100      110      120
m283.pep    AVKPAQADAGKRTDGAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV
            |||| | : | :|:|: | ||| |||||:|||||:|||||:|||||:|||||
g283        AVKPKPA-VDTNAD-SAKENEKDIAEKNQGLEEEKKKIAETERQNKEENCRI SKMNLKAV
              70      80      90      100      110

              130      140
m283.pep    GNSNAKNKDDLIRKYNNAVNKYCRX
            |||||:|||||:|||||:|||||:|||||
g283        GNSNAKNKDDLIRKYNNAVNKYCRX
            120      130      140

```

a283.seq

1	ATGAAC	TTTG	CTTTAT	CCGT	CATTAT	GTGTG	ACCTC	GC	CCCT	CTTTC	CTGCC
51	CGTCCC	GCCT	GCCGG	AGCCG	CCGTCT	TTTAC	TTGGA	AGGAC	GGCG	CGCG	GCA
101	ACAGCT	ATTCC	GGATGT	ATCCG	AAACAG	CTTC	ATCCG	ACCA	AAGCC	AAATC	
151	TTAAAC	CTGC	GGACG	CGCCA	AACCAA	AACCG	GCGGT	CAAAC	CCGCC	CAAGC	
201	CGACGC	AGGG	AAGCG	CACAG	ACGGC	CGGC	ACAGG	AAAAC	AATCC	CGACA	
251	CTGCC	GAGAA	AAACCG	GCAG	CTTGAG	GGAAG	AAAAG	AAAAG	AATTG	CCGAA	
301	ACCGA	ACGGC	AGAAA	CAAGA	AGAAA	ACTGC	CGGAT	TTCAA	AAATG	AACTT	
351	GAAAG	CGGTG	GGAAAT	CTCAA	ATGCA	AAAAA	CAAGG	ATGAT	TTGAT	TCCGA	
401	AATACA	ATAAA	CGCCG	TAAAC	AAATA	CTGCC	GTTAA				

a283.pap

1	<u>MNFALSVIML</u>	<u>TLASFLPVPP</u>	<u>AGAAVFTWKD</u>	<u>GGGNSYSQVP</u>	<u>KQLHPDQSQI</u>
51	<u>LNLRTQTKP</u>	<u>AVKPAQADAG</u>	<u>KRTDGAQEN</u>	<u>NPDTAEKNRQ</u>	<u>LEEEKKRIAE</u>
101	<u>TERONKEENC</u>	<u>RISKMLKAV</u>	<u>GNSAKNKDD</u>	<u>LIRKYNNAVN</u>	<u>KYCR*</u>

	10	20	30	40	50	60
m283.pep	MNFALSVMILTLASFLPVPPAGAAVFTWKDGGGNSYS DVPKQLHPDQSQILNLRTRQTKP					
a283	MNFALSVMILTLASFLPVPPAGAAVFTWKDGGGNSYS DVPKQLHPDQSQILNLRTRQTKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
a283	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
	70	80	90	100	110	120
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
a283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	130	140				

g284.seq.

1	atgccgtctg	aaactcgaaa	tcggtttcag	acggcattgg	tttacgcggc
51	aggttggggc	ttagcgggtc	ttgtaacggc	attcgccttt	gcctgcaaaa
101	gagtcgcggc	cttttcggtt	gcctttgaag	ccttcgcggc	tttttttgaa
151	actgtctttc	ttaaagcctt	ctttcttgaa	accctgcgcg	cgcgttttgc
201	cgccgaagcc	ttctttgcc	ggtttatgat	cgccgcgcgc	gccgccggat
251	ttctatcgc	cccagccgc	ttgccttct	ggcttgcgc	ctgcggattt
301	gcgtttgcgc	gccggctcca	tgccctcgat	ggtcagttcg	ggcagtttgc
351	ggttaatgta	tttttcgatt	ttgtggactt	tgacgtattc	gttcaactcg
401	gcaaacgtaa	tgcgaatacc	cgtgcggcct	gcgcgcgcgc	tcgcgccgat
451	cgcggtgcag	tagtcttcgc	ctgttttcgc	caggtcgtag	tttatgacgt

645

```

501 gggtaatggt cggtagctca ataccgcgtg cggcaacgtc ggtggcaacc
551 aaaattttgc agcggccttt acgcaaattc gtcagcgtgc ggttgcccca
601 gccctgcggc atatcgccgt gcaggcagtt ggcgcgaaa cctttttcgt
651 acaattcatc cgcgatgact tcggtcatcg ctttgggga cgtgaaaatc
701 acacattggt cgatgttggc atcgcgcagg atgtgtcga gcaggcgtt
751 tttgtggcgc atatcgtcgc agtacaacaa ctgctcttcg attttgcctt
801 ggccgtccac gcgttcgact tcgataattt cagagtcttt ggtcagtttg
851 cgcgccagtt tgccgactgc gccgtcccaa gtggcgaga acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

g284.pep

```

1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRVAGFAF AFEAFAGFFE
51 TVFLKAFFLE TFAARFAAEA FFARFMIAAP AAGFPIAPAA FAFRLAACGF
101 AFAGRLHAFD QQFGQFAVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDVVGNG RYVNTACGNV GGNQNEFAAF TQIRQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHREFG RENHTLVDPV IAQDVVEQAV
251 FVAHIVAVQQ LFFDFALAVH AFDFDNFRVF GQFARQFADC AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

m284.seq..

```

1 ATGCCGCTCTG AAACGCGGAA TCAGTTTCAG ACGGCATTGG TTTATGCGGC
51 AGGTTGGGGC TTAGCGGTCT TTGTAACGGC GTTCGCCTTT GCCTGCAAAA
101 GAATCGCCGG CTTTGCGTTT GCCTTTGAAG CCTTCGCCGG TTTTTTTGAA
151 ACCGTCTCTC TTAAAGCCTT CTTCCTTGAA ACCTTCGCCG CGCGTTTTCG
201 CGCCGAAGCC TTCTTTGCTC GGTATATGAT CGCCGCGCCA ACCGCGGGAT
251 TTACGATCGC CCCAGCCGCC TTGCTCTTCG GGCTTGCCGC CTGCGGATT
301 GCGTTTGGCG GTCGGTTCCA TGCCTTCGAT GGTCACTTCG GGCAGTTTTC
351 GGTTAATGTA TTTTTCGATT TTGTGGACTT TGACGTATTC GTTCACTTCG
401 GCAAACGTAA TCGCAATACC CGTGCGGCCCT GCGCGGCCGG TCGCGCCGAT
451 GCGGTGGACG TAGTCTCCG CCTGTTTCGG CAGGTCGTAG TTGATAACGT
501 GGTAAATGGT CGGTACGTCTG ATACCGCGTG CGGCAACATC GGTGGCAACC
551 AAAATTTTGC AGCGGCCTTT ACGCAAATCC ATCAGCGTGC GGTGCGGCA
601 GCCTTGCGGC ATATCGCCGT GCAGGCAGTT TGCGCGGAAA CCTTTTTCGT
651 ACAGTTCATC CGCAATGACT TCGGTATGCG CTTTGGTGGA CGTGAAATC
701 ACGCATTGAT CGATATTGGC ATCGCGCAAG ATATGATCGA GCAGGCGGTT
751 TTTGTGGCGC ATATCGTCGC AGTACAGCAG TTGTCTTCG ATTTTGCCTT
801 GATCGTCCAC GCGTTCGACT TCGATGATT CAGGGTCTTT GGTCACTTTC
851 CGCGCCAGTT TGCCGACCGC GCGTCCCAA GTGGCGGAGA ACAACAAAGT
901 CTGACGGTCG CTCGCGGTTG CTTCACGAT GGTTCGATG TCGTCGATAA
951 AGCCCATATC CAACATACGG TCGGCTTCGT CCAAATCAG CACTTCCAA
1001 CGTTCAAAAT CAACTTTGCC GCTTGCATC AGGTCCATCA GACGGCCGG
1051 CGTGGCGACA ATCAGATCGA CCGTTTGTCT CAGGGCACGG GTTTGGTAGC
1101 CGAAAGACGC GCCGCGGACG ATGCTGACGG TGCGGAACCA ACGCATATTT
1151 TTGCATACG CCAGCGCGTT TTTCTCGACT TGAGCGGCA GTTCGCGGTT
1201 CGGGGTCAAC ACCAAAGCAC GCGGGCCTTT GCCCGGTTTT TCGTGCCTT
1251 TGTCAGTTT TTGCAAGTC GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

m284.pep

```

1 MPSETRNRFO TALVYAAGWG LAVFVTAFAF ACKRIAGFAF AFEAFAGFFE
51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFHAFD QQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNI GGNQNEFAAF TQIHQRAVAP
201 ALRHIAVQAV CGETFFVQFI RNDFGHGFEG RENHALIDIG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALIVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVARRCFHD GFDVVDKAHI QHTVGFVQNG HFQTFKINFA ALHQVHQTAR
351 RGDNQIDRFA QGTGLVAERR AADDADGAEP THIFGIRQV FLDLSRQFAG
401 RGQHQSTRAF ARFFAAGQF LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284 . pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284 . pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDQGQFQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAAGFPIAPAAFAFRLAACGFAFAGRLHAFDQGQFQFVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284 . pep	FFDFVDFDVFVHFGKRNTRACAAAGAPDAVDVVFRLFRQVVVDVNGRNVDTACGNI					
g284	FFDFVDFDVFVHFGKRNTRACAAAGAPDAVDVVFRLFRQVVVDVNGRNVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284 . pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNFAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGRHFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284 . pep	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLDFALAVHAFDFDNFRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284 . pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFAALHQVHQTARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284 . seq
1  ATGCCGCTCTG  AAACTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCGG  CTTTGCGTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTTTTGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201 CGCCGAAGCC  TTCTTTGCTC  GGTTCATGAT  CGCCGCGCCA  ACCGCCGGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 CGGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCACTTCG  GGCAGTTTTC
351 GGTAAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TGCGCCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GGCGCGGAAA  CCTTTTTCGT
651 ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAATC
701 ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCTTT
801 GGTCTGTCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCACTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCT  TCCGGCGTGG  CTTTCGACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001 CGGGCGAAAT  CGACTTTGCC  GCTTTCATC  AAGTCCATCA  GACGGCCCGG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTGGTAGC
1101 CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151 TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201 CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCCCGGTTTT  TCGCTGCGTT
1251 TGGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284 . pep
1  MPSETRNRFT  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

```

```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGREHAFD QQFGQFSVNV FFDFVDFDVF VHFGRNRNT RAACAAGAPD
151 AVDVVFLFR QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNG HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

	10	20	30	40	50	60
m284.pep	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	MPSETRNRFTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDQFGQFSVNV					
a284	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAFAGRFHAFDQFGQFSVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRYVDTACGNI					
a284	FFDFVDFDVFVHFGRNRNTRAACAAGAPDAVDVVFRLFRQVVVDNVGNRYVDTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNFAAFTQIHQRAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGGFGGRENHALIDIG					
a284	GGNQNFAAFAQIHQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHGGFGGRENHALIDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLFFDFALVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
a284	IAQDMIEQAVFVAHIVAVQQLFFDFALVHAFDFFDFRVFGQFARQFADRAVPSGGEQQS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNGHFQTFKINFALHQVHQTARRGDNQIDRFA					
a284	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNGHFQAGEIDFAALHQVHQTARRGDNQIDRFA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m284.pep	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSTRAFARFFAAGQF					
a284	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRRARAFARFFAAGQS					
	370	380	390	400	410	420
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1 atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51 caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat ttggcagta

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151 tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gtttcgggct
201 gtaccaaact ccgtcctggt tcggcgtaaa catttcctcc caaaacctca
251 aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301 gagggggagc accttaaaat cagccgcttc cgcttcgctg ggaaaccgtc
351 cgaactgatg cgccgcagcc tgcacatcac cgacatctcc gccggcgaca
401 tcgccatcgt aaccaaaccg actccgccta aagaagaacg cccgcctcaa
451 ggccctgccg acagcataga cctgcccggc gctgtctatc tcgaccgctt
501 cgagacgggc aaaatcagca tgggcaaaac ctttgacaaa caaaccgtct
551 atctcgaaac cctcaacgcg gcataaccgtt acgaccgtaa agggcaccgc
601 ctcgacctga aggcggccga cagcccggtg agcagttcgt cggggtcagc
651 gtgccttcgc ttgaaaaaac cgtttgcctt cgataccgcc atttacacca
701 aaggcggtat cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751 agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801 cctctcggga aaatccgtca tccaccggtt tgcggaatca ttggataaaa
851 cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901 gtgccttccc tgcgcgatgc cgggctgaat ttcgacctga ccgccatccc
951 gtcgttttca gacggcatcg cgctggaagg ctcgctcgat ttggaaaaa
1001 ccaaagccgg ctttgccgac cgcaacggca tccccgtccg tcaggttttg
1051 ggcggctttg tcctccggca ggacggcagc gtgcataatc gcaatacgtc
1101 cgccgccttg ctcggacggg gcggcatcag gctgtcgggc aaaatcgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacgcg gttcaaaggc aggttgagcg gcagcatcgg
1251 catcggcggc acgaccgcct cgcccaaaat ctcttggaac ctcggcaccg
1301 gcacggcagc cagggacggc agcctcccca tcgcaagcga ccccgcaaac
1351 gaacagcgga aactggtggt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgctca
1451 agctggacat ccgttccgcg gcattcgacc cttcgcgcac cgatccgcaa
1501 ttccggcagc gcaatatcaa cggttcgatt catcttgccg gtgaactggc
1551 aaaagagaaa tttacgggca aaatgcgttt tttgcccgtt acgttcaacg
1601 gcgtgccgat tgcgggcagc gccgacattg tttacgagtc ccgccacctt
1651 ccgcgcggcg ccgtcgattt gcggttgggg cggaacatcg tcaaaacaga
1701 cggcggttcc ggcaaaaaag gcgaccggct taacctcaat atcaccgcac
1751 ccgatttatc ccgtttcggg ttcggactcg cggggtcttt aaatgtacgc
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
1851 ctttccggc acggcgcgca acttacacat cggaacagcg gcagacatcc
1901 gttcgctcga ttttaccctc aaaggctcac ccggcacaag ccgccgatg
1951 cgcgccgata tcaaggcgcg ccgcctttcc ctgtcgggcg gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcaccgca
2051 tccgcacaca cgccgccatg acgctggacg gcaaaccgtt caaactcgat
2101 ttggacgctt caggcgcat caacaggga cttaccgat ggaaaggcag
2151 catcggcatc ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tgcggcaaat
2251 tggcaggcaa tggcgcgag cctcaaccct caacactttt cttgggacag
2301 gaaaaccggc atatcggcaa aaggcgcgcg acggcgctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgcccttcg aacacaatct ggttttaaac
2401 ggcgactggg atgtcgctta cgggcacaac gcgcggcggt acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttcctgaaa acgcgcttcc aaaaacgacc catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcgacgg attaacgcg atttgggcat
2601 cggcaacgcc ttcggcggca atatggcaaa tacaccgctc ggcggcagga
2651 ttacagcctc ccttcccgac ttggcgcat tgaagccctt tctgcccgc
2701 gccgcgcaaa acattaccgg cagcctgaat gcctccgcgc aaatcggcg
2751 acgggtaggc tctccgtccg tcaatgccgc cgtcaacggt agcagcaact
2801 acgggaaaat caacggcaat atcaccgtcg ggcaagccg ctcttcgat
2851 accgcacctt tggcgcgag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaggc agcctgaatg
2951 ccgcgtaac cctcggcggc agcatcgccg acccgcaatt gggcggcagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatactctt
3051 ggacaacggc tcgtgcgtt cgcataattg aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaagggacgg cggaactctc cggcacggtc
3151 agcatggaaa acagcgtgcc cgtgtcgat atcggcgcgg tgttcgacaa
3201 ataccgcac ctgtcccgc ccaaccgcg cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc aggggctggt cggttcgcaa aaatcctcga tgcctccgt
3351 cggcgacgat gtcgtcgat tggcggaagt caagaaagag gcggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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3451 ttctccggt acggcgcgga cgttaccata ggccggcaaac tgaccctgac
3501 cgcgcaaccg ggccggaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aaggcggtta caaagcatat gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgcga
3651 acgcccgtt tccccgtcg gtgcggcggt ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgcca gcagcgcgga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctgggt gatgatttgg gctttaccag caagcgcgag
3901 cgcaacggcg aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 aagcggttg cccgtatcgg cagccgttcg tcggcgcgcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

g285.pep

```

1 MTDTTPTD TD PTENGTRKMP SEHRPAPPAK KRRPLLKLSA ALLSVLILAV
51 CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSLEL RRS LHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLD RFETG KISMGKTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHFFAES LDKTLEEV LV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLSD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGRTARDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTDGGF GKKGDRLNLN ITAPDL SRFG FGLAGSLNVR
601 GHLSDGLDGG IRTFETDL SG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGA AVVD T AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGS LNL QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFEHNLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNTIGSLN ASAQIGGRVG SPSVNA AVNG SSNYGKINGN ITVGQSR SFD
951 TAPLGRLNL TVADAEAFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 SMENSVPD VD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMP SVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GSKLTTLTAQP GGNVRGVGT V RVIKGRYKAY GQDL DITKGT
1201 VSVFGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEP MSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSR S SGGELTYTIR FDRLFSGDKK DSAGNGK GK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

m285.seq

```

1 ATGACCGATA CCGCACC GAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51 CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCCTGAT TTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGGT TCGCGGTAAA CATTTCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGGCT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCC GCCGGCGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCCGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGACCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCGCA CACGCCGTGG AGCAGTTCGT CGGGGGCGGC
651 CTCGGTCCGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGCGGGA CTGAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

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801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA  
 851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC  
 901 GTGCCTTCCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC  
 951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAAACA  
 1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCG TCAGGTTTTA  
 1051 GGCGGCTTTG TCATCCGGCA GGACGGCAGC GTGCATATCG GCAATACGTC  
 1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA  
 1151 CCGAAAAAGA CATCTCGAT TTAATATAG GCATCAACTC CGTCGGCCGG  
 1201 GAAGACGTAC TGCAAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG  
 1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCGAA CTCGGCATCG  
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC  
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG  
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA  
 1451 AGCTGGACAT CCGTTCCCGC GCATTTCGACC CTTCCGCGAT CGATCCGCAA  
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
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 1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT  
 1651 CCGCGTGCCG CCGTCGATT TCGGCTGGGG CGGAACATTA TTAACACAGA  
 1701 CGGCGGCTTC GGCAAAAAG GCGACCGGCT TAACCTCAAT ATCACCGCAC  
 1751 CCGATTATAT CCGTTTCGGT TTCGGAATCG CGGGGTCTTT AAATGTACGC  
 1801 GGACACCTTT CCGGTGATT GGACGGCGGC ATCCGAACCT TTGAAACCGA  
 1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
 1901 GTTCGCTCGA TTTCACGCTC AAAGGTTTCG CCGACACAAG CCGCCCGATA  
 1951 CGCGCCGACA TCAAGGCGAG CCGCCTTCG CTGTCGGGCG GAGCGGCGGT  
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 2051 TCCGCACACA CGCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT  
 2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAGGCGAG  
 2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC  
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 2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG  
 2351 AGTTGCACAA TTTCTTCAA CCGCCCTTCG AACACAATCT GGTTTTAAAC  
 2401 GGCGACTGGG ATGTGCGCTA CGGGCGCAAC GCGCGCGGCT ACCTCAATAT  
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 2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC  
 2551 CTGCTTGACG GCGGCGCGCG TTTCCGGGCG ATTAACGCCG ATTTGGGCAT  
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 2651 TTACCGCCTC CTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC  
 2701 GCCGCGCAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG  
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 2801 ACGGGAATA CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT  
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 2901 ATTCCGCAAC TTCCTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG  
 2951 CCGCCGTAA CCGCGGCGG AGCATCGCCG ATCCGCACTT GGGCGGCAGC  
 3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
 3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG  
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 3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTTCGACAA  
 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCGTACGGTT TCCGGCAACA  
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 3301 AAAACGGATC AGGGGCTGTT CGGTTCCGAA AAATCCTCGA TGCCGTCCGT  
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 3401 CGTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCG  
 3451 TTCGCCGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCCTGAC  
 3501 CGCCCAATCG GCGGAAGCG TACGGGGCGT GGGCACGGTC CGCGTCATCA  
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG  
 3601 GTCTCCTTTG TCGGCCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA  
 3651 ACGCCGCTT TCCCGGCTCG GTGCGGGCGT GGAATATTG GGCAGCTCA  
 3701 ACAGCCCGCG CATTACGCTG ACGGCAACG AACCGATGAG TGAAGGAGAC  
 3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA  
 3801 CAATGCGGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA  
 3851 ACGACCGCAT CCGGCTGGTG GATGATTGTT GCTTTACCAG CAAGCGCAGC  
 3901 CGCAACGCGC AAACCGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT  
 3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT  
 4001 CCAGCGCGGA ACAGTCCGTC AAATGATTG ACCGGCTGAC CCGCGCCATA  
 4051 CAGGCGGTTG CCGGTATCGG CAGCCGTTTCG TCGGGCGGCG AGCTGACATA

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG  
4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

m285.pep  
1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV  
51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET  
101 EGADLKISRF RFAWKPSSELM RRLSHITEIS AGDIAIVTKP TPPKEERPPL  
151 SLPDSIDLPA AVYLDREFETG KISMCKAFDK QTVYLERLDA SYRYDRKGHR  
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF  
301 VPSLPDAGLN FDLTAIPSF S DGIALEGLD LENTKAGFAD RNGIPVRQVL  
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
451 GQRKLVLDTV NIAAGQSSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ  
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL  
551 PRAAVDLRLG RNIKTGSGF GKKGDRNLNL ITAPDLSRFG FGLAGSLNVR  
601 GHLSGDLGG IRTFETDLG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI  
651 RADIKGSRLS LSGGAADVDT ADMLDGTGV QHRIRTHAAM TLDGKPFKFD  
701 LDASGGINRE LTRWKSIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN  
751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENHLVLN  
801 GDWDVAYGRN ARGYLNISQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI  
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRTASLPD LGALKPFPLPA  
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYKINGN ITVGQSRSD  
951 TAPLGRLNL TVADAVERFN FLPGQTVKG SLNAAVTLGG SIADPHLGG  
1001 INGDKLYRN QTGGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV  
1051 GMENSGPDVD IGAVFDKYRI LSRPNRLTV SGNTRLRYSP QKGISVTGMI  
1101 KTDQGLFGSQ KSSMPVSGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR  
1151 FAGYGADVTI GSKLTTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT  
1201 VSFVGLNDP NLNIRAERL SPVGAGVEIL GSLNSPRITL TANEPMSKD  
1251 KSLWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS  
1301 RNAQTGELNP AEQVLTGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI  
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDDK DSAGNGKKG\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m285/g285 96.5% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	:     :     :     :     :					
g285	MTDTTPTDPTENGTRKMPSEHRPAPPKRRPLLKLSAALLSVLILAVCFLGWIAGE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m285.pep	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRAWKPSSELM					
	:     :     :     :     :					
g285	AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDNWSIETEGADLKISRFRAWKPSSELM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m285.pep	RRLSHITEISAGDIAIVTKPTPPKEERPPPLSLPDSIDLPAAVYLDREFETGKISMCKAFDK					
	:     :     :     :     :					
g285	RRLSHITDISAGDIAIVTKPTPPKEERPPQGLPDSIDLPAAVYLDREFETGKISMCKTFDK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
	:     :     :     :     :					
g285	QTVYLERLNAAYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE					
	190	200	210	220	230	240
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF					

652

|||||:|||||  
g285 TIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF  
250 260 270 280 290 300

310 320 330 340 350 360  
m285.pep VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT  
|||||  
g285 VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT  
310 320 330 340 350 360

370 380 390 400 410 420  
m285.pep VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTA FKGRLDGSIGIGG  
|||||  
g285 VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTA FKGRLDGSIGIGG  
370 380 390 400 410 420

430 440 450 460 470 480  
m285.pep TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD  
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g285 TTASPKISWQLGTGTARTDGS LPIASDPANEQRKLVFDTVNISAGEGS LTAQGYLELFKD  
430 440 450 460 470 480

490 500 510 520 530 540  
m285.pep RLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRF LPGTFNGVPIAGS  
|||||:|||||  
g285 RLLKLDIRSRAFDPSRIDPQFPAGNINGSIHLAGELAKEKFTGKMRF LPGTFNGVPIAGS  
490 500 510 520 530 540

550 560 570 580 590 600  
m285.pep ADIVYESRHLPRAAVDLRLGRNIIKT DGGFGKKGDRLN LNITAPDLSRFGFGLAGSLNVR  
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g285 ADIVYESRHLPRAAVDLRLGRNIVKT DGGFGKKGDRLN LNITAPDLSRFGFGLAGSLNVR  
550 560 570 580 590 600

610 620 630 640 650 660  
m285.pep GHLSGDL DGGIRTFETDLSGAARNLHIGKAADIRSLDFTLKGSPDTSRPIRADIKGSRLS  
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610 620 630 640 650 660

670 680 690 700 710 720  
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670 680 690 700 710 720

730 740 750 760 770 780  
m285.pep LDIGGAFLNKLQNRMTLEAGAERVAASAANWQAMGGSLNLQHFSWDKKTGISAKGGAGHL  
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730 740 750 760 770 780

790 800 810 820 830 840  
m285.pep HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK  
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g285 HIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYLNISRQSGDAVLPGGQALGLNAFSLK  
790 800 810 820 830 840

850 860 870 880 890 900  
m285.pep TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA  
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g285 TRFQNDRIGILLDGGARFGRINADLGIGNAFGGNMANTPLGGRITASLPDLGALKPFLPA  
850 860 870 880 890 900

910 920 930 940 950 960  
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a285.seq

1	ATGACCGATA	CCGCACCGAC	AGATACCGAT	CCGACCGAAA	ACGGCACGCG
51	CAAAATGCCG	TCTGAACACC	GCCCTACCCC	GCCGGCAAAA	AAACCGCGCC
101	CAGTGTGAA	GCTGTGGCG	GCACTGCTGT	CTGTCTGTAT	TTTGGCAGTA
151	TGTTTCCTCG	GCTGGCTCGC	CGGCACGGAA	CGGGGTTTGC	GCTTCGGGCT
201	GTACCAAATC	CCGTCTTGGT	TCGGCGTAAA	CATTTCTTCC	CAAACCTCA
251	AAGGCACGCT	GCTCGACGGC	TTCGACGGCG	ACAATCGGTC	GATAGAAACC
301	GAGGGGGCAG	ACCTTAAAT	CAGCCGCTTC	CGCTTCCGCT	GGAAACCGCT
351	CGAACTGATG	GCCCGCAGCC	TGCACATTAC	CGAAATTTCC	CGCCGGCGACA
401	TCGCCATCGT	TACCAAACCG	ACTCCGCCTA	AAGAAGAACG	CCCGCCGCTC
451	AGCCTTCCCG	ACAGCATAGA	CCTGCCTGCC	GCCGTCTATC	TCGACCGCTT
501	CGAGACGGCG	AAATCAGACA	TGGGCAAAGC	CTTTGACAAA	CAAACCGTCT
551	ATCTCGAACG	GCTGGATGCT	TCATACCGTT	ACGACGCGAA	AGGACACCGC
601	CTCGACCTGA	AGGCTGCCGA	CACGCCGTGG	AGCAGTTCGT	CGGGGTTCAGC

651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA  
 701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC  
 751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG  
 801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGATAAAAA  
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 901 GTGCCCTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC  
 951 GTCGTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA  
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 1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGCTGCGCGG  
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 1251 CATCGGTGGC ACGACCGCCT CGCCCAAAT CTCTTGCAA CTCGGCATCG  
 1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAACGGA CCCCAGAAC  
 1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG  
 1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCTGCTCA  
 1451 AGCTGGACAT CCGTTCCCGC GCATTGACC CTTCGCGCAT CGATCCGCAA  
 1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC  
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 1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC  
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 1851 CCTTTCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC  
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 1951 CGCGCCGACA TCAAAGGCAG CCGCCTTCG CTGTCGGGCG GAGCGGAGGT  
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 2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT  
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 2501 TGAACGCATT TTCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC  
 2551 CTGCTTGACG GCGGCGCGCG TTTCCGGGCG ATTAACGCGG ATTTGGACAT  
 2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA  
 2651 TTACCGCCTC CTTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC  
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 3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT  
 3051 GGACAACGGC TCCTGCGTTC CGCATATCGC GGGCAGGAAA TGGGTAATCG  
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 3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA  
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 3351 CGGCGACGAT GTCGTGCTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC  
 3401 CGTCCCGCT CAATATGAAC CTGACTTAG ACCTCAATGA CGGCATCCGC  
 3451 TCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCCTGAC  
 3501 CGCCCAATCG GCGGAAGCG TGCGGGCGGT GGGCACGGTC CGCGTCATCA  
 3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG  
 3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA  
 3651 ACGCGCCCTT TCCCCGTCG GTGCGGGCGT GGAAATATTG GGCAGCCTCA  
 3701 ACAGTCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGAAGGAGAC  
 3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAAGTGCA GCAGCGGCGA  
 3801 CAATGCCGCG CTGTCCGCG CCGCCGCGCG GCTGCTTGCC GGGCAAATCA  
 3851 ACGACCGCAT CCGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC  
 3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT



655

3951 CGGCAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT  
 4001 CCAGCGCGGA ACAGTCCGTC AAAGTGATT ACCGGCTGAC CCGCGCCATA  
 4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTTC TCGGGCGGCG AGCTGACATA  
 4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAAA GACTCCGCCG  
 4151 GAAACAGCAA AGGAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

a285.pep  
 1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV  
 51 CFLGWLAGE AGLRFGlyQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET  
 101 EGADLKISRF RFAWKPELM RRS LHTEIS AGDIAIVTKP TPPKEERPPL  
 151 SLPDSIDLPA AVYLD RFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR  
 201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG  
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEV LV KGFNINPSAF  
 301 VPSLPDAGLN FDLTAIPSF DGIALEGS LD LENTKAGFAD RRGIPVRQVL  
 351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA  
 401 EDVLQTAFCG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN  
 451 GQRKLVLDTV NIAAGQGS LT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ  
 501 LPAGNINGSI NLAGELAKE FTGKMRFLPG TFNGVPIAGS ADIVYESRHL  
 551 PRAAVDLRLG RNIKT DGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR  
 601 GHLSGDL DGG IRTFETDL SG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI  
 651 RADIKGSR LS GGAEVVD T ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD  
 701 LDASGGINRE LTRWKGSGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN  
 751 WQAMGGS LNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFEHNLVLN  
 801 GDWDVAYGRN ARGYLNI SRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI  
 851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLPA  
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSR SFD  
 951 TAPLGGRLNL TVADA EVFRN FLVPGQTVKG SLNAAVTLGG SIADPHLGGS  
 1001 INGDKLYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV  
 1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVSGMI  
 1101 KTDQGLFSGQ KSSMP SVGDD VVVLGEVKKE AAPLPVNMN LTLDLNDGIR  
 1151 FAGYGADVTI GGLTLTAQS GGSVRGVGT VIKGRYKAY GQDLDTKGT  
 1201 VSFVGPLNDP NLNIRAERL SPVGAGVEIL GSINSPRITL TANEP MSEKD  
 1251 KLSWLILNRA GSGSSGD NAA LSAAAGALLA GQINDRIGLV DDLGFTSKRS  
 1301 RNAQTGELNP AEQVLT V GKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI  
 1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSK GK\*

m285/a285 99.4% identity in 1389 aa overlap

	10	20	30	40	50	60
m285.pep	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
a285	MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE					
	10	20	30	40	50	60
m285.pep	AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPELM					
a285	AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPELM					
	70	80	90	100	110	120
m285.pep	AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPELM					
a285	AGLRFGlyQIPSWFGVNISSQNLKGTLLDGFDGDNWSIETEGADLKISRF RFAWKPELM					
	130	140	150	160	170	180
m285.pep	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLD RFETGKISMKGAFDK					
a285	RRSLHITEISAGDIAIVTKPTPPKEERPPLSLPDSIDLPAAVYLD RFETGKISMKGAFDK					
	190	200	210	220	230	240
m285.pep	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK					
a285	QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK					
	250	260	270	280	290	300
m285.pep	TIHSTARLSGSLKDVRAELIDGGNIRLSGKSVIHPFAESLDKTLEEV LVKGFNINPAAF					



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a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTL EEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGGFVIRQDGT
a285	VPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALLGRGGIRLSGKIDTEKDILDNLIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGS LAIASDPANGQRKLVLDTVNIAAGQGS LTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEFTGKMRFPGTFNGVPIAGS
a285	RLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGELAKEFTGKMRFPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLFRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR
a285	ADIVYESRHLFRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLDDGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGS PDSRPIRADIKGSRLS
a285	GHLSGDLDDGGIRTFFETDLSGAARNLHIGKAADIRSLDFTLKGS PDSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAHVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKGSIGI
a285	LSGGAHVVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGAENLKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
a285	LDIGGAENLKLQNRMTLEAGAERVAASAANWQAMGGS LNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLDIGNAFGGNMANAPLGGRITASLPDLGLTKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAAQIGGRVGS PSVNAAVNGSSNYKINGNITVGQSRSFDTAPLGGRNLN

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a285	AAQNITGSLNAAQIGGRVGS	PSVNA	AVNGSSNY	KINGNIT	VGQSR	SFDTAP	LGGRLNL
	910	920	930	940	950	960	
m285.pep	TVADA	EVFRN	FLPVG	QTVKGS	LNA	AVTLGGS	ADPHL
	970	980	990	1000	1010	1020	
a285	TVADA	EVFRN	FLPVG	QTVKGS	LNA	AVTLGGS	ADPHL
	970	980	990	1000	1010	1020	
m285.pep	SLRSH	IAGRK	WVIDSL	KFRHEG	TAELSG	TVGMEN	SGPDVD
	1030	1040	1050	1060	1070	1080	
a285	SLRSH	IAGRK	WVIDSL	KFRHEG	TAELSG	TVGMEN	SGPDVD
	1030	1040	1050	1060	1070	1080	
m285.pep	SGNTR	LRYS	PQKG	ISVTGM	IKTDQ	GLFGS	QKSSMP
	1090	1100	1110	1120	1130	1140	
a285	SGNTR	LRYS	PQKG	ISVTGM	IKTDQ	GLFGS	QKSSMP
	1090	1100	1110	1120	1130	1140	
m285.pep	LTLDL	NDGIR	FAGY	GADVT	IGGKLT	LT	TAQSGS
	1150	1160	1170	1180	1190	1200	
a285	LTLDL	NDGIR	FAGY	GADVT	IGGKLT	LT	TAQSGS
	1150	1160	1170	1180	1190	1200	
m285.pep	VSFVG	PLNDP	NLNIRA	ERRLSP	VGAGVE	ILGSLN	SPRITLT
	1210	1220	1230	1240	1250	1260	
a285	VSFVG	PLNDP	NLNIRA	ERRLSP	VGAGVE	ILGSLN	SPRITLT
	1210	1220	1230	1240	1250	1260	
m285.pep	GSGSS	GDNAAL	SAAAG	ALLAGQ	INDRIG	LVDL	LGFTSK
	1270	1280	1290	1300	1310	1320	
a285	GSGSS	GDNAAL	SAAAG	ALLAGQ	INDRIG	LVDL	LGFTSK
	1270	1280	1290	1300	1310	1320	
m285.pep	LTGKLY	IGYEYS	ISSAEQ	SVKLIY	RLTRAI	QAVARIG	SRSSG
	1330	1340	1350	1360	1370	1380	
a285	LTGKLY	IGYEYS	ISSAEQ	SVKLIY	RLTRAI	QAVARIG	SRSSG
	1330	1340	1350	1360	1370	1380	
m285.pep	DSAGN	GK	GKX				
	1390						
a285	DSAGN	GK	GKX				
	1390						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACACTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCGACA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAGGCCT
351 GCCCGACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCCTA ACGCGGCATA CCCTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTCGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGGCCGAAC TGACGATCGA CCGCGGCAAT ATCCGCCTCT
701 CCGGAAATAT CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCTGCCCC GATGCCGGGC TGAATTTCGA CTGACCGGCC ATCCCGTCGT
851 TTTACAGACG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCGGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTGGGGCGG
951 CTTTGTGATC CCGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGTCTCG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTG GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCTCGCCCC AAAATCTCTT GGCAACTCGG CACCGGCAGC
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGAcCCCC CAAACGAACA
1251 GCGGAAACTG GTGTTGACAC CCGTCAACAT CTCCGCCGGG GAAGGCAGCC
1301 TGACCGGCGA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GCATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCTCT TGCCGGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTGC CCGGTACGTT CAACGGCGTG
1501 CCATTGTCGG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCCGCGCTG GATTGCGGT TGGGGCGGAA CATCGTCAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACCGGACA
1701 CCTTCCGGC GATTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCGGTCG
1801 CTCGATTTTA CCCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATCGCGCG
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTTGTCG
1901 ATACCGCCGG CTTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCGG CCATGACGCT GGACGGCAA CCGTTCAAC TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGCGG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGAAGAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CCGCAATATG GCAATACAC CGCTCGCGCG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTCTGCG CCGCCGCCCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGCTCCT TCGATACCGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CCGGACAAAG CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATTGCAGGCA GGAAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTCAGCAT
3051 GGAAACAGC GTGCCGATG TCGATATCGG CCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAC
3201 TGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATCGCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGGCGGC GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CCGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CGGTCCGCT CATCAAAGG
3451 CGTTACAAAG CATACGGGCA GGATTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT GAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGC GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCTCAACC GTGCCGGCAG CCGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC CGCAGCGGCA GGCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 GCGGCAAAAC GCGGAACTCA ACCCGCCGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CCGGAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAATC GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTTC GGTTCCGACA AAAAGACTC CGCAGGAAAC
4051 GGCAAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:  
g285-1.pap

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAYLD RFETGKISMV KTFDKQTVYL
151 ERLNAAYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GFEGETINST ARLSGSLKDV RAEITIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRDLGS IGIGGTTASP KISWQLGTGT
401 ARTDGSLLAIA SDPANEQRKL VFDTVNISAG EGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLSG DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKGSFG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASAAWQAMG GSNLQHFWS DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPGGOALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSNLASAQI GGRVGSFSPV AAVNGSSNYG
901 KINGNITVGO SRSFDTAPLG GRNLTVADA EAFRNFLPVG QTVKGSNLAA
951 VTGGSIADP HLGGSSINGDK LYRNTQOGI ILDNGLSLRH IAGRKWVIDS
1001 LKFRHEGTAE LSGTSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGGDVVVLG EVKKEAAASL
1101 PVMNLTLDL NDGIRFSGYG ADVTIGKLT LTAQPPGNVR GVGTVRVIK
1151 RYKAYGQDL DITKGTVSFVG PLNDPNLNIR AERRLSVPGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNaQT GELNPAEQVL TVGKQLTGKL YIGYEYGISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GKGR*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGCTCTGC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTG TTGTTCCGGC GTAAACATTT CCTCCAAAA CCTCAAAGGC
151 ACGTGCTCGC ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCAGCTCC GCCTAAAGAA GAACGCCCGC CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCCTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCCTCG
551 TCGGCTTGAA AAAACCGTTT GCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGAATCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGCAAT ATCCGCTCT
701 CGGGAATATC CGTCATCCAC CCGTTTCCGG AATCATTGGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGGCCG CCTTCGTGCC
801 TTCCCTGCCG GATGCCGAC TGAATTTGCA CCTGACGCCC ATCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGTTGCG TCGATTGGA AAACACAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTAGCGCG
951 CTTTGTCTAT CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCTTGCTCGG ACGGGCGCGC ATCAGGCTGT CGGGCAAAAT CGACACGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 CGCGCACGGC ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAACTG GTGCTCGACA CCGTCAACAT CGCCGCCGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTCCGA CATGTGTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCGCGCGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGCGGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTCCGTT GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCGA CATCCGTTCC
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1851 CGACATCAAA GGCAGCGGCC TTTGCTGTC GGGCGGAGCG GCGGTTGTCG
1901 ATACCGCGCA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGC CCATGACGCT GGATGGCAAA CCGTTCAAAT TCGATTGGA
2001 CGCTTCAGCG GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATTCCTCGA CATCGCGGCG GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAAATTCT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
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2501 ACGCCTTCGG CGGCAATATG GCAAAATGCAC CGCTCGGCGG CAGGATTACC
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2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAATC GCGGACGGG
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2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
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3201 GGATCAGGGG CTGTTCCGTT CGCAAAAATC CTCGATGCCG TCCGTGGCGG
3251 ACATGTCTGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
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3351 CCGCTACGGC GCGGACGTTA CCATAGCGCG CAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGGTGGGCA CGGTCCCGCT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CGGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGGC GCGGTGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGGTC ATCCTCAACC GCGCCGGCAG CGGCAGCAGC GCGGACAATG
3701 CCGCCCTGTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GCGCAACTCA ACCCGCCCGA ACAGGTGCTG ACCGTCCGCA
3851 AACCACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCCA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pap

```

1 LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPLSLPDS IDLPAAYILD RFETGKISMG KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAEALIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVRGFNI NPAAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSFPIRADIK GSRLSLSGGA AVVDATDML DGTGVQHRIR
651 THAAMTLDGK PFKEFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSNAAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGO SRSEDTAPLG GRLNLTVADA EVFRNFPVG QTVKGSLNAA
951 VTLGGSIADP HLGGSSINGDK LYRNTQOGI ILDNGLSLRS IAGRKWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVMNMLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL TYTIRFDRFS GSKDKDSAGN
1351 GRGK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

g285-1.pep	LKLSAALLSVLILAVCFLGWIAGTEAGLRFLGYQIPSWFGVNISSQNLRGTLDDGFDGDN
m285-1	LKLSAALLSVLILAVCFLGWLAGEAGLRFLGYQIPSWFGVNISSQNLRGTLDDGFDGDN
	10 20 30 40 50 60
g285-1.pep	70 80 90 100 110 120
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
	70 80 90 100 110 120
g285-1.pep	130 140 150 160 170 180
m285-1	IDLPAAYVLDREFETGKISMGKTFDKQTVYLERLNAARYDRKGHRDLKAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
m285-1	SASVGLKKPFALDTAIYTKGGFEGETIHSTARLSGSLKDVRAELTIDGNNIRLSGKSVIH
	190 200 210 220 230 240
g285-1.pep	250 260 270 280 290 300
m285-1	PFAESLDKTLLEEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGSILDLENTK
	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
m285-1	AGFADRNGIPVRQVLGGFVIRQDGTGVHIGNTSAALLGRGGIRLSGKIDTEKDILDNLIGI
	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
m285-1	NSVGAEDVLQTAFAKGRLDGSIGIGTTASPKISWQLGTGTARTDGLAIASDPANEQRKL
	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
m285-1	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQFPAGDINGSIHLAGE
	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
m285-1	LAKERFTGKMRFLPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGTARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
m285-1	LDFTLKGSPGTSRPMRADIKGRSLSGGAAVVDTAGLTLEGTGAQHRIRTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
m285-1	PFKLDLASGGINRELTRWKGSGIGLDIGGAFNLKLNRMTELEGAERVAASAANWQAMG
	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
m285-1	GSLNLQHFSWDRKKTGISAKGGARGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL

662

	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGGRITASLPDLGALKPFLPAAQNIITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
m285-1	ANAPLGGGRITASLPDLGALKPFLPAAQNIITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSFDTAPLGGRNLNTVADAEAFRNFLPVGQTVKGSLNAAVTLGGSADP					
m285-1	KINGNITVGQSRSFDTAPLGGRNLNTVADAEVFRNFLPVGQTVKGSLNAAVTLGGSADP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVSMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPOKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAASLPVNMNLTLDLNDGIRFSGYGADVTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAASLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSKDKLSWLILNRAGSGSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRFLFGSDKKDSAGNGKX					
m285-1	IGSRSSGGELTYTIRFDRFSGSDKKDSAGNGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTT CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTGCGCGGCA CGGAAGCGGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATTACCGAAA TTTCCGCCGG CGACATCGCC
301 ATCGTTACCA AACCAGCTCC GCCTAAAGAA GAACGCCCCG CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCGCGCGT CTATCTCGAG CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTGT ACAAACAAAC CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGA CTGGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CCGCGCGAAC TGGCGATCGA CCGCGGCAAT ATCCGCCTCT
701 CGGGAATATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTGAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCAG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTAAA TATAGGCATC AACTCCGTCG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAACCGGACA
1251 CGGGAATCTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTC CGACCCCTCG CGCATCGATC CGCAACTTCC
1401 GCGAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAATATCAC AGGCAAAATG CCGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGCTC GATTTGCGGC TGGGGCGGAA CATTATTAAC ACAGACGGGG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTCCGGCG GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGCGCGCGC GCGCAACCTG CACATCGGCA AGCGCGCAGA CATCCGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCGAC ACAAGCCCGC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTC GGGCGGAGCG GAGGTGTGCG
1901 ATACCGCCGA CCTGATGCTG GACGGCACGG CGGTGCGACA CCGCATCCCG
1951 ACACACGCGC CCATGACGCT GGATGGCAA CCGTTCAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGCGG GCAAGTGCGG CAATTTGGCA
2151 GGCATGCGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACCGCC CTTGGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGCGG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAACACGCG CTTTCAAAAC GACCGTATCG GAATCTGTCT
2451 TGACGGCGCG GCGCGTTTCG GCGGATTAA CGCCGATTG GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAATGACAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTCTGCG CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAATC GCGGACGCGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGGCACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT CGGTTGCGAT ATCGCGGCGA GGAATGGGT AATCGACAGC
3001 CTGAAATTCG GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTGCGTAT
3051 GGAACACAGC GGACCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCCTGTC CCGCCCAAC CGCCGCTGCA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAACAA
3201 GGATCAGGGG CTGTTGCGTT CGCAAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGCGGCG GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATACGGGCA GGATTGAGC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CGCTCAACG ACCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCGG CCTCAACAGT
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GCGCCGCGAG TGGCAGCAGC GGCACAAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGCG TTGCGGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCGCGCGA ACAGGTGCTG ACCGTCGGCA
3851 AACCAACTGAC CGGCAAACTC TACATCGGCT ACRAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CCGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAGAGCTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:



## a285-1.pep

1 LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLRG  
51 TLIDGFDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA  
101 IVTKPTPPKE ERPLSLPDS IDLPAAVYLD RFETGKISMV KAFDKQTVYL  
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG  
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL  
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK  
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRRG IRLSGKIDTE  
351 KDILDLNIGI NSVGAEDVLQ TAFKGRDLGS IGIGTTASP KISWQLGIGT  
401 ARTDGSIAIA SDPANGQRKL VLDTVNTAAG QGSLTAQGYL ELFKDRLLKL  
451 DIRSRAFDPS RIDPOLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV  
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD  
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLGGAARNL HIGKAADIRS  
601 LDFTLKGSPP TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR  
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM  
701 TLEAGAERVA ASAANWQAMG GSNLQHFWSV DKKTGISAKG GAHGLHIAEL  
751 HNFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN  
801 AFSLKTFRQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT  
851 ASLPDLGLTK PFLPAAQNI TGSNAAAQI GGRVGSPPSVN AAVNGSSNYG  
901 KINGNITVGO SRSFDTAPLG GRNLTLVADA EVFRNFPVPG QTVKGSNLAA  
951 VTLLGSIADP HLGGSINGDK LYRNQTQGI ILDNGLSLRH IAGRKWVIDS  
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR  
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL  
1101 PVMNMTLIDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIK  
1151 RYKAYGQOLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS  
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND  
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS  
1301 AEQSVKLIYR LTRAIQAVAR IGRSSSGGEL YTTIRFDRFS GSDKKDSAGN  
1351 SKGK\*

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLRGTLIDGFDGDN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLRGTLIDGFDGDN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPLSLPDS					
	70	80	90	100	110	120
	130	140	150	160	170	180
a285-1.pep	IDLPAAVYLDREFETGKISMVKAQDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
m285-1	IDLPAAVYLDREFETGKISMVKAQDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG					
	130	140	150	160	170	180
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	190	200	210	220	230	240
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIALEGS LDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIALEGS LDLENTK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGT VHIGNTSVALLGRRGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGT VHIGNTSVALLGRRGIRLSGKIDTEKDILDLNIGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRDLGSIGIGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRDLGSIGIGTTASPKISWQLGIGTARTDGSIAIASDPANGQRKL					
	370	380	390	400	410	420
	430	440	450	460	470	480

a285-1.pep VLDTVNIAAGQGSLSAQGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE  
|||||  
m285-1 VLDTVNIAAGQGSLSAQGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE  
430 440 450 460 470 480

a285-1.pep 490 500 510 520 530 540  
LAKEKFTGKMREFPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD  
|||||  
m285-1 LAKEKFTGKMREFPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGD  
490 500 510 520 530 540

a285-1.pep 550 560 570 580 590 600  
RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS  
|||||  
m285-1 RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDLGGIRTFTDLSGAARNLHIGKAADIRS  
550 560 570 580 590 600

a285-1.pep 610 620 630 640 650 660  
LDFTLKGPSPTSRPIRADIKGSRLSLSGGAEVVDADLMDGTGVQHRIRTHAAMTLDGK  
|||||  
m285-1 LDFTLKGPSPTSRPIRADIKGSRLSLSGGAEVVDADLMDGTGVQHRIRTHAAMTLDGK  
610 620 630 640 650 660

a285-1.pep 670 680 690 700 710 720  
PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRMTEAGAERVAASAANWQAMG  
|||||  
m285-1 PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLNRMTEAGAERVAASAANWQAMG  
670 680 690 700 710 720

a285-1.pep 730 740 750 760 770 780  
GSLNLQHFSWDKKTGISAKGGAGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL  
|||||  
m285-1 GSLNLQHFSWDKKTGISAKGGAGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL  
730 740 750 760 770 780

a285-1.pep 790 800 810 820 830 840  
NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM  
|||||  
m285-1 NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM  
790 800 810 820 830 840

a285-1.pep 850 860 870 880 890 900  
ANAPLGGRITASLPDLGTLKPFPLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG  
|||||  
m285-1 ANAPLGGRITASLPDLGTLKPFPLPAAQONITGSLNAAQIGGRVGSFVNAAVNGSSNYG  
850 860 870 880 890 900

a285-1.pep 910 920 930 940 950 960  
KINGNITVGQSRSFDTAPLGGRNLTVDAEVEFRNFLPVGQTVKGSLNAAVTLGGSIADP  
|||||  
m285-1 KINGNITVGQSRSFDTAPLGGRNLTVDAEVEFRNFLPVGQTVKGSLNAAVTLGGSIADP  
910 920 930 940 950 960

a285-1.pep 970 980 990 1000 1010 1020  
HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS  
|||||  
m285-1 HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS  
970 980 990 1000 1010 1020

a285-1.pep 1030 1040 1050 1060 1070 1080  
GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP  
|||||  
m285-1 GPDVDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP  
1030 1040 1050 1060 1070 1080

a285-1.pep 1090 1100 1110 1120 1130 1140  
SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLAQSGGSSVR  
|||||  
m285-1 SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLTTLAQSGGSSVR  
1090 1100 1110 1120 1130 1140

a285-1.pep 1150 1160 1170 1180 1190 1200  
GVGTVRVIKGRYKAYQQLDITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS  
|||||  
m285-1 GVGTVRVIKGRYKAYQQLDITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS

666

	1150	1160	1170	1180	1190	1200
a285-1.pep	1210	1220	1230	1240	1250	1260
m285-1	PRITLTANEPMSKDKLSWLIINRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
a285-1.pep	1270	1280	1290	1300	1310	1320
m285-1	TSKRSRNAQTGELNPAEQVLTGKQLTGKLYIGYEYSSISAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
a285-1.pep	1330	1340	1350			
m285-1	IGSRSSGGELTYTIRDFRSGSDKKDSAGNSKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

```

g286.seq
1  atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatatt ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101  aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151  gaatcagtc aattaaacc caaattcccc gtccgcacgc acacgcagga
201  cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251  agcaggaaga ggttttgat aaggaacaga cgggattcct tgccgaagaa
301  gcaccggaca acgttaaaac aatgctccgc agcaaaggct atttcagcag
351  caaggtcagc ctgacggaaa aagacggagc ttatacggtg cacatcacac
401  cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451  atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501  ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaaca
551  gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta cccgcttgcc
601  aagctcggca acacccgggc ggccgtcaac cccgataccg ccaccgcga
651  tttgaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701  aaatcacccg cacacagcgt taccgccgaac aaaccgtctc cggcctggcg
751  cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801  acaggcgctc gaacaaaacg ggcattatcc cggcgcgctc gtacaagccg
851  acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaag tcagcgtaac
901  cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcgggat
951  acggtttggg cggcaaaatc gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggctcg ctgggatatg gacaataacg aaaccacgct
1051 tgccgccggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaaccgt tcgaccaccc aaaacctcga aaaacgcgcc
1151 ttctccggcg gcatctggta tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaattc
1401 gcacctctgc ccgcgagggt tatttcttca cgcccgaata caaaaaactc
1451 ggcacgttca tcatacgcg acaagcgggt tacaccgttg cagcgacaaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcgcgggc gcgtcttccg
1551 tgccgggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

```

g286.pep
1  MONTGTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101  APDNVKTMLR SKGYFSSKVS LTEKDGYATV HITPGPRTKI ANVGVAIIGD
151  ILSDGNLAAY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201  KLGNTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTOR YPEQTVSGLA
251  RFQPGTPYDL DLLLDFQQAL EQNGHYSAS VQADFRLPR GPRPRQSQRN
301  RGQTPQTRNR HPPRFGIRFG RQNRLLRLQP LQRLYRLGR LGYGQIRNHA
351  CRRHQPAQAL SGQLLDKQRF LQPFDPKPR KTRLLRRHLV CARPRGHRCQ
401  AGGGISRRRP ENPRLGCRFG QQPRHDADRL LETPAAQORA APRKRPLPRR

```

451 QNRDDFGHIP VLHRANPHLC PRRLFLHARK QKTRHVHHTR TSGLHRCTRO  
501 CRCPLGADVQ QRRRVFRARL RT\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATCAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC
151	GAATCAGTCA	AATTAAAACC	CAAATTCCCC	GTCCTCATCG	ACACGCAGGA
201	CAGTGAAATC	AAAGATATGG	TCGAAGAACA	CCTGCCGCTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGGCTTCCT	CGCCGAAGAA
301	GCGCCGGACA	ACGTAAAAAC	GATGCTCCGC	AGCAAAGGCT	ATTTACGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCGCG	CACCAAAATC	GCCAACGTCG	GCGTCGCCAT	CCTCGGCGAC
451	ATCCTTTTCT	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GCGATTTCGA	TCAGGACAGT	TGGGAAAAACA
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ATACGCAGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACGTC	GTCGTGGACA	GCGGCCGCCC	CATCGCCTTC	GGCGACTTTG
701	AAATCACCGG	CACACAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCCTTGCG
751	CGTTTCCAGC	CCGGTATGCC	GTACGACCTC	GACCTGCTGC	TCGACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	AGGTCAAAC	GCCACAACT	CGAAACCGGC	ATCCGCCTCG	ATTCGGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAAG
1001	GCTATATCGG	TTCGGTCGTC	TGGGATATGG	ACAAATACGA	AACCACGCTT
1051	GCCGCCGGCA	TCAGCCAGCC	GCGCAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACGCGCCT
1151	TCTCCGGCGG	CGTCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGCGG	AATTCTCGC	AGAAGGCGCG	AAAATCCCCG	GCTCGCTGT
1251	CGATTTGGGC	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAAACGCC
1301	AGCTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CCTCGACGGC
1351	AAAATCGGTA	CGACTTTGGG	CACATTCTCT	TCCTCCACCG	CGCTGATCCG
1401	CACCTCTGCC	CGTGCAGGTT	ATTTCTTCAC	GCCCGAAAAC	AAAAAACTCG
1451	GCACGTTTCT	CATACGCGGA	CAAGCGGGTT	ACACCGTTGC	CCGCGACAAT
1501	GCCGACGTTT	CTTCAGGGCT	GATGTTCCGC	AGCGGCGGCG	CGTCTCCGCT
1551	GCGCGGTTAC	GAACTCGACA	GCATCGGACT	TGCCGGCCCG	AACGGATCGG
1601	TCCTGCCCGA	ACGCGCCCTC	CTGGTGGGCA	GCCTGGAATA	CCAACGCGCG
1651	TTTACGCGCA	CCCTTTCGGG	CGCGGTGTTT	CACGATATGG	GCGATGCCGC
1701	CGCCAATTTC	AAACGTATGA	AGCTGAAACA	CGGTTCCGGA	CTGGGCGTGC
1751	GCTGGTTTCT	CCCGCTTGCG	CCGTTTTCCT	TCGACATCGC	CTACGGGCAC
1801	AGCGATAAGA	AAATCCGCTG	GCACATCAGC	TTGGGAACGC	GCTTCTAA

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

1	MHDTRTMMIK	PTALLLPALF	FFPHAYAPAA	DLSENKAAGF	ALFKNKSPDT
51	ESVKLKPKFP	VLIDTQDSEI	KDMVEEHLPL	ITQQQEEVLD	KEQTGFIAEE
101	APDNVKTMLR	SKGYFSSKVS	LTEKDGAITY	HITPGPRTKI	ANVGVAILED
151	ILSDGNLAAY	YRNALENWQQ	PVGSDFDQDS	WENSKTSVLG	AVTRKAYPLA
201	KLGNLQAAVN	PDTATADLVN	VVDSGRPIAF	GDFEITGTQR	YPEQIVSGLA
251	RFQPGMPYDL	DLLDFQQAAL	EQNGHYS GAS	VQADFRLQ	DRVPVKVSVT
301	EVKRHKLETG	IRLDSEYGLG	GKIAYDYNNL	FNKGYIGSVV	WMDKYETTL
351	AAGISQPRNY	RGNYWTSNVS	YNRSTQNL	KRAFSGGVWY	VRDRAGIDAR
401	LGAEFLEAGR	KIPGSAVDLG	NSHATMLTAS	WKRQLLNNVL	HPENGHYLDG
451	KIGTTLGTFL	SSTALIRTS	RAGYFFTPEN	KKLGTFFIIRG	QAGYTVARDN
501	ADVPSGLMFR	SGGASSVRGY	ELDSIGLAGP	NGSVLPERAL	LVGSLEYQLP
551	FTRTLGSAVF	HDMGDAAANF	KRMKLKHGSG	LGVRWFSPLA	PFSFDIAYGH
601	SDKKIRWHIS	LGTRF*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

		10	20	30	40	50	60
m286.pep		MHDTRTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKN	KSPDTESVKLKPKFP			
		10	20	30	40	50	60
g286		MQNTGTMMIKPTALLLPALFFFP	HAYAPAADLSENKAAGFALFKS	KSPDTESVKLKPKFP			
		70	80	90	100	110	120
m286.pep		VLIDTQDSEIKDMVEEHLPLITQ	QEEVLDKEQTGFLAE	EAPDNVKTMLRSKGYFSSKVS			
		70	80	90	100	110	120
g286		VRIDTQDSEIKDMVEEHLPLITQ	QEEVLDKEQTGFLAE	EAPDNVKTMLRSKGYFSSKVS			
		130	140	150	160	170	180
m286.pep		LTEKDGAYTVHITPGPRTKIANVG	VAILGDI	LSDGNLA	EYRNALENWQQPVGSD	FDQDS	
		130	140	150	160	170	180
g286		LTEKDGAYTVHITPGPRTKIANVG	VAILGDI	LSDGNLA	EYRNALENWQQPVGSD	FDQDS	
		190	200	210	220	230	240
m286.pep		WENSKTSVLGAVTRKAYPLAKL	GNTQA	AVNPDTATADLN	VVDVSGRPIAFGDFEITGTQR		
		190	200	210	220	230	240
g286		WENSKTSVLGAVTRKGYPLAKL	GNTRA	AVNPDTATADLN	VVDVSGRPIAFGDFEITGTQR		
		250	260	270	280	290	299
m286.pep		YPEQIVSGLARFQPGMPYDL	LLDFQQA	LEQNGHYSGASVQADFDRL	-QGDRVPVKVSV		
		250	260	270	280	290	299
g286		YPEQIVSGLARFQPGT	PYDL	LLDFQQA	LEQNGHYSGASVQADFDRL	PRGPRPRQSQRN	
		300	310	320	330	340	350
m286.pep		TEV	KRHKLETGIRLDSEYGLGGK	IAYDY	NLFNKGYIGSVVWMDKYETTLAAGISQPRN		
		310	320	330	340	350	360
g286		RGQTPQTRNRHPPRFGIRFGR	QNRLLQPLQRLYRLGRLGYGQIRNHACRRHQPA	QAL			

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a286.seq
1 ATGCACGACA CCGGTACCAT GATGATTAAG CCGACCGCCC TGCTCCTGCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTCGCCGC GACCTTTCCG
101 AAAACAAGCG GCGCGGTTTC CATTGTTTCA AAAACAAGAG CCCCACACC
151 GAATCAGTTA AATTAAGAAC CAAATTCCTT GTCCGCATCG ACACGCAGGA
201 TAGTGAATTC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGCG
251 AGCAGGAAGA AGTATTGGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCACCGGACA ACGTTAAAGC AATGCTCCGC GCGAAGGCTT ATTCAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAATTC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAATA
501 CTGGCAGCAG CCGGTAGGCA GTGATTTTCA TCAGGAACAG TGGGAAACA
551 GCAAAATCTC CGTCTCGGCG GCGGTAACGC GCAAAGCTAT CCGCGTTGCC
601 AAGCTCGGCA ACACCCGGGC GGCCGTC AACCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCCC CATCGCCTTC GCGACTTTG
701 AATTACCGG CACGCAGCGT TACCCGCAAC AAATCGTCTC CGGCTTTGGC
751 CGCTTCCAAC CGGCGACGCG CTACGACCTC GACCTGCTCG TCGACTTCCA
801 ACAGGCGCTC GACAAAACG CGCATATTTC GCGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAGCT CGAAACCGGC ATCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAG
1001 GCTATATCGG TTCGGTCGTC TGGGATATGG ACAAAATCGA AACACGCTT
1051 GCCCGCGGCA TCAGCCAGCC CGCGCAACTAT CGGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGGCGG CATCTGGTAT GTGCGCGACC GCGCGGGCAT CGATCGCAGG
1201 CTGGGGGCGG AGTTTCTCGC AGAAGGCGCG AAAATCCCCG GCTCGGATAT
1251 CGATTTTGGC AACAGTCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC

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1351 AAAATCGGTA CGACTTTGGG CGCATTCCTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTT CACGATATGG GCGACGCCGC
1701 CGCCAATTTT AAACGTATGA AGCTGAAACA CGGTTGCGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCGC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGYTV HITPGPRTKI ANVGVAI LGD
151 ILSDGNLA EY YRNALENWQQ PVGSDFDQDS WENKTSVLG AVTRKAYPLA
201 KLGNTAAVN PDTATADLN VVDSGRPIAF GDFEITGTOR YPEQIVSGLA
251 RFQPGTPYDL DILLDFQQA LEQNGHYS GASVQADFRLQ GDRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTQNL E KRAFSGGIWY VRDRAGIDAR
401 LGAEFLA EGR KIPGSDIDL G NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLGA FL SSTA LIRTS A RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLSGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKIRWHIS LGTRF*

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m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPFP					
a286	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPFP					
	10	20	30	40	50	60
m286.pep	70	80	90	100	110	120
a286	70	80	90	100	110	120
m286.pep	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	130	140	150	160	170	180
m286.pep	LTEKDGYTVHITPGPRTKIANVGVAI LGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
a286	LTEKDGYTVHITPGPRTKIANVGVAI LGDILSDGNLA EY YRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
m286.pep	190	200	210	220	230	240
a286	190	200	210	220	230	240
m286.pep	WENKTSVLGAVTRKAYPLAKLGNTQA AVNPDTATADLN VVDSGRPIAF GDFEITGTOR					
a286	WENKTSVLGAVTRKAYPLAKLGNTQA AVNPDTATADLN VVDSGRPIAF GDFEITGTOR					
	250	260	270	280	290	300
m286.pep	YPEQIVSGLARFQPGMPYDL DILLDFQQA LEQNGHYS GASVQADFRLQ GDRVPVKVSVT					
a286	YPEQIVSGLARFQPGMPYDL DILLDFQQA LEQNGHYS GASVQADFRLQ GDRVPVKVSVT					
	250	260	270	280	290	300
m286.pep	310	320	330	340	350	360
a286	310	320	330	340	350	360
m286.pep	EVKRHKLETGIRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLG GKIAYDYNNL FNKG YIGSVV WMDKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLKRAFSGGVWYVRDRAGIDARLGAEFLEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLKRAFSGGIWYVRDRAGIDARLGAEFLEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRQLLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNGSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKCLKHSGSLGVRWFSPLAPFSFDIAYGH
a286	LVGSLEYQLPFTRTLSGAVFHDMDAAANFKRMKCLKHSGSLGVRWFSPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTRFX
a286	SDKKIRWHISLGTRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

```

1  atgtttaaac gcagtgtgat tgcaatggct tgtatttttc ccctttcagc
51  ctgtgggggc ggcggtggcg gatcgcccga tgtcaagtcg gcggaacacgc
101 cgtcaaaaacc ggcgcgcccc gttgtgtctg aaaaatgccg ggaaggggtg
151 ctgccgaaag aaaagaaaga tgaggaggca gcgggcggtg cgccgcaagc
201 cgatacgag gacgcaaccg ccggagaagg cagccaagat atggcggcag
251 ttcggcgaga aaatacaggc aatggcggtg cggcaacaac ggacaacccc
301 aaaaatgaag acgcgggggc gcaaaatgat atgccgcaaa atgccgccga
351 atccgcaaat caaacaggga acaaccaacc cgccggttct tcagattccg
401 cccccgcgtc aaaccctgcc cctgcgaatg gcggtagcga ttttggaagg
451 acgaacgtgg gcaattctgt tgtgattgac ggaccgtcgc aaaatataac
501 gttgaccac tgtaaaggcg attcttgtaa tggatgataa ttattggatg
551 aagaagcacc gtcaaaatca gaatttgaaa aattaagtga tgaagaaaaa
601 attaaagcat ataaaaaaga cgagcaacgg gagaattttg tcggtttggt
651 tgctgacagg gtaaaaaagg atggaactaa caaatatata atcttctata
701 cggacaaaacc acctactcgt tctgcacggt cgaggaggtc gcttccggcc
751 gagattccgc tgattcccgt caatcaggcc gatacgtga ttgtggatgg
801 ggaagcgtgc agcctgacgg ggcattccgg caatatcttc gcgcccgaag
851 ggaattaccg gtatctgact tacggggcgg aaaaattgcc cggcggatcg
901 tatgccctcc gtgtgcaagg cgaaccggca aaaggcgaaa tgcttggtgg
951 cacggccgtg tacaacggcg aagtgtctga tttccatatg gaaaacggcc
1001 gtccgtaccc gtccggaggg aggtttgccg caaaagtcga tttcggcagc
1051 aaatctgtgg acggcattat cgacagcggc gatgatttgc atatgggtac
1101 gcaaaaattc aaagccgccca tcgatggaaa cggttttaag gggacttgga
1151 cggaaaatgg cggcggggat gtttccggaa ggttttacgg cccggccggc
1201 gaggaagtgg cgggaaaata cagctatcgc ccgacagatg ctgaaaaggg
1251 cggattccgc gtgtttgccg gcaaaaaaga tcgggattga

```

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

```

1  MFKRSVIAMA CIFFLSACGG GGGGSPDVKS ADTPSKPAAP VVAENAGEGV
51  LPKEKKDEEA AGGAPOADTQ DATAGEGSQD MAAVSAENTG NGGAATTDNP
101 KNEDAGAOND MPQNAAESAN QTGNNQPAGS SDSAPASNPA PANGGSDFGR

```

```

151 TNVGNVSVVID GPSQNTLTH CKGDSCNGDN LLDEEAPSKS EFEKLSDEEK
201 IKRYKKDEQR ENFVGLVADR VKKDGTNKYI IFYTDKPPTR SARRRSLPA
251 EIPLPVNQA DTLIVDGEAV SLTGHSGNIF APEGNYRYLT YGAEKLPGGS
301 YALRVQGEPA KGEMLVGTAV YNGEVLHFHM ENGRPYPSGG RFAAKVDFGS
351 KSDGIIDSG DDLHMGTOKF KAAIDGNGFK GTWTENGSGD VSGRFYGPAG
401 EEVAGKYSYR PDAEKGGFG VFAGKKDRD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```

m287.seq
1 ATGTTTAAAC GCAGCGTAAT CGCAATGGCT TGTATTTTGT CCCTTTCAGC
51 CTGCGGGGGC GCGGTGGCG GATCGCCCGA TGTCAGTCG GCGGACACGC
101 GTTCAAAACC TGCCGCCCCCT GTTGTTCCTG AAAAAGAGAC AGAGGCAAAG
151 GAAGATGCCG CACAGGCAGG TTCTCAAGGA CAGGGCGCGC CATCCGCACA
201 AGGCAGTCAA GATATGGCGG CCGTTCGGA AGAAAATACA GGCAATGGCG
251 GTGCGGTAAAC AGCGGATAAT CCCAAAAATG AAGACGAGGT GGCACAAAAT
301 GATATGCCGC AAAATGCCGC CCGTACAGAT AGTTCGACAC CGAATCACAC
351 CCCGGATCCG AATATGCTTG CCGGAAATAT GGAAAATCAA GCAACGGATG
401 CCGGGGAATC GTCTCAGCCG GCAAACCAAC CGGATATGGC AAATGCGGCG
451 GACGGAATGC AGGGGGACGA TCCGTCGCA GCGGGGCAAA ATGCGCGCAA
501 TACGGGTGCC CAAGGTGCAA ATCAAGCCGG AAACAATCAA GCCGCCGGTT
551 CTTAGATCC CATCCCCGCG TCAAACCTG CACCTGCGAA TGGCGGTAGC
601 AATTTTGAA GGGTTGATT GGCTAATGGC GTTTTGATTG ACGGGCCGTC
651 GCAAAATATA ACGTTGACCC ACTGTAAAGG CGATTCTTGT AGTGGCAATA
701 ATTTCTTGA TGAAGAAGTA CAGCTAAAAT CAGAATTGA AAAATTAAGT
751 GATGCAGACA AAATAAGTAA TTACAAGAAA GATGGGAAGA ATGATAAATT
801 TGTCGGTTG GTTGCCGATA GTGTGCAGAT GAAGGGAATC AATCAATATA
851 TTATCTTTA TAAACCTAAA CCCACTTCAT TTGCGCGATT TAGGCGTTCT
901 GCACGGTCGA GCGGTTCGCT TCCGGCCGAG ATGCCGCTGA TTCCCGTCAA
951 TCAGGCGGAT ACGCTGATTG TCGATGGGGA AGCGGTGAGC CTGACGGGGC
1001 ATTCCGCAA TATCTTCGCG CCCGAAGGGA ATTACCGGTA TCTGACTTAC
1051 GGGGCGGAAA AATTGCCCCG CGGATCGTAT GCCCTTCGTG TTCAAGGCGA
1101 ACCGGCAAAA GCGGAAATGC TTGCGGGCGC GGCCGTGTAC AACGGCGAAG
1151 TACTGCATTT CCATACGGAA AACGGCCGTC CGTACCCGAC CAGGGGCAGG
1201 TTTGCCGCAA AAGTCGATT CCGCAGCAA TCTGTGGACG GCATTATCGA
1251 CAGCGCGGAT GATTTCGATA TGGGTACGCA AAAATTCAA GCCGCCATCG
1301 ATGGAACCG CTTAAGGGG ACTTGACGG AAAATGGCAG CGGGGATGTT
1351 TCCGGAAGT TTTACGGCCC GGCCGGCGAG GAAGTGGCG GAAAATACAG
1401 CTATCGCCC ACAGATGCGG AAAAGGGCGG ATTCGGCGTG TTTGCCGGCA
1451 AAAAAGAGCA GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

```

m287.pep
1 MFKRSVIAMA CIFALSACGG GGGGSPDVKS ADTLSKPAAP VVSEKETEAK
51 EDAPQAGSQ QGAPSAQGSQ DMAAVSEENT GNGGAVTADN PKNEDEVAQN
101 DMPQNAAGTD SSTPNHTPDP NMLAGNMENQ ATDAGESSQP ANQPDMANAA
151 DGMQGDPSA GGQNAAGTAA QGANQAGNNQ AAGSSDPIPA SNPAPANGGS
201 NFGRVDLANG VLIDGPSQNI TLTHCKGDSC SGNNFLDEEV QLKSEFEKLS
251 DADKISNYKK DGKNDKFVGL VADSVQMKGI NQYIIFYKPK PTSFARFRS
301 ARSRRSLPAE MPLIPVNQAD TLIVDGEAVS LTGHSGNIFA PEGNYRYLTY
351 GAEKLPGGSY ALRVQGEPAK GEMLAGAAVY NGEVLHFHTE NGRPYPTRGR
401 FAAKVDFGSK SVDGIIDSGD DLHMGTOKF KAAIDGNGFK GTWTENGSGD
451 SGKFYGPAGE EVAGKYSYR PDAEKGGFGV FAGKKEQD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

m287.pep      10      20      30      40      49
               MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE-----KETE
               |||||
g287          10      20      30      40      50      60
               MFKRSVIAMACIFPLSACGGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPEKKDEEA

```



	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGGGAPSAAQQSSQDMAAVSEENTGNNGGAVTADNPKNEDVQAQNNDMPQNAAGT						
	:     : ::                         :						
g287	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNNGGAATTDNPKNEDAGAQNNDMPQNAA--						
	70	80	90	100	110		
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDFNMLLAGNMENQATDAGESSQPANQPDMANAADGMQGDDPSAGGQNAGNTA						
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFGRVDLANGVLIDGPSQNIITLTHCKGDS						
	::      :						
g287	-ESANQTGNNQFAGSSSDSAPASNPAPANGGSDFGRTNVGNSVVIDGPSQNIITLTHCKGDS						
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSDADKISNYKKDKGKNDKFVGLVADSVMKGINQYIIFYKP						
	: ::  :     :     :     :     :     :     :     :     :						
g287	CNGDNLLEEAPSKSEFEKLSDDEEKIKRYKKDEQRENFVGLVADRVRKKDGNTKYIIFYTD						
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSIGNIFAPEGNYRILT						
	:      :     :     :     :     :     :     :     :						
g287	KPPT----RSARSRRSLPAEIPLVNQADTLIVDGEAVSLTGHSIGNIFAPEGNYRILT						
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNVEVLHFHFTENGPRYPTRGRFAAKVDFFGS						
g287	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYNVEVLHFHMENGRYPYSGRFAAKVDFFGS						
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVLDGIIDSGDDLHMGTKQFKAAIDGNFGKTWTWTENGSGDVSGKFYGPAGEEVAGKYSYR						
g287	KSVLDGIIDSGDDLHMGTKQFKAAIDGNFGKTWTWTENGGDVSGRFYGPAGEEVAGKYSYR						
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKGGFVFAGKKEQDX						
g287	PTDAEKGGFVFAGKKDRDX						
	420	430					

```
a287.seq
1  ATGTTTAAAC GCAGTGTGAT TGCAATGGCT TGTATTGTTG CCCTTTCAGC
51  CTGTGGGGGC GCGGGTGGCG GATCGCCCGT TGTTAAGTCG GCGGACACGC
101 TGTCAAACCC TGCCGCCCTT GTTGTTACTG AAGATGTCGG GGAAGAGGTT
151 CTGCCGAAAG AAAAGAAAGA TGAGGAGGCG GTGAGTGGTG CGCCGCAAGC
201 CGATACGCAG GACGCAACCG CCGGAAAAGG CGGTCAAGAT ATGGCGTCCG
251 TTTCCGCAGA AAATACAGGC AATGGCGGTG CGGCAACAAC GGATAATGCC
301 GAAAATAAAG ACGAGGGACC GCAAAATGAT ATGCCGCAAA ATGCCGCCGA
351 TACAGATAGT TCGACACCGA ATCACACCCC TGCACCGAAT ATGCCAACCA
401 GAGATATGGG AAACCAAGCA CCGGATGCCG GGAATCGCG ACAAACGGCA
451 AACCAACCGG ATATGGCAAA TCGCGCGGAC GGAATCGCG GGGACGATCC
501 GTCGGCAGG GAAATGCGG GCAATACGGC AGATCAAGCT GCAAAATCAG
551 CTGAAAACAA TCAAGTCGGC GGCTCTCAAA ATCCTGCCTC TTCAACCAAT
601 CCTAACGCCA CGAATGGCGG CAGCGATTTT GGAAGGATAA ATGTAGCTAA
651 TGGCATCAAG CTTGACAGCG GTTCGGAAAA TGTAACGTTG ACACATTGTA
701 AAGACAAGT ATGCGATAGA GATTCTTAG ATGAAGAAGC ACCACCAAAA
751 TCAGAATTTG AAAAATTAAG TATTGAAGAA AAAAATTAATA AATATAAAAA
```

**This corresponds to the amino acid sequence <SEQ ID 1204; ORF 287.a>:**

1	<u>MFKRSVIAMA</u>	<u>CIVALSACGG</u>	GGGGSPDVKS	ADTLSPKPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTG	NGGAATTDPN
101	ENKDEGPOND	MPQNAADATS	STPNHTPPAP	MPTRDMGNQA	PDAGESAQFA
151	NQPDMANAAD	GMQGDPPSDS	ENAGNTADQA	ANQAEENNQV	GSQNPPASSTN
201	PNATNGGSD	GRINVANGIK	LDSGSENVTL	THCKDQVCDR	DFLDEEAFFK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNGY	VIIYKDKSAS
301	SSARFRRSA	RSRRSLPAEM	PLIPVQNADT	LIVDGEAVSL	TGHSNGNIFAP
351	EGNYRYLTYG	AEKLSGGSYA	LSVQGEPAKG	EMLAGTAVYN	GEVLNHFHFM
401	GRPSPGGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTKQKFA	VIDGNGFKGT
451	WTENGGGDVS	GRFYGPAGEV	VAGKYSYRPT	DAEKGEGGVF	AGKKEOD*

		10	20	30	40	49	
m287.pep	MFKRSVIAMACIFALSACGGGGGSPDVKSADTL SKPAAPVVSE-----KETE					A	
a287	MFKRSVIAMACIVALSACGGGGGSPDVKSADTL SKPAAPVVTEDEVGEEVL PKEKKDEEA						
		10	20	30	40	50	60
m287.pep	KEDAPQAGSQQGAPSAQGSQDMAAVSEENTGN GGAVTADNPKNED EVAQN DMPQNAAGT						
a287	VSGAPQADTQ--DATAGKGQDMAAVSAENTGN GGAATTDNPENKDEGPONDMPQNAADT						
		70	80	90	100	110	
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQP ANQPDMANAADGM QGDDPSAGGONAGNTA						
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQ PAPANQPDMANAADGM QGDDPSAG-ENAGNTA						
		120	130	140	150	160	170
m287.pep	AQQANQAAGNNQAAGSSDPIASN PAPANGGSNFGRVDLANGV LIDGPSQNITLTHCKGDS						
a287	DQAANQAENNQVGGSQNPASSTNPNATNG GSDFGRIN VANGIKLDSGSENVTLTHCKDKV						
		180	190	200	210	220	230
m287.pep	CSGNNFLDEEVQLKSEFEKLSDADKISNY KKDGN DKFVGLVADSVQMKGINQYII FYKP						
a287	CD-RDFLDEEAPPKSEFEKLSDDEEKINK YKKDEQREN FVGLVADRVEKNGT NKVYIIYKD						
		240	250	260	270	280	290
m287.pep	KP--TSFARFRSARSRRSLPAEMPLIPVNQ ADTLIVDGEAVSLTG HSGNIFAPEGNYRY						
a287	KSASSSARFRSARSRRSLPAEMPLIPVNQ ADTLIVDGEAVSLTG HSGNIFAPEGNYRY						
		300	310	320	330	340	350

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	350	360	370	380	390	400
m287.pep	LTYGAELKPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
a287	LTYGAELSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDDGIIDSGDDLHMGTOQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
a287	GSKSVDDGIIDSGDDLHMGTOQFKAVIDGNGFKGTWTENGSGDVSGRFGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```

g288.seq
1  atgcacaccg gacaggcggg aagccggggt ctgtctcgga cagtcattcc
51  tctaggcata ccgttgccgg tatgctcaag caacctaccc gaacgctcgg
101 cgggcagcgt cattgcgttc tgtttggctt tgctccgaat ggggtttggc
151 ctgccgcata ttgttaccaa atgcgcgggt cgcccttacc gcaccttttc
201 acccttgccg gtgctgccaa agcagccatc ggcgggtttg ctttctgttc
251 cactttccgt cgcgttaccg cgcccgccg ttaaccggca ttctaccctg
301 cggagcccgg actttccctc ccgtatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcggattat aacacgaaac gcaaaaatgc
401 cgtctgaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctggcttcga tgaagccgtc caagtccggc tccaatacgg
501 ctttgtggtt gccgacttcg tagcctgtac gcaagtcttt gatgcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

```

g288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN AKMPSETVQV SDGIQPKLHT
151 LFQAGFDEAV QVAVQYGFVV ADFVACTQVF DA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1207>:

```

m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTGCGTTC TGTTTGGTCT TGCTCCGAAT GGGGTTTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCTTTTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGC GGTTTGTG CTTTCTGTTC
251 CACTTTCGGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC AAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACGG
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1208; ORF 288>:

```

m288.pep
1  MHTGQAVSRV LSRTVIPLGI PLPVCSSNLP ERSAGSVIAF CLVLLRMGFG
51  LPHIVTKCAV RPYRTFSPLP VLPKQPSAVL LSVPLSVALP RPAVNRHSTL
101 RSPDFPPRMP YAIRGDCLPV PCAARIITRN TKMPSETVQV SDGIQPKLHA
151 LFQAGFDEAV QVAIQYGFVV ADFVACTQVF DT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
g288	PCAAARIITRNTKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

a288.seq

1	ATGCACACCG	GACAGGCGGT	AAGCCGGGTT	CTGTCTCGGA	CAGTCATTCC
51	TCTAGGCATA	CGGTTGCCGG	TATGCTCAAG	CAACCTACCC	GAACGCTCGG
101	CGGGCAGCGT	CATTGCGTTC	TGTTTGGTCT	TGCTCCGAAT	GGGGTTTGGC
151	CTGCCGCATA	TTGTTACCAA	ATGCGCGGTG	CGCCCTTACC	GCACCTTTTC
201	ACCCTTGCCT	GTGCTGCCAA	AGCAGCCATC	GGCGGTTTTC	CTTCTGTTC
251	CACCTTCCGT	CGCGTTACCG	CGCCGGCCG	TTAACCGGCA	TTCTACCCTG
301	CGGAGCCCGG	ACTTTCCTCC	CCGTATGCCT	TACGCGATAC	GCGGCGACTG
351	TCTGCCCGTC	CCGTGTGCGG	CGCGGATTAT	AACACGAAAC	GCAAAAATGC
401	CGTCTGAAAC	GGTACAGGTT	TCAGACGGCA	TACAGCCTAA	ACTACACGCC
451	CTGTTTCAGG	CTGGCTTCGA	TAAAGCCGTC	CAAGTCGCCG	TCCAATACGG
501	CTTTGGTGTT	GCCGACTTCG	TAGCCTGTGC	GCAAGTCTTT	AATGCGTGA

This corresponds to the amino acid sequence &lt;SEQ ID 1210; ORF 288.a&gt;:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLKQPSAVL	LSVPLSVALP	REAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFQAGFDKAV	QVAVQYGFV	ADFVACAQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLVCSSNLPERSAGSVIAFCLVLLRMGFGPLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					

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a288                    PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADFVACAQVF  
                               130            140            150            160            170            180

m288.pep            DTX  
                               ::  
 a288                    NAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

g290.seq  
 1    atggcaaaaa tgatgaaatg ggcggtctgtt gcggcggtcg cggcggcagc  
 51    ggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata  
 101    ttacggaagc ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg  
 151    ggcgagattt cgccgtccaa cctgggtatcg gtcggcgcg caggcttcggg  
 201    gcagattaaa aagctttatg tcaaaactcg gcaacaggtc aaaaaggcg  
 251    atttgattgc ggaaatcaat tcgaccacgc agaccaacac gatcgatatg  
 301    gaaaaatcca aattggaaac gtatcaggcg aagctggtgt ccgcacagat  
 351    tgcattgggc agcgcgga aaatataa gcgtcaggcg gcgttggga  
 401    aggatgatgc gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt  
 451    gccgcgcgca aagccaatgt tgccgagttg aaggctttaa tcagacagag  
 501    caaaatttcc atcaataacc ccgagtcgga tttgggtac acgcgcatta  
 551    ccgcgacgat ggacggcacg gtggtggcga ttcccgtgga agaggggcag  
 601    actgtgaacg cggcgcgatc tacgccgacg attgtccaat tggcgaatct  
 651    ggatatgatg ttgaacaaaa tcgagattgc cgagggcgat attaccaagg  
 701    tgaaggcggg gcaggatatt tcgtttacga tttgtccga accggtatcg  
 751    ccgattaagg cgaagctcga cagcgctcga cccgggtgta ccacgatgtc  
 801    gtcggggcgc tacaacagca gtacggatac ggcttccaat gcggtctatt  
 851    attatgcccg ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg  
 901    atgacgacgc agaatacggg tgaatcgac ggtgtgaaaa atgtgttgc  
 951    tattccgtcg ctgaccgtga aaaatcgcg cggcaaggcg ttcgtacgcg  
 1001    tgttgggtgc ggacggcaag gcagtggaa cgcgaatccg gaccgggatg  
 1051    aaagacagta tgaataccga agtgaaaagc ggggtgaaag agggggacaa  
 1101    agtggtcac tccgaaataa ccgccgccga gcagcaggaa agcggcgaac  
 1151    gcgccttagg cggcccgccg cgccgataa

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

g290.pep  
 1    MAKMMKWAAV AAVAAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT  
 51    GEISPSNLVS VQAQASGQIK KLYVKLGQQV KKGDLIAEIN STQTNTIDM  
 101    EKSKLETYQA KLVSAQIALG SAEKKYKROA ALWKDDATSK EDLESAQDAL  
 151    AAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEGQ  
 201    TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT  
 251    PIKAKLDSVD PGLTMSGG YNSSTDASN AVYYYARFV PNPDKLATG  
 301    MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM  
 351    KDSMNTVEKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

m290.seq (partial)  
 1    ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA  
 51    ACTCGGCAAA CAGGTTAAAA AGGGCGATTT GATTGCGGAA ATCAATTGCA  
 101    CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAAACGTAT  
 151    CAGGCGAAGC TGGTGTGCGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA  
 201    ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG  
 251    ATTTGGAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC  
 301    GAGCTGAAGG CTTAATCAG ACAGAGCAAA ATTTCCATCA ATACCGCCGA  
 351    GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG  
 401    TGCGGATTCT CGTGGAAGAG GGCAGACTG TGAACGCGGC GCAGTCTACG  
 451    CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA  
 501    GATTGCCGAG GGCATATTA CCAAGTGAA GGCGGGGCAG GATATTCGT  
 551    TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC  
 601    GTCGACCCCG GGCTGACCAC GATGTCGTCG GCGGTTTACA ACAGCAGTAC  
 651    GGATACGGCT TCCAATGCGG TCTACTATTA TGCCGTTTCG TTTGTGCCGA

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```

701 ATCCGGACGG CAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAATAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TCGCGGTGTT GGGTGGCGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

m290.pep (partial)

```

1 ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTL NTEKSKLETY
51 QAKLVSAQIA LGSAAEKKYR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYSSTDTA SNAVYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLI PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep          10          20          30
                  VSVGAQASGQIKILYVKLGQVKKGDLIAE
g290              30          40          50          60          70          80
                  POAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQVKKGDLIAE

m290.pep          40          50          60          70          80          90
                  INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYRQAALWKENATSKEDLESAQD
g290              90          100         110         120         130         140
                  INSTTQNTIDMEKSKLETYQAKLVSAQIALGSAEKKYRQAALWKDDATSKEDLESAQD

m290.pep          100         110         120         130         140         150
                  AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
g290              150         160         170         180         190         200
                  ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVAIPEEGQTVNAAQST

m290.pep          160         170         180         190         200         210
                  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
g290              210         220         230         240         250         260
                  PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS

m290.pep          220         230         240         250         260         270
                  GGYSSTDTASNAVYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
g290              270         280         290         300         310         320
                  GGYSSTDTASNAVYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG

m290.pep          280         290         300         310         320         330
                  KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
g290              330         340         350         360         370         380
                  KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG

m290.pep          PPRRX
                  ||||
g290              PPRRX
                  390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1  ATGGCAAAAA TGATGAAATG GCGGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTCAGGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AACTTTATG TCAAACTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCCTAAA GAAGATTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATT
551 CCGCAACGAT GGACGGCAGC GTGGTGGCGA TTCTCGTGA AGAGGGGCAG
601 ACTGTGAACG CCGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAAATCGAC GGTGTGAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CCGCAGGGCG TTTGTGCGCG
1001 TGTGGGTGTC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CCGCCGCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1  MAKMMKWAAY AAVAAAAVWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDLIAEIN STSQTNTLNT
101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAANKANVAEL KALIROSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARFV PNPDKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*
```

m290/a290 98.2% identity in 334 aa overlap

					10	20	30
m290.pep					VSVGAQASGQIK	LYVKLGQOV	KKGDLIAE
a290	PQAAYITETVRR	GDISRTVSAT	GEISPSNLVS	VSVGAQASGQIK	KLYVKLGQOV	KKGDLIAE	
	30	40	50	60	70	80	
		40	50	60	70	80	90
m290.pep	INSTSQTNTLN	TEKSKLETYQ	AKLVSAQIAL	GSAEKKYKRQ	AALWKENATS	KEDLESAQD	
a290	INSTSQTNTLN	TEKSKLETYQ	AKLVSAQIAL	GSAEKKYKRQ	AALWKDDATA	KEDLESAQD	
	90	100	110	120	130	140	
	100	110	120	130	140	150	
m290.pep	AFAAAKANVAE	LKALIROSKIS	INTAESELGY	TRITATMDGT	VVAILVEEGQ	TVNAAQST	
	:						
a290	ALAAAKANVAE	LKALIROSKIS	INTAESELGY	TRITATMDGT	VVAILVEEGQ	TVNAAQST	
	150	160	170	180	190	200	
	160	170	180	190	200	210	
m290.pep	PTIVQLANLDM	MLNKMQIAEG	DITKVKAGQD	ISFTILSEPDT	PIKAKLDSVD	PGLTTMSS	
a290	PTIVQLANLDM	MLNKMQIAEG	DITKVKAGQD	ISFTILSEPDT	PIKAKLDSVD	PGLTTMSS	
	210	220	230	240	250	260	
	220	230	240	250	260	270	

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```

m290.pép      GGYNSSTDTASNAVYYYARSFVNPDPGKLATGTTQNTVEIDGVKNVLIIPSLTVKNRGG
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDTASNAVYYYARSFVNPDPGKLATGTTQNTVEIDGVKNVLIIPSLTVKNRGG
                270      280      290      300      310      320

                280      290      300      310      320      330
m290.pép      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISSEITAAEQQESGERALGG
                :|||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISSEITAAEQQESGERALGG
                330      340      350      360      370      380

m290.pép      PPRRX
                |||||
a290          PPRRX
                390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaactct atggtgtcag cccgaccgtg ccaaagcgtg gacggatttg
601 atcggtaaag gcaaattccc ggtcggcggc agcatctgcg acaatcccg
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tcccaacgg gcgcacccaa agcggttaca gccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pép
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSVAAALKAR
51  LEKTYSAQDL KVLVSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGEIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCCF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNFVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPD
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTTG AAAGTGTGTA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAA GAAGTGGCGG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCTGCA CCCCAGATGC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATCGGTAAAG GCAAATCCC GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCC

```



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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence &lt;SEQ ID 1220; ORF 292&gt;:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVAASLKAR
 51 LEKTYSAQDL KVLSVSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:  
 Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEP AVKAESAGKSVAASLKARLEKTYSAQDL					
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESA VKAESAGKSVAASLKARLEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLSVSETPVKGIYEVVVSQRQIIYTDAEGGYMFV GELINIDTRKNLTEERAADLNKIDF					
g292	KVLSVSETPVKGIYEVVVSQRQIIYTDAEGGYMFV GELINIDTRKNLTEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGFVPVGGSIDCNPVAETTS LGEQFGFNGTPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGFVPVGGSIDCNPVAETTS LGEQFGFNGTPTLRLPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPOX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGC GCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTT
451 TGCAAACGCT TGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTT CCGGCCGTGA CCGCGATGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTCAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCC GGTCCGCCGC AGCATCTCGC ACAATCCCGT
651 CGCGGAAACC ACTTCTTGG GCGAACAATT CGGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCG
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292. pep
  1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
  51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFGELIN
 101  IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLKV AVFSDPDCPF
 151  CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
 201  MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSMP
 251  QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

      10      20      30      40      50      60
m292. pep MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
a292      MKTKLIKILTPFTVLPLLACGQTPVSNANAEPVKAESAGKSPAASLKARLEKTYSAQDL
      10      20      30      40      50      60

      70      80      90     100     110     120
m292. pep KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFGELINIDTRKNLTEERAADLNKIDF
a292      KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFGELINIDTRKNLTEERAADLNKIDF
      70      80      90     100     110     120

      130     140     150     160     170     180
m292. pep ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
a292      ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFMMPIAGLHPDA
      130     140     150     160     170     180

      190     200     210     220     230     240
m292. pep ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
a292      ARKAQILWCQPDRAKAWTDWMRKGKFPVGGSSICDNPVAETTSLSGEQFGFNGTPTLVFPNG
      190     200     210     220     230     240

      250     260
m292. pep RSQSGYSMPQLEEIIRKNQX
a292      RSQSGYSMPQLEEIIRKNQX
      250     260
  
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
  1  atgcgtatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
  51  gggttcgggt gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
 101  gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
 151  tggcatcggg tgccggcggt caagtcgaat cggcggacgc gtggcgtgaa
 201  gccgttgaaa aaaccttatc tggcgagggg ggcggaatgc agatgcaggc
 251  gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
 301  ccgaggcggt gcgggaagcg gtatgcggac atcgggggcg atagtatac
 351  aatccgtatc cgagttttcc ggttgagca tcgtatgagt atttatgccg
 401  tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcggt
 451  ttttttgaag tgctggtttt gtccgtcctg catacgggac ggggtgcgcg
 501  cgaggcgccg gcggaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
 551  tgatgccgtt tgcggtcgga ctgctgttcg ccagggggaa tctagagtcg
 601  actgcagcag catgccctc...
  
```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
  1  MRITCAPMSL LSAAVSVRA VRTSSNRFP ALRRYSAFRP TIFPKPAGTP
  51  WHRVRRFSN RRTRGVKPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
 101  PRCCKRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
 151  FFEVLVLSVL HTGRVSREAR REVEKAMSyr AVRMPFAVG LLFARGTLES
 201  TAAACP...
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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```

m294.seq
1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTTCGGGT GTGAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATTATCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
151 TGGCATCGGG TCGGCGGTT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
451 TT'TTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCTCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTACGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC GGTGCGTTGG
751 TCGAAATACA TACAGCCGT CGTCTTACC CATATGCTGC TGATTGTCTT
801 TT'TGGCAAAA GCGATGTTT ATATCAGCTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

```

m294.pep
1  MRITCAPMSL LSAAVWSIRV VRTSSNRFFA AFRRYSAFQP TIFPKPADTP
51  WHRVRREFKS RMRGGKPLK KPYRPRGGC RCRRAWTALS HNAIERARES
101 PRRCGKRYAD IGGSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPEVVG LLFASGIVMA
201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVMG
251 SKYIHAVVET HMLLIVFLAK AMFYISW*

```

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFFAALRRYSAPRTIFPKPAGTPWHRVRREFKS					
m294	MRITCAPMSLLSAAVWSIRVVRTSSNRFFAALRRYSAPRTIFPKPAGTPWHRVRREFKS					
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARESPRRCGKRYADIGGSDTIRI					
m294	RMRGGKPLKKPYRPRGGCRRRAWTALSHNIAERARESPRRCGKRYADIGGSDTIRI					
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
m294	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVVLVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
g294.pep	AVRVMPEVVGLLFARGTLESTAAACP					
m294	AVRVMPEVVGLLFASGIVMAANRYLSILGEFFATSFGTMLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

```

a294.seq
1  ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
51  GATTTCGGGT GTGAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
101 GATTATCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGCACGCCT
151 TGGCATCGGG TCGGCGGTT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
201 GCCGTTGAAA AAACCTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
351 AATCCGTATC CGAGTTTTC GGTGAGTA CCGTATGAGT ATTTATGCCG
401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCTTTGT CGGCGGCGTG
451 TTTT'TGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCTCG
501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTACGGG
551 TGATGCCGTT TGTGGTCGGA CTGCTGTTTCG CCAGCGGCAT CGTGATGGCG
601 GCAAACCGCT ATCTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

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701 TCGCCATCGC CGTCGTCAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG  
 751 TCGAAATACA TACACACCGT CGTCTTTACC CATATGCTGC TGATTGTCTT  
 801 TTTGCAAAA GCGATGTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294 . pep  
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFFA AFRRYSAFRP TIFPKPAGTP  
 51 WHRVRRFKSN RRTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES  
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV  
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMPEVVG LLFASGIVMA  
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW  
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW\*

m294/a294 94.9% identity in 277 aa overlap

m294 . pep	10	20	30	40	50	60
	MRITCAPMSLLSAAVWSIRVVRTSSNRFFA AFRRYSAFQPTIFPKPADTPWHRVRRFKSN					
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFFA AFRRYSAFRPTIFPKPAGTPWHRVRRFKSN					
	10	20	30	40	50	60
m294 . pep	70	80	90	100	110	120
	RRMRGGKPLKKPYRPRGGGCRRAWTALSHNIAERARES PRRCGKRYADIGDDSDTIRI					
a294	RRTRGGKPLKKTYPRAECRCRRARTALSHNIAERARES PRRYGKRYADIGDDSDTIRI					
	70	80	90	100	110	120
m294 . pep	130	140	150	160	170	180
	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGV FFEVLVLSVLHTGRVSREARREVEKAMSYR					
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGV FFEVLVLSVLHTGRVSCEARREVEKAMSYR					
	130	140	150	160	170	180
m294 . pep	190	200	210	220	230	240
	AVRVMPEVVG LLFASGIVMAANRYLSILGEPFATSFGTML TLKILLAFSV LAHFAIAVVK					
a294	AVRVMPEVVG LLFASGIVMAANRYLSILGEPFATSFGTML TLKILLAFSV LAHFAIAVVK					
	190	200	210	220	230	240
m294 . pep	250	260	270			
	MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVVFTHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295 . seq  
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt  
 51 gttgccacgc cgccagcagt ttttccgcct cgtcttcgcc ccgataaacg  
 101 cgcgtgctgc cgcacacggc aaccggccgg cctccgatgc gtttttcaaa  
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg  
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc  
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggctgcggg  
 301 acggatcagg cggcggactt tcagataacc gttcagcgat tttccgaca  
 351 gccgcgcatt cgccaaaaac agcggcacac ccgctcgcgc gcattccttc  
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcggggc  
 451 gtgttcgcgc aaaaactgcc gtacccacgt tttttgtca tacggaagat  
 501 agcggcattg cgcacgcgga aacagaactt gcgcggttc ccgtcccgtc  
 551 ggggtcatct cgtcatcag cagcggcgca tcgggaaaac gccgcgcgaa  
 601 ctgcgcgtatc aagggtctgg cggcacgcgt ttctccgacc gaaacggcgt  
 651 gtatccaaac cgcgcggta acgggattcg gatcgggctt gccgaaacgc  
 701 tcgtccctat gcgcccggta tgcgggggca cttccggagc gtttgtccaa  
 751 ataacgccgt atccatatcg gcgcaagcag ccacaatata tcataaagcc  
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc  
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

g295.pep  
 1 MLGMRHDDQ QGIAAILLPR RQOFFRLVFA PINARAAAHG NRPASDAFFK  
 51 LPRQRHFHVR RHQVVFQIAA HLHGCRAQFR QPRRIRLRLR QTARQSGCG  
 101 TDQAADFQIT VQRFFRQPRI RQQRHTRSP AFLHQIGPDF GFHQNAEHRA  
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PSRRGHLRHQ QRRIGKTPPQ  
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRMRL AETLVPMRPV CRGTSGAFVQ  
 251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq  
 1 ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGCGCATCG CCGCGATATT  
 51 GTTGCCACGC CGCCAGCAGT TTTCCGCGCT CGTCTTCACC CCGATAAACG  
 101 CGCGTGCTGC CGCACACGGC AACCGGCCCG CCTCCGATGC GTTTTCAAA  
 151 CTGCCCGGCC AGCGTTTTCA TCTGTCCGA CGGTATGATG TCGTATTGG  
 201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTCGC CAACCGCGCC  
 251 GCATCCGCCT CTGTCTGCGC CAGACACCCC GTCAGCGAAG CGGCGGCAGG  
 301 ACGGATCAGG CGCGGCACTT TCAGATAACC GTTCAACGAT TTTCCGACA  
 351 GCCCGGCATT CGCCAAAAC AGCGGCACAC CCGCGCGCCG GCATTCCCTC  
 401 ATCAGGTTGG GCCAGATTTC GGTTTCCATC AAAATGCCGA ACATCGGGCG  
 451 GTGTTCCGCG AAAAAGTCC GTACCCACGT TTTTGTGCA TACGGAAGAT  
 501 AGCGGCATTG CGCATCGGGA AACAGAACTT CGCGGTTTC CCGCCCCGTC  
 551 GGGGTCTCAT GCGTCATCAG CAGCGCGGCA TCGGGAAGC GCCGCCGCA  
 601 CTGCGGTATC AAGGACTGGG CGGCACGCGT TTCTCCGACC GAAACGGCGT  
 651 GTATCCAAC CGCGCCGTA ACGGGATTTC GATACGGCTT GCCGAAACGC  
 701 TCGTCCCGAT CGGCCGATA TGCCGGGCA CTTCGGGAGC GTTTGTCAA  
 751 ATAACGCCGT ATCCATATCG CGCGAAGCAG CCACAATACA TCATAAGCC  
 801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC TGAACGGTTC  
 851 AGACGGCATT TCGGCAACGG AATCAAATAT CGTAG

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295.pep  
 1 MLGMRHDDQ QRIAAILLPR RQOFFRLVFT PINARAAAHG NRPASDAFFK  
 51 LPRQRHFHVR RYDVVFQIAA HLHGCRAQFR QPRRIRLRLR QTARQSGGR  
 101 TDQAADFQIT VQRFFRQPRI RQQRHTRAP AFPHQVGPDF GFHQNAEHRA  
 151 VFAQKLPYPR FFVIRKIAAL RIGKQNLRGF PPRRHLRHQ QRRIGKTPPQ  
 201 LAYQGLGGTR FSDRNGVYPN RAGNGIRIRL AETLVPMRPI CRGTSGAFVQ  
 251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV XTVQTAFRQR NQIS\*

m295/g295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMRHDDQ	QRIAAILLPR	RQOFFRLVFT	PINARAAAHG	NRPASDAFFK	LPRQRHFHVR
g295	MLGMRHDDQ	QGIAAILLPR	RQOFFRLVFA	PINARAAAHG	NRPASDAFFK	LPRQRHFHVR
	70	80	90	100	110	120
m295.pep	RYDVVFQIAA	HLHGCRAQFR	QPRRIRLRLR	QTARQSGGR	TDQAADFQIT	VQRFFRQPRI
g295	RHQVVFQIAA	HLHGCRAQFR	QPRRIRLRLR	QTARQSGCGT	TDQAADFQIT	VQRFFRQPRI
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
g295	RQQRHTRSP	AFPHQVGPDF	GFHQNAEHRA	VFAQKLPYPR	FFVIRKIAAL	RIGKQNLRGF
	190	200	210	220	230	240
m295.pep	PPRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRIRL	AETLVPMRPI
g295	PSRRGHLRHQ	QRRIGKTPPQ	LAYQGLGGTR	FSDRNGVYPN	RAGNGIRMRL	AETLVPMRPV
	250	260	270	280	290	
m295.pep	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	XTVQTAFRQR	NQISX
g295	CRGTSGAFVQ	ITPYPYRRKQ	PQYIIPLEH	LSISCKTNAV	RTVRTAFRQR	NQIS

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCGGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTGCG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCCGCGC
251 GCATCCGCTT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAC AGCGGCACAC CCGTCCGCGC GCATTCCTTC
401 ATCAGATTGG GCCAGATTTC GGTTCATC AAAATGCCGA ACATCGGGCG
451 GTGTTCCGCG AAAAATGCC GTACCCACGT TTTTGTGCA TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCACTC GCGTCATCAG CAGCGGCGCA TCGGAAAAC GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TTCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCGATA TGCAGGGGCA CTCCCGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ OGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLEF RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQRSGGR
101 TDQAADFQIT V*RRFRQPRI RQQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FFVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPO
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

m295.pep	10	20	30	40	50	60
	MLGMARHDDQORIAAILLPRRQOFFRLVFTPINARAAAHGNRPASDAFFKLPQRQFHLEF					
a295	MLGMARHDDQOGIAAILLPRRQOFFRLVFTPINARAAAHGNLPVSDAFFKLPQRQFHLEF					
	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
	RYDVVFGLIAHLHGCRAQFRQPRRIRLRLCLRQTFRQRSGGRTDQAADFQITVQRFFRQPRI					
a295	RHQVVFGLIAHLHGCRAQFRQPRRIRLRLCQTARQRSGGRTDQAADFQITVXRFFRQPRI					
	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
	RQQRHTRAPAFPHQVGPDEFGFHQNAEHRVFAQKLPYPRFFVIRKIAALRIGKQNLRGF					
a295	RQQRHTRAPAFHLHQIGPDFGFHQNAEHRVFAQKLPYPRFFVIRKIAALCIRKQNLRGF					
	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
	PPRRGHLRHQRRIGKTPFQLAYQGLGGTRFSDNRGVYPN RAGNGIRIRLAETLVPMRPI					
a295	PSRRGHLRHQRRIGKTLPLAYQRLGGTRFPDRNGVYPN RAGNGIRIRLAETLAPMRPI					
	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
	CRGTSGAFVQITPYPYRRKQPQYIIPLEHLSISCKTNAVXTVQTAFRQRNQISX					
a295	CRGTSGAFVQITPYPYRRKQPQYIIPLEHLSISCKTNAVRTVRTAFRQRNQISX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
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51  GCTTGCCGTT TCGATTATTC TGGTGTcgcG GGCATACATT Gcttcgacag
101  aggggaccga ggcgctcaga ccgcAGCGCG Tggaacaaa ACTGCCGCCG
151  CTGTCTtTGGg ggcgcaacgg CGTtcagacy gcaTATTGGG TGCAGGAGGC
201  GGTGcagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251  CGCGGGGacga gattgCCcga ATcacGGAAA aataTggcgG CGAAGCCGAT
301  TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCGA
351  CGGCGAGTGC CGCGAAGTGC AGTTTtttaC CGACGAAGAC GGCAGCGCA
401  aTc tGGTTCG TTTGGAAAA AAAGGCGGCA TATGGCGCGG GTCGGCTTCT
451  GATGCGGATA TGAAGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501  GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551  AATCCTTAAG CGGGATTTTT GCCGGCGGCT TCAGCCTTGA CGGTTTGAAG
601  GAAAGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651  GCAAGGTGGC GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701  CAAACCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751  GGC AATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801  CAAATCgag CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851  GTA TGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901  GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951  CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCA
1051 CAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGAGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

```

g297.pep
1  MAVFPLSAKH RYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101  LRHLRADQSV HVLVGGDQSA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151  DADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201  EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251  GNY YDEDRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301  AAPQQTpVRA SADGVITFKG RKGyGNAVM IRHANGVETL YAHLSAFSQA
351  QGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401  DKAFAFAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

```

m297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTCCCGTT TCGATTATTT TGGTGTcgcG GGCATACATT GCTTCGACAG
101  AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151  CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201  GGTGCAGCCG GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251  CGCGGGACGA GATTGCCCGA ATCAGGAAA AATATGGCGG CGAAGCCGAT
301  TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTGG TCGGCGGCGA
351  CGGCGGCGCG CGCGAAGTGC AGTTTtttaC CGACGAAGAC GGCAGGCGCA
401  ATCTGGTTCG TTTGGAAAAG AAAGGCGGCA TATGGCGCGG GTCGGCTTCT
451  GAGGCGGATA TGAAGGTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501  GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATCCGCG
551  AATCCTTAAG CGGGATTTTC GCCGGCGGCT TCAGCCTTGA CGGTTTGAAG
601  GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651  GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701  CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751  GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801  CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851  GTATGCACCC CATCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901  GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951  CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGCAGGCG
1051 GAAGGCAATG TCGCGGCGCG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGC CGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCGGAATT GACGCGAGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

```

m297.pep
1  MAVFPLSAKH RYALRALAV SIILVSAAYI ASTERTERVV PORVEQNLPP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101  LRHLRADQSV HVLVGGDQGA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151  EADMKVLPTL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHQQVA AGDILAAEVV KGSTRHQAFY YRSDKEGGGG  
 251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY  
 301 AAPQGTTPVRA SADGVITFKG RKGgyGNAVM IRHANGVETL YAHLSAFSQA  
 351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA  
 401 DKAFAAQKQ KADALLARLR GIPVTVSQSD \*

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQVEQNLPPLSWGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQVEQKLPPLSWGNGVQT					
	10	20	30	40	50	60
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
m297.pep	REVQFFTDEDEGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVVPV					
g297	REVQFFTDEDEGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVVPV					
	130	140	150	160	170	180
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHQQVAAGDILAAEVVKGGTRHQAFY					
g297	EIRESLSGIFAGRFSLDGLKEGDAVRLLYDSLYFHQQVAAGDILAAEVVKGGTTHQAFY					
	190	200	210	220	230	240
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
m297.pep	AAPQGTTPVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTTPVRASADGVITFKGRKGGYGNVAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
m297.pep	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPVNPVSVVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

a297.seq

1 ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC  
 51 GCTTGCCGTT TCGATTATTT TGGTGTGCGC GGCATACATT GCTTCGACAG  
 101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAAA ACTGCCGCCG  
 151 CTGTCTTGGG GCGGCAGCGG TGTTTCAGACG GCATATTGGG TGCAGGAGGC  
 201 GGTGCAGCCA GCGGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG  
 251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT  
 301 TTGCGGCATT TGGTGCCTGA CCAGTCGGTT CATGTTTTGG TCGGCGCGCA  
 351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTTAC CGACGAAGAC GCGGAGCGCA  
 401 ATCTGGTGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT  
 451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTGC TGGTCAAAAC  
 501 GTCGGCGCGC GGTTCGCTGG CGCGGCGCGA AGTGCCCGTC GAAATTCGCG



```

551 AATCCTTAAG CGGGATTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGC GCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGCGCGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGGTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTCAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTCT GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGGC
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

a297.pep

```

1 MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV RQORVEQKLPP
51 LSWGGSGVQT AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGG REVQFFTED GERNLVALEK KGGIWRSSAS
151 EADMKVLP LRSVVVKT SAR GSLARAEV PV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHQQVA AGDILAEV V KGGTRHQAFY YRSDKEGGGG
251 GNYDEDGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGT PVRASADGVIT FKG RKG GYGNV M IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERV RQORVEQKLPP LSWGGSGVQT					
a297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERV RQORVEQKLPP LSWGGSGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG					
a297	AYWVQEAQVP GDSDLADVLAR SGMARDEIAR ITEKYGGEAD LRHLRADQSV HVLVGGDGGG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTED GERNLVALEK KGGIWRSSASEADMKVLP LRSVVVKT SARGSLARAEV PV					
a297	REVQFFTED GERNLVALEK KGGIWRSSASEADMKVLP LRSVVVKT SARGSLARAEV PV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHQQVAAGDILAEVVKGGTRHQAFY					
a297	EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSLYFHQQVAAGDILAEVVKGGTRHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
a297	YRSDKEGGGGNYYDEDGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGT PVRASADGVIT FKG RKG GYGNV M IRHANGVETL YAHLSAFSQAEGNVRGGEVI					
a297	AAPQGT PVRASADGVIT FKG RKG GYGNV M IRHANGVETL YAHLSAFSQAEGNVRGGEVI					
	310	320	330	340	350	360

689

	370	380	390	400	410	420
m297 . pep	GFVVGSTGRSTGPHLHYEARINGQVPNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQVPNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297 . pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298 . seq

```

1 ATGAAAACT TTCTTCCCT TTTCCCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCTCG TCCGGCGAAA cgcggccgac ggCTCAAGAC GGCAGTTCGG
251 CATCTTGGAA GCCTGAAGCC GCCGCATCCG AAGCGCGCCC GCCGCGCGG
301 GGAACAGAAT GGAACAAGG CACCGAAGCC GCCGCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCCCGGAG ATTGCTGAT GCAGGGCGTT GCGCTTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTGAAT GGCGGAAAAC
501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCG GAACGACCCG TGGGATTTC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCTTGGAA GCGGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAAA ATCATCTGA TTCCACCGC
801 GCAACACTG AGCGGCGGGA AAGGCGGCTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GAAAAAATA ATGGAATAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298 . pep

```

1 MKNFLSLPAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPFAG
101 GTEWKQGTEA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIER TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AANTHRVQVW NLGIPYMKKV KLDGQMRYLD
251 KLLSEHLKGG IILPTAQTG SGGKGRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298 . seq

```

1 ATGAAAACT TTCTTCCCT TTTCTCTCC ATACTGATGT CTGCCCTGAT
51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCTCG TCCGGCGAAA CGCCGCGGAC GGCTCAAGAC GGCAGTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAACAAGA CACCGAAGCC GCCGCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCCGCG ACTCGCTGAT GCAGGGCGTT GCCCTTTCG
401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTGAAT GGCGGAAAAC
501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCTTGGAA GCGGCACACA CGCACCGCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATGCTTT CGGAACATT GAAAGGCAAA ATCATCTGA TTCCACCGC
801 GCACACCTG AGCGGCGGGA AAGACGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GCAAAAATA ATGGAATAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

m298.pep  
 1 MKNFLSLFSS ILMSALIAVW FSONPINAYW QQTYHRNSPL EPLAAYGWNW  
 51 SGAAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG  
 101 ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS  
 151 KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL  
 201 KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGIPIYMKA KLDGQMYLD  
 251 KLLSEHLKGI IILPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA  
 301 EGQKLLAAKI MEKIVFEPST QPSSTQP\*

m298/g298 94.8% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWNWRSAAALQENAY					
g298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWNWRSAAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
g298	ALSDGIKTFISGETPPTAQDGGSDMPPEAAASEAAPAGGETEWKQDTEAAAVRSGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQYQYIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
g298	FAGDSLMOGVAPFVQKSLKQYQYIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWFDFPVGKLYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGIPIYMKA					
g298	LAVFLGPNDPWFDFPVGKRYLKFASDEWAQEYLKRVDRIEAAHTRVQVVWLGIPIYMKV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMYLDKLLSEHLKGI IILPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
g298	KLDGQMYLDKLLSEHLKGI IILPTAQTLSGGKGRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
g298	EGQKLLAEKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

a298.seq  
 1 ATGAAAACT TTCTTCCCT TTTGCCTCC ATACTGATGT CTGCCCTGAT  
 51 TGCCGTGTGG TTCAGCCAAA ACCCATCAA CGCCTACTGG CAGCAGACCT  
 101 ACCACCGCAA CAGCCCCTC GAACCGCTT CCGCTACGG ATGGTGGCGG  
 151 AGCGGTGCGG CATTGCAAGA AACGCCTAC GCCCTTTCAG ACGGCATCAA  
 201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCAGTTCGG  
 251 CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC  
 301 GAAACAGAA GGAACAAAA CACCGAAGCC GCCCGCTCC GAACAGGGGA  
 351 CAAAGTCTTT TTCGCCGCG ACTCGCTGAT GCAGGGCGTT GCACCCTTCG  
 401 TGCAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC  
 451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC  
 501 GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT  
 551 TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC  
 601 AAATTCGCTT CCGACGAATG GCGCGAAGAA TACCTGAAAC GCGTCGACCG  
 651 CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA  
 701 TCCCTTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

```

751  AAACTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
801  GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851  ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901  GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTGA
951  ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298 . pep
  1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101  ETEWKQNTA AAVRTGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESVNLS
151  KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201  KFASDEWAE YLKRVDRIE AAHTHYVQVW WLGIPYMKKA KLDGQMRYL
251  KLLSEYLKGI ILIPTAHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301  EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298 . pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298 . pep	ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGSDMPSEAAAPETAPQTGETEWKQNTA AAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298 . pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298 . pep	LAVFLGPNDPWFDFPVGKLYLKFADEWAEYLKRVDRILEAAHTRVQVWVWLGIPYMKKA					
a298	LAVFLGPNDPWFDFPVGKRYLKFADEWAEYLKRVDRILEAAHTHYVQVWVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298 . pep	KLDGQMRYLDKLLSEHLKGIILIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
a298	KLDGQMRYLDKLLSEYLKGIILIPTAHTLSGGKDRYTDVNVNGKPVRYRSKDGIFHTA					
	250	260	270	280	290	300
	310	320				
m298 . pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299 . seq
  1  ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
 51  GGCAGAAGCC CTGCCCCTCG CCTCCGTCAG CCCCGACACC GTTACCGTTT
101  CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151  AACGCGCGCG CCTCGCCTTG GATGAAAAAA CTCCGATCCG TCGCACAAAG
201  CAGCGGCGAG GCCTTCCGCA TCCTGCAAAAT CGGCGACTCG CATACCGCGC
251  GCGACTTCTT TACCGACGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301  GACGCGCGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351  GCGCGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCAAC AGCAGGAACA
401  ATACCGGAGA TTTCCCGCTC GGCGGCATCC TCGCCCAAAC CGGACGCGGC
451  GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

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g299	MNPKHFIASFALFAATQAEALPVASVSPDVTVTSPSAPYTDNGLLTDYGNAAASPMWKK
	10 20 30 40 50 60
m299.pep	LQSVAQGSGETFRILQIGDSHTAGDFFTDLSLRKRLQKTWGDGGIGWVYPANVKGQORMAAV
g299	LRSLVAQGSGEAFRLQIGDSHTAGDFFTDALSRKRLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAQTL
g299	RHSGNWQSFTRNNTGDFPLGGILAHGTSGGSMTLTASDGIASKQRVSLFAKPLLAQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGRPVRLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
g299	LIIGAPESLKNLTGVCGRPVLLTEVQQMQRVARQGQTMFWSWQAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVFHSAKGYRRAAEMLADSLEELVRSAAIRQX
g299	GWAAKDGVFHSAQGYRRAAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

a299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTITTC	GCCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTCG	CCTCAGTCAG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCCGC	CCCCTACACC	GATACAAACG	GGCTGCTGAC	CGACTACGGC
151	AACGCCTCCG	CCTCGCCTTG	GATGAAAAAA	CTCCAATCCG	TCGCACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAAC	GCCTACAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TTACCCCGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGCCGTC	CGGCACAACG	GTAACCTGGCA	AAGCCTCACC	AGCAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCCACAC	CGGCAGCGGC
451	GGCAGCATGA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCAAACCCC	TGCTTGCCGA	ACAAACCCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGCGGCT	GGCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATC	GAAAATCCCG	CCGGCGGCAT	TACCGTTTCC	GCGATGGGCA
701	TCAACGGCGC	ACAATTAACC	CAGTGGTCGA	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCAAACGGG	CGCCGATCTA	GTCATCCTTG	CCTACGGTAC
801	CAACGAAGCC	TTCGGCGACA	ACATCGACAT	TGCCGATACC	GAACAGAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTACCTGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATGCGG
951	CACACGCCCC	GTCCGCCTGA	CCGAAGTCCA	ACAGATGCAG	CGGCGCATCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	GATGGGCGGC
1051	GTTTGCAGCA	TGAAAACTG	GCTCAACCAC	GGATGGGCGC	CCAAAGACGG
1101	CGTACACTTT	TCCGCCAAAG	GCTACCAACG	GTCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAACTCGTC	CGCTCCGCTG	CAATCAGGCA	ATAA

This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
  1  MNPKHLLIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
 51  NASASPWMKK LQSVAGGSGE TFRILQIGDS HTAGDFFTDS LKRRLQKTWG
101  DGGIGWVYPA NVKGQORMAAV RHNGNWQSLT SRNNTGDFPL GGILAHGSG
151  GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201  AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251  NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301  LIIGAPESLK NTLGVCGRTP VRLTEVQQMQ RRIARQQQTM FWSWQAMGG
351  VCSMKNLNLH GWAADGVHF SAKGYQSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

m299.pep	10	20	30	40	50	60
	MNPKHLLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHLLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
m299.pep	70	80	90	100	110	120
	LQSVAGGSGETFRILQIGDSHTAGDFFTDSLKRRLQKTWGDGGIGWVYPANVKGQORMAAV					
a299	LQSVAGGSGETFRILQIGDSHTAGDFFTDSLKRRLQKTWGDGGIGWVYPANVKGQORMAAV					
	70	80	90	100	110	120
m299.pep	130	140	150	160	170	180
	RHNGNWQSLTSRNNTGDFPLGGILAHGSGSMTLTASDGIASKQRVSLFAKPLLAEQTL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHGSGSMTLTASDGIASKQRVSLFAKPLLAEQTL					
	130	140	150	160	170	180
m299.pep	190	200	210	220	230	240
	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
m299.pep	250	260	270	280	290	300
	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFNGDNIDIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
m299.pep	310	320	330	340	350	360
	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRVARQQQTMFWSWQAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRRIARQQQTMFWSWQAMGGVCSMKNLNLH					
	310	320	330	340	350	360
m299.pep	370	380	390			
	GWAADGVHFSAGKYRRAAEMLADSLEELVRSAAIRQX					
a299	GWAADGVHFSAGKYQSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
  1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
 51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101  TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151  GCCTCTGCCG TCGGTGCGTA TTTTCGACTA TCCGTCCCCG ATCCGCGTCC
201  TGTGTTGGGCG AAAGGACGTG CCGATGACGG TTTGATTACAC GTTGTCAGCC
251  TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301  TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGTTTCTT TATTGGGCGT
```

```

351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAATGCG TTTTATATGG
701 CAGCCAGTAC GTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTGTGTGT
1001 TTGCGCTGCC GGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTGTGCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTAA TTTTAATTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCGCGCAA TGGCGGTAA
1301 CTGCGCGGAT TTTCGTCCTT ATGCTGATGT TGGCCGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCG GGCTGATTAT GGCACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TTCTGCATT GGTATTGT
1551 TTTGGGCTG CCCGTCGGT CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRVGA KGRADDGLIH VVSLLDADGL IKILHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLISALM RLLLTSPRK LTTFMVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLALI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVNVAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAVFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAO WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNIIITPM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIANIAL FCIWVFLGL PVGPGTPTFY PVP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCCGACTA TCCGTCCTCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCCGGCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTGCT
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CCTTATCAAT CAGATTGTG ACAAGAAGAA AAAGACATTC GGCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GCGGTGGTGT
851 TTGTTGCCCT ATCCGCCCTA TTGGCTTGGG GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTTTAAA
951 ATCGATTGTT GTTTTATTTT TCTGTGTTG TGCATGyCG GGCmTTGTTT
1001 ATGGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

```



```

1051 ATGGCCGAAT CGATGAGTAC TCTGGsGCTT TmTTTGswCA kCATCTTTTT
1101 TGCCGCACAG TTTGTCGCAT TTTTAAATTG GACGAATATT GGGCAATATA
1151 TTGCCGTTAA AGGGGCGACG TTCTTAAAAG AAGTCGGCTT GGGCGGCAGC
1201 GTGTTGTTTA TCGGTTTTAT TTTAATTGT GCTTTTATCA ATCTGATGAT
1251 AGGCTCCGCC TCCGCGCAAT GGGCGGTAAC TCGCGCGATT TTCGTCCCTA
1301 TGCTGATGTT GGCCGGCTAC GCGCCCGAAG TCATTCAAGC CGCTTACCGC
1351 ATCGGTGATT CCGTTACCAA TATTATTACG CCGATGATGA GTTATTTCGG
1401 GCTGATTATG GCGACGGTGA TCAAATACAA AAAAGATGCG GCGGTGGGTA
1451 CGCTGATTTC TATGATGTTG CCGTATTCCG CTTTCTTCTT GATTGCGTGG
1501 ATTGCCTTAT TCTGCATTG GGTATTGTT TTGGGCTGC CCGTCGGTCC
1551 CGGCGCGCCC ACATTCTATC CCGCACCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1256; ORF 302>:

m302.pep

```

1  MHSIYFFKEK QMSQTDTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAVGAYFGL SVPDRPVGA KGRADDGLIY IVSLLNADGF IKILTHTVKN
101 FTGFAPLGTV LVSLGVGIA EKSGLISALM RLLLTSPRK LTTFMVVFTG
151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 STIDPLLACI THQAAVVGPE ANWFFMVAST FVIALIGYFV TEKIVEPQLG
251 PYQSDLSQEE KDIRHSNEIT PLEYKGLIWA GVVFVALSAL LAWSIVPADG
301 ILRHPETGLV SGSPFLKSIV VFIFLLFALX GXVYGRVTRS LRGEQEVVNA
351 MAESMSTLXL XLXIFFFAAQ FVAFFNWTNI QGYIAVKGAT FLKEVGLGGS
401 VLFIGFILIC AFINLMIGSA SAQWAVTAPI FVPMLLAGY APEVIAQAYR
451 IGDVSTNIIT PMMSYFGLIM ATVIKYKDA GVGLISMML PYSAFFLIAW
501 IALFCIWVFEV LGLPVGPGAP TFYPAP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 302 shows 94.0% identity over a 533 aa overlap with a predicted ORF (ORF 302.ng)

from *N. gonorrhoeae*:

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTDTRDGRFLRTVEWLGNNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
g302	MHSIYFFKEKQMSQTDARRSGRFLRTVEWLGNNMLPHPVTLFIIFIVLLLIASAVGAYFGL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDRPVGAKGRADDGLIYIVSLLNADGFIKILTHTVKNFTGFAPLGTVLVSLGVGIA					
g302	SVPDRPVGAKGRADDGLIHVSLDADGLIKILTHTVKNFTGFAPLGTVLVSLGVGIA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLTSPRKLTTFMVVFTGILSNTASELG YVVLIPLSAII FHSLGRHPL					
g302	EKSGLISALMRLLLTSPRKLTTFMVVFTGILSNTASELG YVVLIPLSAII FHSLGRHPL					
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSANLFLSTIDPLLACITHQAA-----VVGPEANWFFMVASTFVI					
g302	AGLAAAFAGVSGGYSANLFLGTIDPLLAGITQAAQIIHPDYVVGPEANWFFMAASTFVI					
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW					
g302	ALIGYFVTEKIVEPQLGPGYQSDLSQEEKDIRHSNEITPLEYKGLIWAGVVVVALSALLAW					
	250	260	270	280	290	300
	300	310	320	330	340	350

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>>:

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

a302.ppep

1 MHSIYFFKEK QMSQTDQTRD GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI

51 ASAAGAYFGL SVPDRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN

101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTKSPRK LTTFMVVFTG

698

```

151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMEA SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIIIPMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QRDGRFLRTVEWLG	NMLPHPVTLFII	FIVLLLIASAVG	AYFGL	
a302	MHSIYFFKEKQMSQTD	QRDGRFLRTVEWLG	NMLPHPVTLFII	FIVLLLIASAAG	AYFGL	
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADGFI	KILTHTVKNFTGFAP	LGTVLVSL	LGVGIA	
a302	SVPDPRPVGAKGRADD	GLIHVVSLLDADGLI	KILTHTVKNFTGFAP	LGTVLVSL	LGVGIA	
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLTK	SPRKLTTFMVVFTGIL	SNTASELGYVVLIP	LSAIIFHSLGRHPL		
a302	EKSGLISALMRLLLTK	SPRKLTTFMVVFTGIL	SNTASELGYVVLIP	LSAIIFHSLGRHPL		
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYSAN	LFLSTIDPLLACITHQA	-----VVGPEANW	FFMVASTFVI		
a302	AGLAAAFAGVSGGYSAN	LFLGTIDPLLAGITQAA	QIIHPDYVVGPEANW	FFMVASTFVI		
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEPQL	GPYQSDLSQEEKDIR	SNEITPLEYKGLIW	AGVV FVALSALLAW		
a302	ALIGYFVTEKIVEPQL	GPYQSDLSQEEKDIR	SNEITPLEYKGLIW	AGVV FVALSALLAW		
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPETGL	VSGSPFLKSIVVFIF	LLFALGXGVYGRVTR	SLRGEQEVVNAMEA		
a302	SIVPADGILRHPETGL	VSGSPFLKSIVVFIF	LLFALPGIVYGRVTR	SLRGEQEVVNAMEA		
	360	370	380	390	400	410
m302.pep	SMSTLXLXIXIIFFAAQ	FVAFFNWTNIGQYIA	VKGATFLKEVGLGGS	SVLFIGFILICAFI		
a302	SMSTLGLYLVIIFFAAQ	FVAFFNWTNIGQYIA	VKGATFLKEVGLGGS	SVLFIGFILICAFI		
	420	430	440	450	460	470
m302.pep	NLMIGSASAQWAVTAPI	FVPMMLAGYAPEVIQA	AYRIGDSVTNIIIP	MMSYFGLIMATV		
a302	NLMIGSASAQWAVTAPI	FVPMMLAGYAPEVIQA	AYRIGDSVTNIIIP	MMSYFGLIMATV		
	480	490	500	510	520	
m302.pep	IKYKKGAGVGT	LISMMLPYSAFFLIA	WIALFCIWVFLGL	PVGPGAPTFYPAPX		
a302	IKYKKGAGVGT	LISMMLPYSAFFLIA	WIALFCIWVFLGL	PVGPGAPTFYPAPX		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

## g305.seq

```

1  ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTTT GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TATTTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGCC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GTGTGCCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGCCG TTCCGATGAT GGTTCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CCGTTTGATT TTGATAGGCT TTATTGCCG TTTTGTTCG GGTTCGGTAG
701 CCGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

## g305.pep

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

## m305.seq (partial)

```

1  AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTGGC GGTAGTGTTT GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GGCAwACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTyTG GcCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGCGTG TGCCGATGAT GGTTCGCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CCGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCa GGCTTGGTAG
701 CCGTAAAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

## m305.pep (partial)

```

1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51  QLGAVLAVVF EYRQRFNSVL HGLGKDRKAN RFVLNLAIAP IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

## g305/m305

	10	20	30	40	50	60
g305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
m305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF					
	10	20	30	40	50	60

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI					
	:					
m305	XGFXILWVEKQRSRAEPKIADVDALRPIDALMIGVAQVFALVPGTSRSGSTMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1   ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCC
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTTGGC GGTAGTGTTC GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTT
301 GGCAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTC GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAATTTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCCA AGTGTTTGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGGCCG TTCCGATGAT GGTTCAGCA
601 ACGGCTTATG ATGTCCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTGTGTTCA GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1   MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVLNLAI AF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFFILWVEK QRSRAEPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHNKVFETIAIQLGAVLAVVF					
	:					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHNKVFETIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	:					
a305	EYRQRFNSVLHGVGKDRKANRFVLNLAIAFIPAAVMGLLFGKQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRSRAEPKIADVLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
a305	GGFFILWVEKRSRAEPKIVDLDALRPIDALMIGVAQVFALVPGTSRSGSTIMGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

g306.seq

```

1  ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCCGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAT  CGGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCCT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAGA
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCG  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

g306.pep

```

1  MFMNKFSSQSG  KGLSGFFFL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NOPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREPEP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKA VKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMKNFQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

m306.seq (partial)

```

1  ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGMAWAA  CCAGCYTAAG
151 GAAGACATCC  AACCTGAWCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAAWGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAW  ACAAGCGTGA  AAACCGTCTA  AAGAAACAGA  GAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACCG

```

702

601 ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG  
 651 CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA  
 701 GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG  
 751 ATGCGGTGA

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

m306.pep (partial)  
 1 ..GLFFGLILAT VIIAGILFYL NQSGQNAFKI PASSKQPAET EILKPNQXK  
 51 EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP  
 101 EREEPDQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA  
 151 SKEEKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR  
 201 IICKWARMPT VRARKGSPVN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP  
 251 MR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

m306/g306

	10	20	30	40
m306.pep	GLFFGLILATVIIAGILFYL NQSGQNAFKI PASSKQPAETEILKPX			
g306	MFMNKFSQSGKGLSGFFGLILATVIIAGILLYLNQGGQNAFKI PAPSQKQPAETEILKPK			
	10	20	30	40
	50	60	70	80
m306.pep	NQKKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED			
g306	NQPKEIDIQPEPADQNALSEPDVAKEAEQSDAEXAADKQPVADKADEVEEKAGEPEREED			
	70	80	90	100
	110	120	130	140
m306.pep	GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKAAKEKVAPKP			
g306	GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKAAKEKVAPKP			
	130	140	150	160
	170	180	190	200
m306.pep	TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSPVNWQSWA			
g306	TPEQILNSRSIEKARSAAAKEVQKMNFGQGSQRIICKWARMPNPGARKGSPVNWQSWA			
	190	200	210	220
	230	240	250	
m306.pep	YLPRWSVIRRDIKRFTGCKAAICLPMRX			
g306	YLPKWSAIRRDIKRFTACKAAICPPMRX			
	250	260		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

a306.seq  
 1 ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGTTTTTTT  
 51 CTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC  
 101 TGAACCGAG CGGTCAAAAT GCGTTCAAA TCCCGTTCC GTCGAAGCAG  
 151 CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT  
 201 CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA  
 251 AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCGTT  
 301 GCCGACAAAG CCGACGAGGT TGAGGAAAAAG GCGGACGAGC CGGAGCGGGA  
 351 AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG  
 401 AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA  
 451 AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAGA  
 501 AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC  
 551 AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

a306.pcp

**m306/a306 93.7% identity in 252 aa overlap**

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

g307.seq

1	atgaaaacct	tcttcaaaaac	cctttcgacc	gcgtcactcg	cgctcatcct
51	cgcagcctgc	ggcgggtcaaa	aagacagcgc	gcccgcagcc	tctgccgccc
101	ccccttctgc	cgataacggc	gcggcgaaaa	aagaaatcgt	cttcgggcag
151	accgtgggcg	acttcggcga	tatggtcaaa	gaacaaatcc	aagccgagct
201	ggagaaaaaa	ggctacacgc	tcaaattggt	cgaatttacc	gactatgtgc
251	gccgaattct	ggcatctggc	gaggggcgagt	tggacatcaa	cgtcttccaa
301	cacaaaccct	atcttgacga	tttcaaaaaa	gaacacaacc	tggacatcac
351	cgaagccttc	caagtgcgga	ccgcgccttt	gggactgtat	ccgggc aaac
401	tgaatctgct	ggaagaagtc	aaagacggca	gcaccgtatc	cgcgcccaac
451	gaccgcgtcca	acttcgcacg	cgctctgggt	atgctgaacg	aactgggttg
501	gatcaaaact	aaagacggca	tcaatccgct	gaccgcatcc	aaagccgaca
551	tcgcggaaaa	cctgaaaaac	atcaaaatcg	tccagcttga	agccgcacaa
601	ctgccgcgca	gcgcgcgcga	cgtggatttt	gcgctctgtca	acggcaacta
651	cgccataaag	agcggcatga	agctgaccga	agccctgttc	caagagccga



q307.ppt

1	MKTFFKTLST	ASLALILAAC	GGQKDSAPAA	SAAAPSADNG	AAKKEIVFGT
51	TVGDFGDMVK	EQIQAELEKK	GYTVKLVEFT	DYVRPNLALA	EGELDINVFO
101	HKPYLDDPFK	EHNLDITEAF	QVPTAPLGLY	PGKLKSLEEV	KDGSTVSAFN
151	DPSNFARALV	MLNELGWIKL	KDGINPLTAS	KADIAENLKN	IKIVELEAAQ
201	LPRSRAVDVF	AVNNGNYAIS	SGMKLTEALF	QEPSFAYVNW	SAVKTADKDS
251	OWLKDVTEAY	NSDAFKAYAH	KRFEGYKYPA	AWNEGAAK*	

```
m307.seq (partial)
```

1 ..CAATGGCTTA AAGACGTAAC CGAGGCTAT AACTCCGACG CGTTCAAAGC  
51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCTGCC GCATGGAATG  
101 AAGGCGCAGC CAAATAA

m307.pep (partial)

1 ..OWLKDVTEAY NSDAFKAYAH KRFEGYKSPA AWNEGAAK\*

Homology with a predicted ORF from *N. gonorrhoeae*

from *N. gonorrhoeae*:

m307/g307

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEQYKSPA
                               |||||
g307                          SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEQYKYPA
                               230      240      250      260      270      280

                                39
m307.pep                      AWNEGAALKX
                               |||||
g307                          AWNEGAALKX

```

a307.seq

1	ATGAAAACCT	TCTTCAAAC	CCTTTCGCC	GCCGCACTCG	CGCTCATCCT
51	CGCCGCCTGC	GGCGGTCAA	AAGATAGCG	GCCCGCGCA	TCCGCTTCTG
101	CGCGCGCGCA	CAACGGCGCG	GCGAAAAAG	NAATCGTCTT	CGGACGACC
151	GTGGCGGACT	TGGCGATAT	GGTCAAAGAA	CAATCTCAAC	CCGAGCTGGA
201	GAAAAAAGGC	TACACCGTGA	AACTGGTCTGA	GTTTACCGAC	TATGTGCGCC
251	CGAATCTGGC	ATTGGCTGAG	GGCGAGTNGG	ACATCAACGT	CTTCCAACAC
301	AAACCCATTAC	TTGACGACTT	CAAAAAAGAA	CACAATCTGG	ACATCACCGA
351	AGTCTTCCAA	GTGCCGACCG	CGCCTTTTGG	ACTGTACCCG	GGCAAGCTGA
401	AATCGTGGAA	AGAAGTCAA	GACGGCAGCA	CCGATCTCCG	GCCCAACGAC
451	CCGTCCAAC	TCGCCCCGCT	CTTGGTGATG	CTCGACGAAC	TGGGTTGGAT
501	CAAATCAA	GANGGCATCA	ATCCGCTGAC	CGCATCCAA	GCGGACATTG
551	CGGAAAACCT	GAAAAACAT	AAAATCGTCG	AGCTTGAAGC	CGCGCRACTG
601	CGCGTAGCC	CGCGCCAGCT	GGATTTTGN	GTCGTCAACG	GCAANTACGC
651	CATAAGCAGC	GGCATGAAGC	TGACCTGAAGC	CTGTTTCCAA	GAAACCGAGCT
701	TTGCCTATGT	CAACTGGTCT	GCCGTCAAAA	CCGCCGACAA	AGACAGCCAA
751	TGGCTTTAAG	ACGTAACCGA	GGCCTATAAC	TCCGACGCGT	TCAAAGCCTA
801	CGCGCACAAA	CGCTTCGAGG	GCTACAAATC	CCCTGCCGCA	TGGAATGAAG
851	CGCGAGCCAA	ATAA			

a307.pep

1 MKTFFKTLA AALALILAAC GGOKDSAPAA SASAAADNGA AKKXIVEGTT

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFOH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLKSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLNKI  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

m307.pep                               10      20      30
                                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

m307.pep          39
          AWNEGAAXX
          |||||
a307          AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCTT  GTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAGCCGCGA
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1278; ORF 308.ng&gt;:

```

g308.pep
1  MLNRVFYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RMMVRRLLI
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPLE  NLAHLNMRKR  VTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTCTT  GTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAAC
201 TTTGCGCGCG  CAAGATGTCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CCGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTTC  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGCT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GWAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  gCG...

```

This corresponds to the amino acid sequence &lt;SEQ ID 1280; ORF 308&gt;:

m308.pep (partial)

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMKR  XTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSLFGID  TPDSA EWQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNLMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGM A					
g308	VTEMGGVVFPVPVPAMYRKQPQTADDIVAHSAHTLSLFGIDTPDLA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTCGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGTGCGCG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTGCTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNLMXR  VTEMGGVVFP  PVPAMYRKQP
201 TADDIVAHSV  AHALSLFGID  TPDSA EWQGM  AD*

```

## m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308 .pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPQAVLWERRMMVRRLLIIGISGASGFQY					
a308	MLNRIFYRILGVADNLYPRLSDFCFFTTIAGLPQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
m308 .pep	GVKALELLRAQDVETHLVVSKGAEMARASEYARDEVYALADVFVHPIGNIGACIASGTF					
a308	GVKALXLLRAQDIETHLVVSKGAEMARASEXYARDXVYALADVHPIGNIGACIASGTF					
	70	80	90	100	110	120
m308 .pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
a308	KTDGMLVAPCSMRTLASVVGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180
m308 .pep	KTDGMLVAPCSMRTLASVVGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
a308	KTDGMLVAPCSMRTLASVVGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR					
	130	140	150	160	170	180
m308 .pep	XTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGM					
a308	VTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMAD					
	190	200	210	220	230	
m308 .pep	XTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGM					
a308	VTEMGGVVFPVPAMYRKPTADDIVAHSAHALSLFGIDTPDSEWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

## g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
51  TCCGTGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTGTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCCT TGTGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGCCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCG GTAACGGAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACGCG TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

## g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTTIA GLPLQAVLWE RMMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLTRA
151 ADVVLKERRR LVLVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLAEWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

## m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTGCCG ACAATTTGTA
51  TCCGCGTTTA TCGGATTCTT GTTTTTCAC TATAATAGCC GGTGTGCCG
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGCAATC GATCGGCAAT ATCGGGCGT GCATTGCCAG
351 CCGTACGTTT AAAACGGATG GGATGCTGGT CGCCCTGT TCGATGCGGA
401 CGCTTGCCCT TGTGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGG
451 GCGGATGTGG TTTGAAGGA AAGCGGCGG CTGGTGCTGA TGGTGCCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCG GTAACGGAA
551 TGGGCGGCGT GGTGTTTCCC CCTGTTCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCT TGTGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

## m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTTIA GLPLQAVLWE RMMVRRLLI

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51 GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TAYARDEVYA  
 101 LADVFHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA  
 151 ADVVLKERRR LVLVRETPL NLAHLNMXR VTEMGGVVFP PVPAMYRKPO  
 201 TADDIVAHSV AHALSIFGID TPDSA EWQGM AD\*

m308-1/g308-1 97.0% identity in 232 aa overlap

	10	20	30	40	50	60
m308-1.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
g308-1	MLNRVFYRILGVADNLYPCLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308-1.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
g308-1	GVKALELLRAQDVETHLVVSKGAEMARASEDTYTKDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308-1.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMXR					
g308-1	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMXR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308-1.pep	VTEMGGVVFPVPAMYRKPOQTADDIVAHSAHLSIFGIDTPDSA EWQGMADX					
g308-1	VTEMGGVVFPVPAMYRKPOQTADDIVAHSAHLSIFGIDTPDLA EWQGMADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq  
 1 ATGTTAAATC GGATATTTTA TCGGATATTG GGTGTTGCCG ACAATTTGTA  
 51 TCCGATTATTA TCGGATTCTT GTTTTTTCAC TATAATAGCC GGTITGCCGT  
 101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC  
 151 GGCATCAGTG GGGCGAGCGG TTTCCAATAC GGCCTGAAGG CTTTGGANCT  
 201 TTTACGCGCG CAAGATATCG AAACGCACCT TGTGGTATCG AAAGGTGCGG  
 251 AGATGGCGCG CGCTTCGGAA ACGGNTTATG CGAGAGACGA NGTATATGCC  
 301 TTGGCGGACT TNGTGATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG  
 351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCCCCCTGT TCGATGCCGA  
 401 CGCTTGCCTC GGCTCGTCAC GGCTTCGGCG ACAACCTCTT GACGCGTGGC  
 451 GCGGATGTGG TTTGAAGGA AAGCGGCGCG CTGGTGCTGA TGGTGCCGGA  
 501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAANCGG GTAAACGGAA  
 551 TGGCGGCGGT GGTGTTTCCC CCTGTTCCCTG CGATGTACCG CAAACCGCAG  
 601 ACGGCGGACG ACATAGTGGC GCACAGTGT GCACACGCTT TGTGCTGTT  
 651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1288; ORF 308-1.a&gt;:

a308-1.pep  
 1 MLNRIFYRIL GVADNLYPYL SDFCFFTTIIA GLPLQAVLWE RRMVRRLLI  
 51 GISGASGFQY GVKALXLLRA QDIETHLVVS KGAEMARASE TXYARDXVYA  
 101 LADXVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVVAH GFGDNLLTRA  
 151 ADVVLKERRR LVLVRETPL NLAHLNMXR VTEMGGVVFP PVPAMYRKPO  
 201 TADDIVAHSV AHALSIFGID TPDSA EWQGM AD\*

a308-1/m308-1 96.1% identity in 232 aa overlap

	10	20	30	40	50	60
a308-1	MLNRIFYRILGVADNLYPYLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
m308-1	MLNRVFYRILGVADNLYPRLSDFCFFTTIIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a308-1	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
m308-1	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a308-1	KTDGMLVAPCSMRTLASVVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNMXR					

```

m308-1      KTDGMLVAPCSMRTLASVAHGFCDNLLTRAADVVLKERRRLVLMVRETPLNLAHLNDNMRK
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPPVPAMYRKQTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              |||
m308-1      VTEMGGVVFPPVPAMYRKQTADDIVAHSAHALSLFGIDTPDSAEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

```

g311.seq
1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtcgccct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgtttgg
101 gtttggaaac gcaaatacaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaacagtc agggcgggcg gtaaacagg
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgcccgttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaacattg cttgcggaac tgggcgcgg
351 gttggaacaa tatgcggaag aagggttcgc gccatttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttggg aggcgggaac agccggctca agtgggcgtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgcgg taccgcgatt
701 tgcgcctttt gggcgcggag tggcggaag aggcggatgg aaatgtcccg
751 atcgtcggtt gcgcgctgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgca caggctttgg
851 gcatacgcaa ccactaccgc caccgcgaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtaa cggttgacgc gtcaccgat gacggacatt
1001 atctcggcgg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggtt
1151 gcggctcgat aatgatgatg cagggccgtt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcgcgcgcg cgaagtcgc
1251 cgaagccctg ccgctgcatt ttttggcgga aaataccgtg cgcggtggcg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaagcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

```

g311.pep
1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGGILIEIV RAGGKTAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETI LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVLEHLE TAEGETVVS GEISLRPDNR SVSVPKRPDS
201 ERFLLEGGN SRLKAWVEN GTFATVGSAP YRDLSPGLAE WAKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGTTIM PGFHLMKESL
351 AVRTANLNRP AGKRYFPPTT TGNAVASGMM DAVCGSIMMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

```

m311.seq (partial)
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTGCGCT GTTGCggCAG TGGCGTGTCT GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCArATTAAg TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAACCGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCCTGCGG TCCGACnACA GGCCGTTTTC CGTGnCGAAG CCGCGGGATT

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401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAA ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCGCT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGTT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCGGTC GCCAGCGGCA TGATGGATGC
951 GGTTCGCGC TCGGTTATGA TGATGCACGG GCGTTTGAAA GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCGAT GTCATCATT CCGGCGGCGG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGG GCGGAAAATA CCGTGCCTG
1101 GCGGACAAC CTCGTCATT ACGGGTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT....

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGGLIETV RTGGKTAVAV GIGINFLPX EVENAASVQS LFTASRRGN
101 ADAVLLXXX XXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WVNGTFATV GSAPYRDLSP LGAWEAKAD GNVRIVGCAV CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPPEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTTGNAV ASGMDAVCG SVMMHGRLK EKTGAGKPD VIITGGGAAK
351 VAEALPPAFL AENTVRVADN LVIYGLNMI AAEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

m311/g311

```

              10      20      30      40      50      60
m311.pep  MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGGLIETV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGGLIETV
              10      20      30      40      50      60

              70      80      90      100     110
m311.pep  RTGGKTAVAVGIGINFLPXEVENAASVQSLFQTASRRGNADAVALLLXXX-----
          |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      RAGGKTAVAVGIGINFLPKEVENAASVQSLFQTASRRGNADAVALLETLTLLAELGAVLEQ
              70      80      90      100     110     120

m311.pep  -----XXXXXXXXX
          :
g311      YAEFGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDGRGVLHLETAEGEQTVVS
              130     140     150     160     170     180

              120     130     140     150     160     170
m311.pep  XEISLRSDXRPVSVXKRRDSEFLLLDDGGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      GEISLRPDNRSVSPKRPDSEFLLLEGGNSRLKWAVVNGTFATVGSAPYRDLSPLGAE
              190     200     210     220     230     240

              180     190     200     210     220     230
m311.pep  WAEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQALFGIRNHYRHPPEHGS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPPEHGS
              250     260     270     280     290

```

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```

      240      250      260      270      280      290
m311 .pep  WFNALGSRRF SRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR
          |||
g311       WFNALGSRRF SRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR
      300      310      320      330      340      350

      300      310      320      330      340      350
m311 .pep  HAGKRYFPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVDVITGGGAAKVAEA
          |||
g311       PAGKRYFPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKTGAGKPVDVITGGGAAKVAEA
      360      370      380      390      400      410

      360      370      380      389
m311 .pep  LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH
          |||
g311       LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
      420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311 .seq
1  ATGTTCA GTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTT
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATGGGCGC GCATTCTGAT TGAACGGTTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTCGT GCTGCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTTGCT GGAACCGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTGCAA TATGCGCGGG ACGGATTTGC GCCTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGGCGG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGCG GTGGACGGAC AAGGCGTTCT
501 GCACTTGAA ACGGCAGAGG GCAACAGAC GGTCTGTCAG GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCCG TGCCGAAGCG GCGGGATTCT
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGCGTCA AGTGGGCGTG
651 GGTGAAAAC GGCACGTTCT CAACCGTCGG TAGCGCGCGG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATTC AAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAATCG AGTGGCTGCC GTCTCCGCA CAGGCTTTTG
851 GCATACGCAA CCACTACCGC CACCCGAGG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGAGCGCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CCGTTGACGC GCTACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGCGGTT TGAAAGAAAA AACCGGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GCGCGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CGCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311 .pep
1  MFSFGWVFD R PQYELGSLSP VAAVACRRAL SRLGLKTOIK WPNDLVVGRD
51  KLGGILIE TV RTGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLE TL LAELDAVLLQ YARDGFAPFV AEYQANRDH GKAVLLLRDG
151 ETVFEGTV KG VDGQGVHLLE TAEGKQTVVS GEISLRDDR PVSVPKRRDS
201 ERFLLLDG GN SRLKWAVVEN GTFATVGSAP YRDLSP LGAE WAEKVDGNVR
251 IVGCAVCG EF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRR FS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLNR H AGKRYFPFPT TGNASVSGMM DAVCGSVMM HGRLEKKTGA
401 GKPVDVIIT G GGAAKVAEAL PPAFLAENTV RVADNLVIH LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap



712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLDVQIKWPNDLVVGRDKLGGILIETV					
a311	MFSFGWVFD RPQYELGSLSPVAACRRALSRLGLKTQIKWPNDLVVGRDKLGGILIETV					
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVA VVGIGIN FVLPKEVENAASVQSLFQTASRRGNADA VLLXXXXXXXXX-----					
a311	RTGGKTVA VVGIGIN FVLPKEVENAASVQSLFQTASRRGNADA VLLLETLAELDAVLLQ					
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGV DQGVLHLETAEGKQTVVS					
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDXRPVS VVKRRDSEFLLLDGNSRLKWAVVENGTFATVGSAPYRDLSP LGAE					
a311	GEISLRSDDRPVS VPKRRDSEFLLLDGNSRLKWAVVENGTFATVGSAPYRDLSP LGAE					
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQALFGIRNHYRHPEEHGSDR					
a311	WAEKVDGNVRIVGCAVCGEFKKAQVQEQ LARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR					
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSRFRSNACVVVSCGTAVTV DALTDGHYLGGT IMPGFHLMKESLAVRTANLNR					
a311	WFNALGSRFRSNACVVVSCGTAVTV DALTDGHYLGGT IMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPFPTTTGN AVASGMMDAVCGSVMMHGR LKEKTGAGKPDVVIITGGGA AKVAEA					
a311	HAGKRYPFPTTTGN AVASGMMDAVCGSVMMHGR LKEKTGAGKPDVVIITGGGA AKVAEA					
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLAENTVRVADNLVIYGLLN MIAAEGREYEH					
a311	LPPAFLAENTVRVADNLVIHGLLN LIAAEGGESEHTX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTTCGG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTCGCGCA CTTGCGTGCC GCGCGCCTTT
501 GGGGTGTTTG GGTTCGAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GCATTCTGA TTGAACAGT CAGGCGGGCG
601 GGTAAACGG TTGCGTGGT CCGTATCGGC ATCAATTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GCGCGGGCAA TGCCGATGCC GCCGTATTGC TGGAACATT GCTTGGCGAA
751 CTGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTT

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801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGC CGCAGCG CGAAACCGTG TCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCATTGGA AACGGCAGaa ggCGAACAGA cggtcGtcag
951 cggcGaaATC AGcctTGGGc CCgacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aaggcgggaa cagccggctc
1051 aAGTGGgctt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcCC
1101 gtaCCGCGAT TTGTGCGCTT TGGGCGCGGA GTGGCGGAA AAGCGGGATG
1151 GAAATGTCCG CATCGTCGGT TGGCGCGTGT GCGGAGAATC CAAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCGCTCCGA ACCGCGAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTCGCA GCGGCATGAT
1551 GGACGCGGAT TGCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1 MTVLKPSHWR VLAELADGLP QHVSQAREA DMKPQQLNGF WQMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTLKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRGGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTAVAVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLAE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVVDG
301 RGVHLHLETAE GEQTVVSSEI SLRPDNRVS VPKRPDSERF LLLEGGNSRL
351 KWAWVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHPE EHGSDRWFA LGSRRFSRNA
451 CVVVSCTGAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRNAPGK
501 RYFPPTTTGN AVASGMDAV CGSIMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAELPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1 ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAGTAAAG GGCAGGGGCG GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTGTTGACG GCCGAGTAT
451 GAGTTGGGTT CGCTGTGCGC TGTGCGGCA GTGGCGGTGC GCGCGCCTT
501 GTCGCGTTTA GTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCGGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GGAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GGCAGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCATTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CCGCGAAATC AGCCTGCGGT CCGACGACAG GCCGTTTCC GTGCCGAAGC
1001 GCGCGGATTG GGAACGTTTT CTGCTGTTGG ACGCGGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGGAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGCCTGTGT GCGGAGAAT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACCga
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA GCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTTACGG GTTGTGTAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTAA

This corresponds to the amino acid sequence &lt;SEQ ID 1298; ORF 311-1&gt;:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARM DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDROPY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILIETVRTG
201 GKTAVVVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVVG
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHPE EHGSDFWNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTTCN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR					
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVFDROPYELGSLSPVAACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m311-1.pep	DLVVGRDKLGGILLETVRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRTGGKTAVVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVG					
g311-1	AVLLETLLAELGAVLEQYAEAGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVVG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m311-1.pep	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAUVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRSVSVKRPDSERFLLLEGGNSRLKWAUVENGTF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m311-1.pep	ATVGSAPYRDLSPGLGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQALARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPGLGAEWAEKADGNVRIVGCAVCGESKKAQVQEQALARKIEWLPSSAQAL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGF					
g311-1	GIRNHYRHPPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGF					
	430	440	450	460	470	480
	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYFPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYFPFTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
	490	500	510	520	530	540
	550	560	570	580	590	

**a311-1.seq**

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

a311-1.pwp

1	MTVLKPSHR	VLAELADGLP	QHVSQALARMA	DMKPQQLNGF	WQOMPAHIRG
51	LLRQHDGYKR	LVRLPFLAVDA	EGRLRELGERS	GFQTALKHEC	ASSNDEILEL
101	ARIAPDQWHR	TICVTHLQSK	GRKGQRGRKWS	HLRGLECLMFS	FGWVDFDRPQ
151	ELGSLSPVAA	VACRRALLSRL	GLKTKIWPNN	DLVVGDRKLG	GILIIETVRTY
201	GKTVAVVVGIG	INFVLPKEVE	NAASVQSLFQ	TASRRGNADA	AVLLETTLAE
251	LDAVLLQYAR	DGFAPFVAEY	QAA NRDHGKA	VLLLLDGETV	FECTVKGVGDG
301	QGVHLHETAE	GKQTVVSGEI	SLRSDRPVPS	VPKRRDSERF	LLLDGGNSRL
351	KWAVVENGTG	ATVGSAPYRD	LSPLGAEWAE	KVDGNVRIVG	CACVGEFFKA
401	QVQEQLARKI	EWLPSSAQAL	GIRNHYRHPE	EHGSDRW FNA	LGSRRFRSNA
451	CVVVS CGTAV	TVDALTD DGH	YLG GTIMP GF	HLMEKSLAVR	TANLNRRHAGK
501	RYPFPTTTGN	AVASGMMDAV	XCVSMMHGR	LKEKTGAGKP	VDVIIITGGGA
551	AKVAEALPPA	FLAENTVRVA	DNLVIHGLLN	LIAEGGGESE	HT*

**a311-1/m311-1** 98.5% identity in 591 aa overlap

	10	20	30	40	50	60
a311-1.pep	MTVLKPSHWVLAELADGLPQHVSQ	LARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR				
m311-1	MTVLKLSHWVLAELADGLPQHVSQ	LARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR				
	10	20	30	40	50	60
	70	80	90	100	110	120
a311-1.pep	LVRPLAVFDAEGLRELGERSGFOTALKHECASSNDEILELARIAPDKAHTICVTHLQSK					
m311-1	LVRPLAVFDAEGLRELGERSGFOTALKHECASSNDEILELARIAPDKAHTICVTHLQSK					
	70	80	90	100	110	120

716

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECLMFSFGWVFDPRQYELGSLSPVAACRRALSRLGLKTQIKWPN					
m311-1	GRGRQGRKWSHRLGECLMFSFGWVFDPRQYELGSLSPVAACRRALSRLGLDQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILITVVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	DLVVGRDKLGGILITVVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
m311-1	AVLLETLLVLEDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPSVSPKRRDSEFLLLDGGNSRLKWAWVNGTF					
m311-1	QGVHLHLETAEGKQTVVSGEISLRSDDRPSVSPKRRDSEFLLLDGGNSRLKWAWVNGTF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPLGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAAL					
m311-1	ATVGSAPYRDLSPLGAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGF					
m311-1	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	HLMKESLAVRTANLNRHAGKRYFPPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLIAEGGESEHTX					
m311-1	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLNMIIEAGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgcAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCGCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCTCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGGCTGCG
551 CCAAAATCGT CGTGTCTGTC AACCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCC ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGTCCA GCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGT CGTGGCACC GACCCCGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CGGTACGCAC

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCGG CCGAGGCAGG CGTGTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCGGTC TGCTCCGTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTC GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATCCGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGG TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTTCGTC CCGGGGCGG AGGATTCCCG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1 MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51 TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVSGP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFVNRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1 ATGAGTATCC AATCCGCGCA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51 CCAGAAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACACTG GCAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GCGCGAAACT
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAAGGGA TGTGCGcTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACcGTC AAACGCACGG CGGAAATCAC GCCCGAAGGT TTCGGCTGCG
551 CTAAATTTGT CGTGTCTGTC AACGCGGTGG AAGACAACCC GTTTWTGGCG
601 GGCGCGTTTC ATGGTTCCGG CGATGCCGTT ATCAATGTCT GCGTATCCGG
651 CCCAGGTGTC GTAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAACTG CTTTCAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCGCGCA AGCcTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCC GCCCGT CGGCGACTCA GTGGCACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGGTTTGA GTGGCGCGTT TATCCCCGTT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CAcGGTCGAG TTCGGCGGCT TGTGGGgCTA
1251 CGCGCCTGTG ATGCCGGTCA AAGAAGGTTT GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1 MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51 TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGCAKIVVFC NAVEDNPFXA
201 GAFHGS GDV INVGVSGPGV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPVGDS VARILEEMGL SVCGTHGTTA
301 ALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 EAMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCFV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMVADQNFVVRTITIGIDLHDCISSDINVLNQNIYNKITTVGKDLVTT					
g312	MSIQSGEILETVKMVADRNFDVVRTITIGIDLHDCISTDIDVLNQNIYNKITTVGKDLVAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m312.pep	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVVAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVVAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLRISPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLRISVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
	190	200	210	220	230	
m312.pep	FGCAKIVVFCNAVEDNPFKAGAFHGSG--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDVAVKKGMMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDVAVKKGMMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
g312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRRGGRIAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAATTTC GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAC CGACATCGAC GTGTTGAACC AAAATATTTA CAACAAAATT
151 ACCACGGTCG GCAAAGACTT GGTGGCGACA GCAAATATC TGTCTGCCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCTGTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAC
```

a312.pep

1	MSIQSGEILE	TVKMVADQNF	DVRTITIGID	LHDCISTDID	VLNQNIYNKI
51	TTVGKDLVAT	AKYLSAKYGV	PIVNQRISVT	PIAQIAAATH	ADSYVSVQAT
101	LDKAAKAIGV	<u>SFIGGFSALV</u>	QKGMSPSDEV	LIRSIPEAMK	TTDIVCSSIN
151	IGSTRAGINM	DAVRLAGETI	KRTAEITLEG	FGCAKIVVFC	NAVEDNPFMA
201	GAFGHSGEAD	AVINUVGSGP	GVVKAALENS	DATTLTEVAE	VVKKTAFKIT
251	RVGELIGREA	SKMLNIPFGI	LDLSLAPTPA	VGDSVARILE	EMGLSVCGTH
301	GTTAALALLN	DAVKKGGGMA	SSAVGGLSGA	FIPVSEDEGM	IAAAEAGVLT
351	LDKLEAMTAV	<u>CSVGLDMIAV</u>	PGDTPAHTIS	GIIADEAAIG	MINSKTTAVR
401	LIPTVGKTVG	DSVEFGLLG	YAPVMPVKEG	SCEVFVNRGG	RIPAPVQSMK
451	N*				

		10	20	30	40	50	60
m312.pep		MSIQSGEILETVKQMVADQNFDVRTITIGIDLHDCISSDINVLNQNIYNKITTGVGKDLVTT					
a312		MSIQSGEILETVKQMVADQNFDVRTITIGIDLHDCISTDIDVLNQNIYNKITTGVGKDLVAT					
		10	20	30	40	50	60
		70	80	90	100	110	120
m312.pep		AKYLSAKYGVPPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAGAIGVSFIGGFSA					
a312		AKYLSAKYGVPPIVNQRISVTPIAQIAAATHADSYVSVAQTLDKAAGAIGVSFIGGFSA					
		70	80	90	100	110	120
		130	140	150	160	170	180
m312.pep		QKGMSPSDEVLIRSIPEAMKTDDIVCXSSINIGSTRAGINMDAVKLAGE					
a312		QKGMSPSDEVLIRSIPEAMKTDDIVCSSINIGSTRAGINMDAVRLAGETIKRTAEITL					
		130	140	150	160	170	180
		190	200	210	220	230	
m312.pep		FGCAKIVVFCNAVEDNPFKXAGAFHGSG--DAVINVGVS					
a312		FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS					
		190	200	210	220	230	240
		240	250	260	270	280	290
m312.pep		VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
a312		VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTPAVGDSVARILEEMGLSVCGT					



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	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRRGGRIPAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc  cgcgcaccta  cggatcgggc  aatcccgggc  cgaccaatgt
51  tttagcgagc  ggcaaaaaaa  aggcggccgc  gctgacgctc  ttggcgcatg
101 cgcgcaaagg  tttggttgcc  gttttgcttg  cacgcgtgct  tcaagaaccg
151 ctcggtttat  ccgacagcgc  aatcgccgcc  gtcgcactcg  ccgcgctggt
201 cgggcatatg  tggccggtgt  ttttcggatt  taaggcgggc  aaaggcgtgg
251 caacggcatt  gggcggtgct  ctggcactct  ctcccgcaac  tgccttggtc
301 tgcgcgttga  tttggcttgt  gatggcattc  ggcttcaaag  tatcctccct
351 tgccgcgctg  gtcgccacaa  ccgccgcccc  ccttgccgca  ctgtttttta
401 tgccgcatac  ttcttggtat  ttccgaaccc  tcgcaatcgc  catattggtg
451 ttgctccgcc  ataagagcaa  catcctcaac  ctgattaaag  gcaaagaaag
501 caaaatcggc  gaaaaacgct  ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAAILV
151 LLRHKSNILN LIKGKESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC  CGCGCACCTA  CGGATCGGGC  AATCCGGGGG  CAACCAATGT
51  TTTACGCAGC  GGCAAAAAAA  AGGCGGCCGC  GCTGACGCTC  TTGGCGCATG
101 CCGCCAAAGG  TTTAGTTGCC  GTTTTGCTTG  CACGCGTGCT  TCAAGAACCG
151 CTCGGTTTAT  CCGACAGCGC  AATCGCGGCC  GTCGCACTCG  CCGCGCTGGT
201 CGGGCATATG  TGGCCGCTGT  TTTCGGATT  TAAAGCGGGC  AAAGGCGTGG
251 CAACGGCATT  GGGCGTGCTT  CTGGCACTCT  CTCCCGCAAC  TGCCTTGGTC
301 TGCGCGTTGA  TTTGGCTTGT  TATGGCATT  GGCTTCAAGG  TGTCTCCCT
351 TGCCGCATTA  ACCGCCACAA  TCGCCGCACC  GGTGCGCGCA  TCCTTCTTTA
401 TGCCGCACGT  CTCGTGGGTT  TGGCGGACCG  TCGCCATTGC  TTTGCTGGTG
451 TTGTTCCGCC  ACAAAGTAA  TATCGTCAAG  CTGCTCGAAG  GCAGAGAAAG
501 CAAAATCGGC  GGCAGCCGCT  GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYGS NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGVL LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSIV WATVAIALLV
151 LFRHKSNIIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLEGRESKIGGSRX					
	:    :    :    :    :    :    :    :    :    :    :    :    :    :    :					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

1	ATGGACGACC	CGCGCACCTA	CGGATCGGGC	AATCCGGGGG	CAACCAATGT
51	TTTACGCAGC	GGCAAAAAAA	AGGCGGCCGC	GCTGACGCTC	TTGGGCGATG
101	CCGCCAAAGG	TTTGGTTGCC	GTTTGTCTTG	CACGCGTGCT	TCAAGAACCG
151	CTCGGTTTAT	CCGACAGCGC	AATCGCGGCC	GTCGCACTCG	CCGCGCTGGT
201	CGGGCATATG	TGGCCGGTGT	TTTTCGGATT	TAAAGGCGGC	AAAGGCGTGG
251	CAACGGCATT	GGGCGTGCTT	CTGGCACTCT	CTCCACAAC	TGCCTTGGTC
301	TGCGCGTTGA	TTTGGCTTGT	GATGGCATTG	GGCTTCAAGG	TGCTCTCCCT
351	TGCCGCATTA	ACCGCCACAA	TGCGCGCCCC	CCTTGCCGCA	CTGTTTTTTA
401	TGCCGCATAC	TTCTTGGATT	TTCGCAACCC	TCGCAATCGC	CATATTGGTG
451	TTGCTCGGCC	ATAAGAGCAA	CATCCTCAAC	CTGATTAAAG	GCAAAGAAAG
501	CAAAATCGGC	GAAAAACGCT	GA		

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

1	MDDPRTYGS	NGPATNVLR	S	GKKKAAALT	L	LGDAAKGLV	A	VLLARVLQEP
51	LGLSDSAIAA	VALAALVGHM	WPVFFGFKGG	KGVATALGVL	L	ALSPPTALV		
101	CALIWLVMF	GFKVSSLAAL	TATIAAPLAA	LFMPHTSWI	F	FATLAIAILV		
151	LLRHKSNIILN	LIKGESKIG	EKR*					

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKGVATALGVLLALSPPTALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNLIKGESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgatttgtgtt
 51  cacgctgctt gtagtcagtg tcggtctggt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggcaaca cagccggcgc cgggctgtaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcggttacg
251  gtcattactc tgttgccgga gaggcggttt acgaccatcc gttccaatgg
301  ggttccaaac gtaccgggtc tgatttggca cgtgtgggcg gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcga aagcgctga ggctttggca aacaaatccg
551  agctggatgc tgtagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaaggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GGC GGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTC GTCCGTTC CG TCGGAAACC GAGCGTTACG
251  GTCATTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401
      10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
g401      MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          10      20      30      40      50      60

      70      80      90     100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
```

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```

g401      |||||
          IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          .70      80      90      100      110      120

          130      140      150      160      170      180
m401 . pep HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
          |||||
g401      HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
          130      140      150      160      170      180

          190      200
m401 . pep NKSELDAVVAYLQGLGLALKNVRX
          |||||
g401      NKSELDAVVAYLQGLGLALKNVRX
          190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401 . seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAA
151 GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACC GAGCGTTACG
251 GTCATTACTC TGTGCCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGCA CGTGTGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATT CCGTGGCTTG CACGCAATAA AGTCGATGC
451 GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401 . pep
1  MKLQQLAEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

          10      20      30      40      50      60
m401 . pep MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
a401      MKLQQLAEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
          10      20      30      40      50      60

          70      80      90      100      110      120
m401 . pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          |||||
a401      IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGRYSEW
          70      80      90      100      110      120

          130      140      150      160      170      180
m401 . pep HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
          |||||
a401      HRIHLLNPRDVVPESNMPAF PWLARNKVDVDATVANMKALRKVGTPYSDEEIIAKAPEALA
          130      140      150      160      170      180

          190      200
m401 . pep NKSELDAVVAYLQGLGLALKNVRX
          |||||
a401      NKSELDAVVAYLQGLGLALKNVRX
          190      200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggatTATTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGtttttcgTT CGCagcAcag tccgtgcctc aggCATTtTC atttattcctt
151 gcctGttttc tgACCGgtat cgcgcgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GCGCGGGTAT TgccgaTttt ttgatTTTGG GTGCTGCGTG GTTGTGACG
301 GGTttttTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATTT TCCCACtTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCGC CAACGTTGCC
451 GGCAGTGCAAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttgtt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTGTTTTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTTC
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTTGATT GAAAACAAAC
701 ACGGCATTGT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 CGGAATGTAT ACGACGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGCATA
951 CCGTAGCCTT ATCGCGGAcg agcgcgCAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCTATTCC ACTAACCTGT TGAGTGCgGA ATTTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTccct AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cgGTTGATTT GGCCGGAAG CCGCAGgcac
1351 gTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGtctctCG
1401 TATGCTGATT CGGATGACGG AacctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPOAFSFLI
51  ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLIT
101 GFSGFVHHAG IPITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPEMQSMIV ABINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSSTDAA AQKVSRMLI RMTEPSAGAE VIITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATTT ATATGChTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTtTC ATTtACCCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTttttTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCGC CAACGTTGCC
451 GGCAGTGCAAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTtCTT
501 GTCCACCCAA CAGATTtACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTCC
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTYAC TGCCGGATTTC

```

651	TGTCTTTCAA	AATATTGCTG	ACCGTCCGGA	TA <del>g</del> GCTGATT	GAAAA <del>C</del> AAAC
701	ACGGCATTGT	TGCGGTTTAC	CATAGAGATG	GTGATAAGGT	TGTTTTATGGG
751	GCGAATGTAT	ACGACGGCGC	ATACAATACC	GATGTATTCA	ATAGTGTCAA
801	CGGCATCGAA	CGTGCCTATC	TGCTACCCTC	CCTGAAAGTCT	GGCATACGCC
851	GCATTTTCGT	CGTTGGAATC	AGTACAGGTT	CGTGGGCGCG	CGCTCTGTCT
901	GCCATTCCGG	AAATGCACTG	GATGATCGTT	GCGGAAATCA	ATCCGGCATA
951	CCGTAGCCTT	ATCGCGGACG	AGCCGCAAAT	CGCCCCGCTT	TTGCAGGACA
1001	AACGTGTTGA	AATTGTATTG	GATGACGGTA	GGAAATGGCT	GCGTCGCCAT
1051	CCTGATGAAA	AATTCGACCT	GATTTTGATG	AATACGACTT	GGTACTGGCG
1101	TGCCTATTCC	ACCAACCTGT	TGAGTCGGGA	ATTTTTAAAA	CAGGTGCAAA
1151	GCCACCTTAC	CCCGGATGGT	ATTGTAATGT	TTAATACCAC	GCACAGCCCG
1201	CATGCTTTTG	CTACCGCCGT	ACACAGTATT	CCCTATGCAT	ACCGCTATTG
1251	GCATATGGTA	GTCGGCTCGG	CAACCCCGGT	AGTTTTCCCT	AATAAAGAAC
1301	TGCTCAAGCA	ACGTCTCTCC	CGGTTGATTT	GGCCGGAAAG	CGGCAGGCAC
1351	GATATTGACA	GCAGCACCGT	GGATGCTGCA	GCACAAAAGG	TGTGTCCTCG
1401	TATGCTGATT	CAGATGACGG	aACCTTCGCC	TGGGGCGGAA	GTGTTATTCCG
1451	ACGATAATAT	GAGTTGTAGAA	TACAAATACG	GACAGGGGAT	TTAA

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pcp

1	MDIVNTKPMI	SLIYMXSFLS	GLLSLGIEVL	WVRMFSFAAQ	SVPQAFSFTL
51	ACFLTGIAVG	AYFGKRICRS	RFVDIPFIGQ	CFLWAGIADF	LILGAAWLLT
101	GFGSGFVHHAG	IFITLSAVVX	XLIFPLVHHV	GTDGNKSGRQ	VSNVYFAXVA
151	GSALGPVLIG	FVILDFLSTQ	QIYLLICKIS	AAVPLFCTLF	QKSRLRNAVS
201	VAVSLMFGIL	MFLLPDSVFQ	NIADRPRLI	ENKHGIVAVY	HRDGDKVVYG
251	ANVYDGAynt	DVFNsvNGIE	RAYLLPSLKS	GIRRI FVVGL	STGSWARVLS
301	AIPEMQSMIL	AEINPAYRSL	IADEPQIAPL	LQDKRVEIVL	DDGRKWLLRH
351	PDEKFDLIM	NTTWYRSL	TNLLSAEFLK	QVQSHLTQDG	IVMFWNTTHSP
401	HAFATAVHSI	PYAYRYGHMV	VGSATPVVFP	NKELLKQRLS	RLIWPESGRS
451	VFDSSTVDAA	AQKVVSRLMI	QMTEPSAGAE	VITDDNMIVE	YKYGRGI*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/q402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGLIEVLWVRMFSFAAQSVQPAFSFTLACFLTGI					
	:       :     :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGLIEVLWVRMFSFAAQSVQPAFSFILACFLTGI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQOIYLLICKIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQOIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVVYGANVYDGAyntdVFNsvNGIERAYLLPSLKSgIRRIfvVGLSTGSwarVL					

726

g402	HRDGDKVVYGANVYDGAYNTDIFNSVNGIERAYLLPSLKSIGIRRFVVGLSTGSWARVLS
	250 260 270 280 290 300
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
g402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRRHPDEKFDLILM
	310 320 330 340 350 360
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
g402	NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV
	370 380 390 400 410 420
m402.pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAQKVVSRLIQMTEPSAGAE
g402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSTVDAAQKVVSRLIRMTEPSAGAE
	430 440 450 460 470 480
m402.pep	VITDDNMIVEYKYGRGIX
g402	VITDDNMIVEYKYGRGI
	490

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

```

a402.seq
1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTGTTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTC
651 TGTCTTTCAA AATATTGCTG ACCGTCGGGA TAGGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCAGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCGGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAAG CGGCAGGCAC
1351 GTATTTGACA GCAGCACCCT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

```

a402.pep
1  MDIVNTPKNT SLIYMLSFLS GLLSLGIEVL WVRMFSEFAQ SVPOAFSFTL

```

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT  
 101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA  
 151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS  
 201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG  
 251 ANVDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSGWARVLS  
 301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRRH  
 351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP  
 401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH  
 451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI\*

## m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402. pep	MDIVNTKNTSLIYMXSFLSGLLSLGIEVLWVRMFSAQSVFQAQSFSLACFLTGIAVG					
a402	MDIVNTKNTSLIYMLSFLSGLLSLGIEVLWVRMFSAQSVFQAQSFSLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402. pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402. pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQOIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQOIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402. pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402. pep	HRDGDKVYGANVDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
a402	HRDGDKVYGANVDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSGWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402. pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM					
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402. pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402. pep	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLKQRLSRLIWPESGRHVFDSSSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402. pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1  ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGGC GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGGGAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1  MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTG LTTSLSLINA PALSRQSDG SGRSSLGLN
151 IGGMDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIQPYGNHTG NSAPSV EADN
301 SHEGYGSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAACGCT
101 TTGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTTCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACGGAAG GATTAATGGT CGATTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGGGAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK

```

```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTPRYETT AETTSGLTG LTSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDPS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAANKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFQELVAASARAANKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	:					
m406	KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTPRYETTAETTSGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTSLSTLNAPALSRQSDGSGSRSSGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	:					
m406	LTSLSTLNAPALSRQSDGSGSKSSLGLNIGMGDYRNETLTTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	:					
m406	FLRGIDVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDPSDIQPYGNHTGNSAPSVEADN					
	:					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDPSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGPX					
	:					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT CGAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTCTCC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
1  MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGLTGG LTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLHLVQTVF FLRGIDVVP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSCKGIK PTEGLMVDFF DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGP *

```

m406/a406 98.8% identity in 320 aa overlap

	10	20	30	40	50	60
m406.pep	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR					
a406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARAANKDMDLQALHGR					
	10	20	30	40	50	60
m406.pep	70	80	90	100	110	120
	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG					
a406	KVALYIATMGDQSGSLTGGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGLTGG					
	70	80	90	100	110	120
m406.pep	130	140	150	160	170	180
	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
a406	LTSLSTLNAPALSRTQSDGSGSKSSLGLNIGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
m406.pep	190	200	210	220	230	240
	FLRGIDVVPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
a406	FLRGIDVVPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
m406.pep	250	260	270	280	290	300
	IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
a406	IKPKTNAFEAAAYKENYALWMGPYKVSCKGIKPTTEGLMVDFFSDIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
m406.pep	310	320				
	SHEGYGYSDEVVRQHRQGPX					
a406	SHEGYGYSDEAVRRHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
1  atggtcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
51  ggcaggcgga gatggcaaga tgcagcatca ctttgacggc agggttgcgt

```

```

101  tcgtcaaacg attcggacac caagccgctg tctcggctga ggcgaggggt
151  cagctgggtc atgtcggtcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgctgccgc
501  cgaccaggtt ggcttattcg ttggatttga agtcggacat acggacgatg
551  gttttacgcy gataaaccga tgcggcaagc gttgccacgc cttcgccgat
601  tttatcgacy tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttccgc tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701  ttccgggtgga tgcgatttg gcggttgatg ataaattcca tacgcgccaa
751  gccgatgcct tcgtgggca gattggcgaa gctgaatgcg agttcgggat
801  tgcgcagctt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgcacctgg taatttgtag gtccagcagg ccggcataga taaagccggt
901  atcgccttcg gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcaggt gcgtccgccg cggttggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggagcattc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgagg tttgacgggt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgcgt agtgtccaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg gaacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggggtt gcttgccttg agcgtgggtt
1551 tgaacacata aaattcgtcc ggggtgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLADT DIFVLLAAGG DGKMQHHFDG RYAFVKRFGH QAAVSVEAEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQSA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFFM RFVYAADQV GVFVGFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRGC VTGDAADNFR FQFVVLVVKF QQGFVRDADL AVDDKFHTRO
251 ADAFAQIGIE AECEFGIADV HHDGDCFWH IVQGDIGNLY VQAGIDKAG
301 IAFGTGYGNF LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFP I R IGHVGNQYVA GFDGIHLGSI FNQAHALTD FLTDGTTFAQ
401 DGFFAVDQVA AQVAAFFLG FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVCQ LGDFFVNGE AVAVFFGDFD VGYRFAGGFP VGENHFDVFR
501 THGLAQDGGF ACFERGFEBI KFVRVDRALY DVFAQTVRGG NKDDLVVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc agggttgcgt
101 tcgtcaaacg attcggatac caagccgctg tcgcggctga gaccgaggggt
151 cagttgggtc atgtcggtcg agccgatgga gaagccgtcg aagtattgca
201 ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251 aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtttt
301 gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351 caacgttggy caacccatt tcatcgcgga cgcgtttcaa ggctttgcat
401 tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451 acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501 cgaccaggtt ggcttattcg ttggatttga agtcggacat acggacgatg
551 gttttacgcy gataaaccga tgcggccaat gtcgccacgc cttcgccgat
601 tttatcgacy tagaagtcga caggggacgc gtaaccggcg atacggcggg
651 taatttccgc ttttaattcg tcgtcttggt tgtcaaattc caacaargct

```

```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacgtt catcatgact tttacagggtg ctttaggcat attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggg
901 atcgccctcg gcacaggata cggtaacttc ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggcgcgcg cggttggtta cgatggcaga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttctgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaaagcg gcgcagggtt cggttgccct
1251 cttcttggga ttttacgggt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgccc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgcaa ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcctcgg ggaatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgttttga
1501 acccatggtt ttacgcagga tggcgggcgt gcccggtttg agcgtggggt
1551 tgaacacatr aaattcgccc ggggtgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggatgc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHFFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRR
151 TEAQHRVFFM RFVYVAADQV GVFVGFVGVH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAVGNDRGR
351 STPHHGFPPIR IGHVGNEYVA GFDGIHLGSI FNQAHALTD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVGNGE AVAVFLGDI VGYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFVRVDRTLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	:   :     :     :     :     :     :					
g501	MVGRTLTAADTDIFVLLAAGGDGKMQHFFDGRVAFVKRFGHQAAVSVEAEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHHNQAAVFAAFQAVFFQGFNDNGFGFAQSADERNHDFNVG					
	:     :     :     :     :     :     :     :     :					
g501	EAVEVLQELFRQYRVARQLAHHNQAAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQGETVFEVVDITRRITTEAQHRVFFMRVYVAADQVGVFVGFVGVH					
	: : : :     :     :     :     :     :     :					
g501	QTHFVTNAFQGFQGETVFEALGNITRRITTEAQHRVFFMRVYVAADQVGVFVGFVGVH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					
	:     :     :     :     :     :					

g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLVVKFQQGFVRVDADL
	190 200 210 220 230 240
m501 . pep	250 260 270 280 290 300
	AVDDKPFHTRQADAFAGQVGEAECEFGIADVHHD FYRCFRHIVXGDI GNLYVQQTGIDKAG
g501	AVDDKPFHTRQADAFAGQI GEAECEFGIADVHHD FDGCFWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501 . pep	310 320 330 340 350 360
	IAFGTGYGNFLT V FQFGC IAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
g501	IAFGTGYGNFLT V FQEFGR IAAADDGRNTQFARDDGGVAGASAAVGHGDSSTFHHGFPPIR
	310 320 330 340 350 360
m501 . pep	370 380 390 400 410 420
	IGHVGN EYVAGFDGIHLGSI FNQ AHLALTD FLTDGA AFAXYGFVAVDGEAAQVAVALFLG
g501	IGHVGNQYVAGFDGIHLGSI FNQ AHLALTD FLTDGTTFAQDGF FAVDGVAAQVA AAFVLG
	370 380 390 400 410 420
m501 . pep	430 440 450 460 470 480
	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDGGQRVVQLGDF FVGNGEAVAVFFGDFD
	430 440 450 460 470 480
m501 . pep	490 500 510 520 530 540
	VGYGFTGF CFVGKNHFDVFXTHGFTQDGG LARFERGF EHXKFVRVDR TLYDVFAQTVRGG
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGF EHIKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501 . pep	550
	NKDDLIVXGFGVGEHHHT
g501	NKDDLIVVAGFGVGEHHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501 . seq (partial)

1	ATGGTCGGAC	GGGCCTTGAC	CGCAGATGCC	GACATATTTG	TTCTGCTTGC
51	GGCAGGCCGA	GATGGCAAGG	TGCAGCATCA	CTTTGACGGC	AGGGTTGCGT
101	TCGTCAAACG	ATTCGGATAC	CAAGCCGCTG	TCGCGGTCGA	GACCGAGGGT
151	CAGTTGGGTC	ATGTCGTTTC	AGCCGATGGA	GAAGCCGTCG	AAGTATTGCA
201	GGAATTGTTC	CGCCAATACC	GCGTTGCTCG	GCAGCTCGCA	CATCATAATC
251	AGGCGCAGGC	CGTTTTTGCC	GCGTTCCAAG	CCGTTTTCTT	TCAGGGCTTT
301	GACAACGGCT	TCGGCTTCGC	CCAAAGTGCG	GACGAACGGA	ATCATGATTT
351	CAACGTTGGT	CAACCCATT	TCATCGCGGA	CGCGTTTCAA	GGCTTTGCAT
401	TCCAAGGCGA	AACAGTCTTT	GAAGTTGTCG	GCGACATAAC	GCGCCGCACC
451	ACGGAAGCCC	AACATCGGGT	TTTCTTCATG	CGGTTCGTAT	ACGTTGCCGC
501	CGACCAGGTT	GGCGTATTCG	TGGGATTTGA	AGTCGGACAT	ACGGACGATG
551	GTTTTACGCG	GATAAACCGA	TGCGGCCAAT	GTCGCCACGC	CTTCGGCGAT
601	TTTATCGACG	TAGAAGTCGA	CAGGGGACGC	GTAACCGCG	ATACGGCGGG
651	TAATTTCCGC	TTTTAATTCG	TCGTCTTGTT	TGTCAAATTC	CAACAAGGCT
701	TTGGGGTGGA	TACCGATTTC	GCGGTTGATG	ATAAATTC	TACGCGCCAA
751	CCGATGCCT	TCGCTGGGCA	GGTTGGCGAA	GCTGAATGCG	AGTTCCGGAT
801	TGCCGACGTT	CATCATGACT	TTTACAGGTG	CTTAGGCAT	GTTGTCCAAA
851	GCAACATCGG	TAATTTGTAC	GTCCAGCAGG	CCGGAGTAGA	TGAAGCCGGT
901	ATCGCCTTCG	GCACAGGATA	CGGTAACCTC	TTGACCGTTT	TTACGCAATT
951	CGGTTGCATT	GCCGACGCCG	ACAACGGCAG	GAATACCCAG	TTTCGCGCGG

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1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCGTACCGAC TTTCTGACCG ATGGCGCGGC CTTCCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CGGTCGCCIT
1251 CTTCTGCGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTGCCT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGAC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

## a501.pep

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNFG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNER F*FVVLVVKF QQGFVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDYFRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQFGCI AAADNGRNTQ FARDDGGVAG TSAFVGHDDG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAFAAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVQAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTG
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

m501.pep	10	20	30	40	50	60
	MVGXALTADADIFVLLAAGGDGKVQHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRLTADADIFVLLAAGGDGKVQHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG					
m501.pep	70	80	90	100	110	120
	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNFG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNFG					
m501.pep	130	140	150	160	170	180
	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVGH					
a501	QPHFIADAFQGFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFVGH					
m501.pep	190	200	210	220	230	240
	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQGFVDTDL					
m501.pep	250	260	270	280	290	300
	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDYFRCFRHVVQSNIGNLYVQAGVDEAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDYFRCFRHVVQSNIGNLYVQAGVDEAG					
m501.pep	310	320	330	340	350	360
	IAFGTGYGNFLTIVFQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPIR					
a501	IAFGTGYGNFLTIVFQFGCIAAADNGRNTQFARDDGGVAGTSAPVGHDDGGSAPVGHHRFPIW					

	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLT DGA AFAXYGFVAVDGEAAQVAVALFLG					
a501	:     :     :     :     :     :     :     :     :     :     :     :					
	370	380	390	400	410	420
	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLT DGA AFADGFFAVDRKAAQVAAFFLG					
m501.pep	430	440	450	460	470	480
a501	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGGQCVMRQLSNFFVGNGEAVAVFLGDID					
	430	440	450	460	470	480
	FDGFGTGLQDVEFAVQAVASPFVHRAAVVFFDGGQCVMRQLGDFVGNGEAVAVFFGDID					
m501.pep	490	500	510	520	530	540
a501	VGYGFTGFCFVGKNHFDVFXTHGFTQDGLARFERGFEHKKFVRVDRTLVDVFAQTVRGG					
	490	500	510	520	530	540
	VGYRFAGFCFVGKNHFDVFXAHGFAQDGRFACFQRGFEHIEFVGIDCALYDVFAQTVGXS					
m501.pep	550	559				
a501	NKDDLIVXGFGVEGEHHTX					
	:     :     :					
	DKDDLIVVTGFGIEGEHH					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

g502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccggtt	gctccctgac
51	cgtcgccgtc	gcttcgcgac	aggcggggcg	ggtggacgcg	ctcaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	aaccgtccaa
151	agcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tctgcgccc
201	gggctcttc	aatgggaat	acactttgcc	ctacagacag	actattgtcg
251	gcgacggtca	aaccgtttgg	ctctacgatg	ttgatttggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	catcgggcgg	agccccgcgg	ccatcctgtc
351	gaacaaaacc	gccctcgaaa	gcagttacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	cggggcaacg	cccaaacgca	acaacgcggg
451	ctaccaatac	atccgcatcg	gcttcaaagg	cggcaacctc	gccgccatgc
501	agcttaa				

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

g502.pep

1	MMKPHNLFQF	LAVCSLTVAV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTQVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTLPYRQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	RGNAQTQRRR
151	LPIHPHRLQR	RQPRRHAA*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

m502.seq

1	atgatgaaac	cgcacaacct	gttccaattc	ctcgccggtt	gctccctgac
51	cgtcgccgtc	gcttcgcgac	aggcggggcg	ggtagacgcg	cttaagcaat
101	tcaacaacga	tgccgacggt	atcagcggca	gcttcaccca	amccgtccaa
151	wgcaaaaaga	aaacccaaac	cgcgcacggc	acgttcaaaa	tctgcgacc
201	gggctcttc	aatgggaat	acaccaaact	t.acaggcaa	accatcgtcg
251	gcgacggtca	aacygtttgg	ctmtacgatg	tygatctggc	acaagtgacc
301	aagtcgtccc	aagaccaggc	cataggcgsc	agccccgcgg	ccatcctgtc
351	gaacaaarcc	gccctcgaaa	gcagctacac	gctgaaagag	gacggttcgt
401	ccaacggcat	cgattatgtg	ggcaacgccc	aaacgcaaca	acgccggcta
451	ccaatacatc	cgcacggtc	tcaaaggcgg	caacctcgcc	gccatgcagc
501	tyaa				

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

m502.pep

1	MMKPHNLFQF	LAVCSLTVAV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQXVQ
51	XKKKTQTAHG	TFKILRPGLF	KWEYTKLYRQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGX	SPAAILSNIX	ALESSYTLKE	DGSSNGIDYV	GNAQTQRRRL
151	PIHPHRLQRR	QPRRHAA*			



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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502 . seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCGGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTCG
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCGC	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502 . pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKKTQTAHG	TFKILRPGLF	KWEYTSPIKQ	TIVGDGQTVW	LYDVDLAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502 . pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502 . pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSPIKQQTIVGDGQTVWLYDVDLAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502 . pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAAX					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAAX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1  ATGatGAAAc  cgcaCaacct  gttccaaTtc  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTGGACGCG  CTCAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGCCC
201 GGGCCTCTTC  AAATGGGAAT  ACACTTTGCC  CTACAGACAG  ACTATTGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATCGGCGGC  AGCCCCGCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGTTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CGGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601 GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKTQTAHG  TFKILRPGLF  KWEYTLPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIIG  SPAILSNKT  ALESSYTLKE  DGSSNGIDYV  RATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTNPQLS  RGAFKFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1  ATGATGAAAC  CGCACAACT  GTTCCAATTC  CTCGCCGTTT  GCTCCCTGAC
51  CGTCGCCGTC  GCTTCCGCAC  AGGCGGGCGC  GGTAGACGCG  CTTAAGCAAT
101 TCAACAACGA  TGCCGACGGT  ATCAGCGGCA  GCTTCACCCA  AACCGTCCAA
151 AGCAAAAAGA  AAACCCAAAC  CGCGCACGGC  ACGTTCAAAA  TCCTGCGACC
201 GGGCCTTTTC  AAATGGGAAT  ACACCAAACC  TTACAGGCAA  ACCATCGTCG
251 GCGACGGTCA  AACCGTTTGG  CTCTACGATG  TTGATCTGGC  ACAAGTGACC
301 AAGTCGTCCC  AAGACCAGGC  CATAGGCGGC  AGCCCCGCG  CCATCCTGTC
351 GAACAAAACC  GCCCTCGAAA  GCAGCTACAC  GCTGAAAGAG  GACGGTTCGT
401 CCAACGGCAT  CGATTATGTG  CTGGCAACGC  CCAAACGCAA  CAACGCCGGC
451 TACCAATACA  TCCGCATCGG  CTTCAAAGGC  GGCAACCTCG  CCGCCATGCA
501 GCTTAAAGAC  AGCTTCGGCA  ACCAAACCTC  CATCAGTTTC  GCGGTTTGA
551 ATACCAATCC  CCAACTCTCG  CGCGGCGCGT  TCAAGTTTAC  CCCGCCCAA
601 GCGGTGGACG  TGTGAGCAA  CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1  MMKPHNLFQF  LAVCSLTVAV  ASAQAGAVDA  LKQFNNDADG  ISGSFTQTVO
51  SKKKTQTAHG  TFKILRPGLF  KWEYTKPYRQ  TIVGDGQTVW  LYDVDLAQVT
101 KSSQDQAIIG  SPAILSNKT  ALESSYTLKE  DGSSNGIDYV  LATPKRNNAG
151 YQYIRIGFKG  GNLAAMQLKD  SFGNQTSISF  GGLNTNPQLS  RGAFKFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	KQFNNDADGISGSFTQTVO	SKKKTQTAHG			
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	KQFNNDADGISGSFTQTVO	SKKKTQTAHG			
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVW	LYDVDLAQVTKSSQDQAIIGGSPAILSNKT				
g502-1	TFKILRPGLFKWEYTKPYRQTIVGDGQTVW	LYDVDLAQVTKSSQDQAIIGGSPAILSNKT				
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
	130	140	150	160	170	180
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAG	YQYIRIGFKGGNLAAMQLKDSFGNQTSISF				
	130	140	150	160	170	180

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```

                190      200
m502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
g502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACT GTTCCAATC CTCGCCGTT GTCCTCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGCGGGGCG GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT AACTTCGCC TTACAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTGTCTCC AAGACCAGGC CATAGGCGGC AGCCCCGCGC CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAA
601 GGCCTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTVQ
51 SKKKTQTAHG TFKILRPLGF KWEYTSYPYQ TIVGDGQTVW LYDVLQVVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTISIF GGLNTNPQLS RGAFKFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep      MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                |||||
m502-1          MMKPHNLFQFLAVCSLTVAVASAQAGAVDALKQFNNDADGISGSFTQTVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep      TFKILRPLGFKWEYTSYPYQTIVGDGQTVWLYDVLQVTKSSQDQAIGGSPAAILSNKT
                |||||
m502-1          TFKILRPLGFKWEYTKPYQTIVGDGQTVWLYDVLQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep      ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                |||||
m502-1          ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTISIF
                130     140     150     160     170     180

                190     200
a502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
m502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgctcgcatc ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcgaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaatatgcg ttcgttcaga ccgttgtgtg cgagaaatgc
201 gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

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m503.seq  
 1 atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat  
 51 ttcggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga  
 101 tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt  
 151 gccagtgcgg cggaaatgcg ttcgctcaga ccgttgtgtg cgaggaatgc  
 201 gcggtag

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

m503.pep  
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF  
 51 ASAAEMRSLR PLCARNAR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

m503/g503

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNFASAAEMRSLR					
	:					
g503	MSAPSASVILFHAASISASSCSGKGVSKIHWIRISLPTRASSETTSSTSNFARAAEMRSEF					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNAR					
g503	PLCARNAR					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

a503.seq  
 1 ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT  
 51 TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA  
 101 TTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT  
 151 GCCAGTGGG CCGAAATGCG TTCGCTCAGA CCGTTGTGTG CGAGGAATGC  
 201 GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

a503.pep  
 1 MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF  
 51 ASAAEMRSLR PLCARNAR\*

m503/a503 100.0% identity in 68 aa overlap

	10	20	30	40	50	60
m503.pep	MSAPPASATILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNFASAAEMRSLR					
a503	MSAPPASATILFHAASISASSCSGKGVSKIHWIRISLPTRASSATSSTSNFASAAEMRSLR					
	10	20	30	40	50	60
	69					
m503.pep	PLCARNARX					
a503	PLCARNARX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

g503-1.seq  
 1 ATGGCGCGGT CGTTGTACAG GGAGGCGAAA ACCTGGCGCA TCGCTTTTTT  
 51 AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA  
 101 ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG  
 151 GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTGTGTC ATGCCGCTTC  
 201 GATTTCCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC  
 251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT  
 301 TTTGCCAGAG CGGCGGAAAT GCGTTCGTTC AGACCGTTGT GTGCGAGAAA  
 351 TGC GCGGTAG

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

## g503-1.pep

```

1  MARSLYREAK TWRIAFLLS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSETSSTSN
101 FARAAMERSF RPLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

## m503-1.seq

```

1  ATGGCAGCGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51  AACGTTATCC AAGCCGTTGA TGTTCAAGAA GGTTTCCTGT TGCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCGG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTTCGGA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TCGCGGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

## m503-1.pep

```

1  MARSLYREAN TWCIASLTLK KPLMFKKVSC CPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRIAFLLSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPSASVI					
m503-1	MARSLYREANTWCIALTLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFARAAMERSFRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

## a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51  AACGTTTTCC AAGCCGTTGA TATCAGGAA GGTTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCGG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTTCGGA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTTCTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TCGCGGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

## a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51  EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*

```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRIASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATEMSAPPASAT					
m503-1	MARSLYREANTWCIALTLKPLMFKKVSCCPANDASGRSSAVAEERTATEMSAPPASAT					
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFASAAEMRSLRPLCARNARX					
m503-1	ILFHAASISASSCSGKGVSKIHWRISLPTRASSETSSTSNFASAAEMRSLRPLCARNARX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

g504.seq

```

1 atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggt gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tottgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgcgcgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgtga cgcgacccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cagcgcgagc ggcttgacag agcaataccg ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgcct atacggggct gacggaatat cccgcgccta
1001 tgctgctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcgggtgc gcttttggtc tatctcggct cggatttgtt
1101 ggttttggtt acagtattta tgttttatgt gcccataaaa cggcggtggg
1151 tattgttttc aaacdgcata atccgttttg ctatgtcttc ggcccgcagc
1201 gaacgggatt tgcagaagga atttccaaaa cagtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

g504.pep

```

1 MLVQDLPEFV KLKPFHIDFY NTGMPDRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTOEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDAPAEI REQFMLAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQODKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPKK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

m504.seq..

```

1 atattggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51 cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 tgacggacaa ggcaaccggt gagaaactcg agcgcacccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcgggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tottgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgatccgt gatgcggcag ggcaggcggt
501 cgaatataaa aactatatgc tgccggtttt gcaggacag gattattttt
551 ggattaccgg cagcgcgagc ggcttgacag agcaataccg ctggctgcgt
601 atccccttgg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaac
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcgtttcct
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgag

```

1051 atgaccggtt ccccggtg cgttttggtc tatctcggct cgggtgctgtt  
 1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg  
 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgagc  
 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg  
 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep..

1 ILVQDLPFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN  
 51 HPLTLHGITI YQASFADGGS DLTFKAWN LG DASREPVVLK ATSIHQFPLE  
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN  
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR  
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN  
 251 TLNIFAQKGY LGLDEFITSN IPKEQDKMQ GYFYEMLYGV MNAALDETIR  
 301 RYGLPEWQQD EARNRFLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ  
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS  
 401 ERDLQKEFPK HVESLQRLGK DLNHD\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng)  
 from *N. gonorrhoeae*:

m504/g504

m504.pep	10	20	30	40	50	60
	ILVQDLPFV KLKKFHIDFYNTGMPRDFASDIEVTDKATG EKLERTIRVNHPLTLHGITI					
g504	MLVQDLPFV KLKKFHIDFYNTGMPRDFASDIEVTDKATG EKLERTIRVNHPLTLHGITI					
	10	20	30	40	50	60
m504.pep	70	80	90	100	110	120
	YQASFADGGS DLTFKAWN LG DASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED					
g504	YQASFADGGS DLTFKAWN LG DASREPVVLK ATSIHQFPLE IGKHKYRLEF DQFTSMNVED					
	70	80	90	100	110	120
m504.pep	130	140	150	160	170	180
	MSEGAREKSLKSTLXDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPVLQEQ					
g504	MSEGAREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPILQDK					
	130	140	150	160	170	180
m504.pep	190	200	210	220	230	240
	DYFWITGTRS GLQQQYRWLR IPLDKQLKAD TFMALREFLK DGEGRKRLVADATKGAPAEI					
g504	DYFWLTGTRS GLQQQYRWLR IPLDKQLKAD TFMALREFLK DGEGRKRLVADATKDAPAEI					
	190	200	210	220	230	240
m504.pep	250	260	270	280	290	300
	REQFMLAAENTL NIFAQKGYLGLDEFITSN IPKEQDKMQGYFYEMLYGV MNAALDETIR					
g504	REQFMLAAENTL NIFAQKGYLGLDEFITSN IPKGQDKMQGYFYEMLYGV MNAALDETIR					
	250	260	270	280	290	300
m504.pep	310	320	330	340	350	360
	RYGLPEWQQD EARNRFLHSMDAYTGLTEY PAPMLLQLDGFSEVRSSGLQ MTRSPGALLV					
g504	RYGLPEWQQD EARNRFLHSMDAYTGLTEY PAPMLLQLDGFSEVRSSGLQ MTRSPGALLV					
	310	320	330	340	350	360
m504.pep	370	380	390	400	410	420
	YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS ERDLQKEFPK HVESLQRLGK					
	:     :     :     :     :					

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g504 YLGSVLLVLGTVFMFYVPKKRAWVLSN-KIRFAMSSARSERDLQKEFPKHVESLQRLGK  
 370 380 390 400 410

m504 . pep DLNHD  
 |||||  
 g504 DLNHD  
 420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

a504 . seq

```

1 ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTGAATA AATTCCATAT
51 CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
151 CATCCTTTGA CCTTGACCG CATCACGATT TATCAGGCGA GTTTTGCCGA
201 CGGCGGTTTC GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
251 GCGAGCCTGT CGTGTGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
301 ATTGGAACAA ACAATATCG TCTTGAGTTC GATCAGTTTA CTCTATGAA
351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA
401 CGCTGAACGA TGTCCGCGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GCGAGGCGGT
501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
551 GGATTACCGG CACGCGCAGC GGCTTGCAGC AGCAATACCG CTGGCTGCGT
601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
651 GTTTTGAAGA GATGGGGAAG GCGCAAAACG TCTGGTTGCC GACGCAACCA
701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TCGGAAAAAC
751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
801 TACGTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCTT
951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TGCGTTCGTC GGGTTTGCAG
1051 ATGACCCGTT CCCCGGGTGC GCTTTTGGTC TATCTCGGCT CGGTGCTGTT
1101 GATTATTGGT ACGGTATTGA TGTTTTATGT GCGCGAAAAA CGGGCGTGGG
1151 TATTGTTTTT AGACGCAAAA ATCCGTTTTG CCATGTCTTC GGCCCGCAGC
1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
1251 GCTCGGCAAG GACTTGAATC ATGACTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

a504 . pep

```

1 ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKES LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQQD EARNRFLLS MDAYTGLTEY PAPMLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERDLQKEFPK HVESLQRLGK DLNHD*
  
```

m504/a504 99.8% identity in 425 aa overlap

```

m504 . pep 10 20 30 40 50 60
ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI
|||||
a504 ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI
10 20 30 40 50 60

m504 . pep 70 80 90 100 110 120
YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
|||||
a504 YQASFADGGSDLTFKAWNLDASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
70 80 90 100 110 120

m504 . pep 130 140 150 160 170 180
MSEGAREKESLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKNYMLPVLQEQ
  
```



a504	MSEGAEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ	130	140	150	160	170	180
m504.pep	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI	190	200	210	220	230	240
a504	DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI	190	200	210	220	230	240
m504.pep	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR	250	260	270	280	290	300
a504	REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR	250	260	270	280	290	300
m504.pep	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV	310	320	330	340	350	360
a504	RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTRSPGALLV	310	320	330	340	350	360
m504.pep	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK	370	380	390	400	410	420
a504	YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSERDLQKEFPKHVESLQRLGK	370	380	390	400	410	420
m504.pep	DLNHD						
a504	DLNHD						

g505.seq	1	atgtttcgtt	tacaattcag	gctgtttccc	cctttgcgaa	ccgccatgca
51	catcctgttg	accgccctgc	tcaaatgcct	ctccctgctg	tcgctttcct	
101	gtctgcacac	gctgggaac	cggctcggac	atctgcgcgt	ttacctttta	
151	aaggagacac	gcgcgcgcac	cgtcgccaat	atgcggcagg	cgggtttgaa	
201	ccccgcacag	cagacggtca	aagcgtttt	tgcggaaaacg	gcaaaatgcg	
251	gtttggaact	tgcccccgcg	tttttcaaaa	aaccggaaga	catcgaaaaca	
301	atgttcaaag	cggtacacgg	ctgggaacac	gtgcagcagg	ctttggacaa	
351	gggcgaaggg	ctgctgttca	tcacgccgca	catcggcagc	tacgatttgg	
401	gcggacgcta	catcagccag	cagcttcctg	tccacctgac	cgccattgtac	
451	aagccgcgca	aaatcaaagc	gatagacaaa	atcatgcagg	cgggcagggt	
501	gcgcggcaaa	ggcaaaaccg	cgcccaccgg	catacaaggg	gtcaaaacaaa	
551	tcatcaaggc	cctgcgcgcg	ggcgaggcaa	ccatcatcct	gcccgaccac	
601	gtcccttctc	cgcaggaagg	cggcggcgctg	tgggcggatt	tttccggcaa	
651	acctgcatac	accatgacac	tggcggcaaa	attggcacac	gtcaaaggcg	
701	tgaaaaccct	gtttttctgc	tgogaacgcc	tgcccgcagg	acaaggcttc	
751	gtgttgacac	tccgccccgt	ccaaggggaa	tgaacggca	acaaaggcca	
801	cgatgcgcgc	gtgttcaacc	gcaataccga	atattggata	cgccgttttc	
851	cqacgcagta	tctgtttatg	tacaaccgct	ataaaacgcc	gtaa	

g505.pep

1	MFRLQFRLFP	PLRTAMHILL	TALLKCLSL	SLSCLHTLGN	RLGHLAFYLL
51	KEDRARIVAN	MRQAGLNPD	QTVKAVFAET	AKCGLELAPA	FFKKPEDIET
101	MFKAVHGEH	VQALDKGEG	LLFITPHIGS	YDLGGYISQ	QLPFHLTAMY
151	KPKKIKAKD	IMQAGRVRG	GKTAPTGIQG	VKQIKKALRA	GEATIIIPDH
201	VPSPEGGGV	WADFFGKPAY	GMTLAAKLAH	VKGVKTLFFC	CERLPDQGGF
251	VLHIRPVOGE	LNGNKAHDA	VFNRTTEYWI	RRFPTQYLFM	YNRYKTP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

## m505.seq (partial)

```

1  GGCATGTTTC GTTTACAATT CAGGCTGTTT CCCCCTTTGC GAACCGCCAT
51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
101 CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
151 TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
201 GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
251 GCGGTTTGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
301 ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
351 CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
401 TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTCCCCTG GACCGCCATG
451 TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
501 GGTTTCGCGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
551 AAATCATCAA AGCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
601 ACGTCCCCTC CCCTCAAGAA GCGGGGGAAG GCGTATGGGT GGATTCTTTC
651 GGCAAACCTG CCTATACCAT GACGCTGGCG GCAAATTGG CACACGTCAA
701 AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GCGGACAAG
751 GTTTCGATT GCACATCCGC CCCGTCCAAG GGGAATTGAA CGGCGACAAA
801 GCCCATGATG CCGCCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
851 TTTCCGACG CatATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

## m505.pep (partial)

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSLP LSLCLHTLGN RLGHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGEH VQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFGKPA YMTLAAXLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPFTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

## m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSLCLHTLGNRLGHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFKKPEDIETMFKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGLLELAPAFKKPEDIETMFKAVHGEHVQALDKHEG					
	70	80	90	100	110	120
m505.pep	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGGYISQQLPFLTAMYKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIIPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	240
m505.pep	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFGKPAYTMTLAAXLAHVKGVKTLFF					
g505	VKQIIKALRAGEATIIIPDHVPSPQEGG-GVWADFFGKPAYTMTLAAXLAHVKGVKTLFF					
	190	200	210	220	230	
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTH					
g505	CCERLPGGQGFVLRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTH					
	240	250	260	270	280	289
m505.pep	CCERLPGGQGFDLHIRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTH					
g505	CCERLPGGQGFVLRPVQGEELNGDKAHDAAVFNRNAEYWIRRFPTH					
	240	250	260	270	280	289

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

```
a505.seq
1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TCGCGAAACG GCAAAAGGCG
251 GTTTGGAAGT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAACCG CGCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

```
a505.pep
1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSCSLHTLGN RLGHlafyLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLELAPA FFRKPEDiet
101 MFKAVHWEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VVVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*
```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHlafyLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCSLHTLGNRLGHlafyLLKEDRARIVAN					
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDietMFKAVHWEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDietMFKAVHWEHVQQALDKHEG					
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPKIKAIKIMQAGRVRGKGKTAPTSIQG					
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVVDFFGKPAYTMTLAAXLAHVKGVKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVVVDFFGKPAYTMTLAAXLAHVKGVKTLFF					
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQELNGDKAHDAAVFNRNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

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## m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCAGCCCC AAAACGGTCA AAGCCGTTT TCGGGAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGGAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGA AAAACCG GCGCTACCAG CATAAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GCGGAAGCAA CCATCGTCTT GCCCGACCAC
601 CCCCCTCTCC CTCAAGAAGG GGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATGGCA CACGTCAAAG
701 GCGTGA AAC CCTGTTTTC TGCTGGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATGGAACG GCGACAAGC
801 CATGATGCC GCGTGTTC ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTT ATGTACAACC GCTACAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

## m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL PLSC LHTLGN RLGH LAFYLL
51  KEDRARIIVAN MRQAGLNPD KTVKAVFAET AKGGL ELAPA FFRK PED IET
101 MFKA VHGWEH VQALDKHEG LLFITPHIGS YDLGG RYISQ QLPF PLTAMY
151 KPPK IKAIDK IMQAGRVRGK GKTAPTSIQG VKQII KALRS GEATI VLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLA AKLA HVKG VKTLPF CCERLP GGQ
251 FDLH IRPVQG ELNGDKA HDA AVFN RNAYW IRRFP TQYLF MYNRY KMP*

```

## m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSLSLSC LHTLGNRLGH LAFYLLKEDRARIIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGL ELAPAF FRKPED IETMFKA VHGWEHVQALDKHEG					
g505	MRQAGLNPDPTQTVKAVFAETAKGGL ELAPAF FRKPED IETMFKA VHGWEHVQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGG RYISQQLPFP LPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPTSIQG					
g505	LLFITPHIGSYDLGG RYISQQLPFP LPLTAMYKPPK IKAIDKIMQAGRVRGKGKTAPTGIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATI VLPDHVPSPQEGGEGVWVDFFGKPAYMTLA AKLAHVKG VKTLPF					
g505	VKQIIKALRAGEATI ILPDHVPSPQEGG-GVWADFFGKPAYMTLA AKLAHVKG VKTLPF					
	190	200	210	220	230	240
m505-1.pep	CCERLP GGQGF DLH IRPVQGE L NGDKA HDA AVFN RNAYW IRRFP TQYLF MYNRY KMPX					
g505	CCERLPDGGQGFV L H IRPVQGE L NGNKA HDA AVFN RNTEY W IRRFP TQYLF MYNRY KTPX					
	240	250	260	270	280	290

## m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGH LAFYLLKEDRARIIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120

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m505-1.pep	MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMPKAVHGWHEHVQQALDKHEG
a505	MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDMETMPKAVHGWHEHVQQALDKHEG
	70 80 90 100 110 120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTTSIQG
a505	LLFITPHIGSYDLGGYISQQLPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTTSIQG
	130 140 150 160 170 180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
a505	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
	190 200 210 220 230 240
m505-1.pep	CCERLPGGQGFDLHIRPVQGEINLGDKAHDAAVFNRNAEYWRPPTQYLFMYNRYKMPX
a505	CCERLPGGQGFDLHIRPVQGEINLGDKAHDAAVFNRNAEYWRPPTQYLFMYNRYKMPX
	250 260 270 280 290 299

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

g506.seq

```

1  ATGCGCGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51  TGTCAAACAA AGCCTGTTTC TGCGCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GGCGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGGCGC GGCCTTGTCG GTGCGCTGGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GGCGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC
451 ATCGGCGAAG AAGTTTTTCG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTC GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTTGGTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAATTTCA CCCAAAAACG
751 TTCGCCGCTC TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGGG CTTCGGGCAG CAGCGTCCAG AAGTCCCATG TGTGTGTGGC
901 GGAACGCATA TTGGTGCGCG GATCGCGTTT GACGGCTTTG TTCAGGTCGG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCCACT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACCGCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAAGCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGGCGCGC CGTTGTTTCA
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCCCT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

g506.pep

```

1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHVQ EQGARLAEV VIVLAVVPVC
51  RVAVDFORRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEVVFGLAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFG IGFRHDLDVH

```

201 RPFRELAALD GFVQVALMAF AVVGDDFCFS FVGQVFNPLL AAEMEFHPKT  
 251 FARFVPEAVG MRTEAVHMAV AGGNTAVAH DGNLVQGFQ QRPEVPVVC  
 301 GTHIGARIAF DGFVQVGEFA RVAQEEHGRV VADHIPVAFF GIEFQRKTAD  
 351 VAFRIGCAAL ACHGGETGEH LGFFADFAEN FGAGVFGDVV CYGKRTERAR  
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQG AARAGGQAVL IVGNGRAVVH  
 451 GQMGYGAFGG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES  
 501 TFYFPFAKTM DAIIRQDFRY \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1377>:

m506.seq

1 ATGGCGGTAT TTGATGAAGT CGGGCGCGTC GCCCATTGCG GCGGCGGTGT  
 51 TGCCGAACAA TGCTGTTC TCGCGTCTG TCATCAGGT GAACAGGGCG  
 101 CGCGGTTGGC TGAAATAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC  
 151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGGAATCG GGTGTGTGCT  
 201 GCCATTGGCC GAAGCTGTyG GGTTCGTAGT GCGGCAGGCT GCCGyAGTTG  
 251 CCGTCGCGCG GGCCTTGCCC GTyGCGsTgr TTgTGTgAA CAsGGCAACG  
 301 CGGACGATTG ACGGGAATTT GCGGGAAGTT TACGCCCCAA CCGTAGCGTT  
 351 GTGCGTCGGC GTAATTGAAC AAACGCGCTT GCAGCATTTT ATCTsGGCTG  
 401 GCGCCGACAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCCAC  
 451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CTCAAACGGA TGATAAGGTA  
 501 CTTTTTCCGC GTCTGCTTCA GGCATGACTT GGATGTACAT CGTCCATTTC  
 551 GGAAACTCGC CGCGTTCGAT GGCTTCsTAT AAGTCGCGCT GATGGCTTTC  
 601 GCGGTCGTCG GCGATGATTT TGGCGGCTTC TCGTTGGTC AGGTTTTTAA  
 651 TGCCTTGTTG GGTGCGGAAA TGGAATTTCA CCAAAAACG CTCGCTGCT  
 701 TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA TATGGCGGTA  
 751 GCGGCGCGGG ATGCGCGGCT CGCTCATCAC GATGGTAACT TGGTGCAGTG  
 801 CTTGCGGCAG CAGCGTCCAG AAGTCCCAGT TGTGTGTGCG AGAGCGCATA  
 851 TTGGTGCAGG GGTGCGGTTT GACGGCTTTG TTCAGGTGCG GGAACCTACG  
 901 CCGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC ACATCCCAGT  
 951 TGCCTTCTTC GGTATAAAAT TTCAAGGCAA AACCGCGGAT GTCGCGTTCT  
 1001 GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC GGGCGAACAT  
 1051 CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TCCTTTGGCG TGCCATACGGC  
 1101 GTTCGGGGAT GACTTCGCGC ACGAAGTCGG CGAGTTTTTC AGTCATCGCT  
 1151 CTTGTTCCTT TTCTCAGGTT GGTCAAATGG GGGTAAACGG CTTACAGTAC  
 1201 GATTTGGCGG AAAGCGTATT CGTAACCGGT TTCTTGATTG CAATAAATT  
 1251 CTTGAATCGA CATTTTATT CCCTTTTGTA AAAACTATGG ATGCGACTAT  
 1301 ACGCCAAGAT TTTCGCTATT AA

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

m506.pep

1 MAVFDEVGRV AHC GG GVAEQ CLFLRVVHV EQGARLAEIV VIVLAVVPVC  
 51 RVAVDQRRF GESGLLLPLA EAVGFVVRQA AXVAVGAALP VAXXAVNXAT  
 101 RTIDGNLAEV YAQTVALCVG VIEQTRLQHF IXAGADTGNE VARCEGGLFH  
 151 IGEVFGIAV QLEFAHFNQR IVFRPNFGQ VKRMIRYFFR VCFRHDLDVH  
 201 RPFRLAAFD GFXXVALMAF AVVGDDFGGF FVGQVFNALL GAEMEFHPKT  
 251 LACFVPEAVG MRTEAVHMAV AGGDAVAH DGNLVQCFQ QRPEVPVVC  
 301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIKFQKTD  
 351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYKRTERRAR  
 401 TFGVHTAFGD DFAHEVGEFF IQPQILRQR AARTGGQAVL IVGNRAVVH  
 451 GQMGYRAFGG SHRSCSFSQV GQMGGKRLTV RFGGKRIRNR FLDCNKFLES  
 501 TFYFPVKTM DATIRQDFRY \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

m506/g506

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQEQGARLAEIVVIVLAVVPVCRVAVDQRRF					
g506	MAVFDEVGRIAHGCGGVVQSLFLRVVHVQEQGARLAEVVVIVLAVVPVCRVAVDQRRF					
	10	20	30	40	50	60

		70	80	90	100	110	120
m506.pep	GESG	LLLLPLAE	AVGFVVRQA	AXVAVGAALP	VAXXAVNXATRT	IDGNLAEVYAQT	VALCVG
g506	GEVG	LLLLPLAE	AVGFVVRQA	AVVAVGAALS	VALVAVNRATRT	IDGDLAEVHTQA	VTLRVG
		70	80	90	100	110	120
		130	140	150	160	170	180
m506.pep	VIEQ	TRLQHFIX	AGADTGNE	VARCEGGLF	HIGEEVFGI	AVQLEFAHFN	QRIVFFRPNFGQ
g506	VIEQ	TGLQHFIR	ARADTGNE	VARCEGGLF	HIGEEVFGI	AVQLEFAHFN	QRIVFFRPNFGQ
		130	140	150	160	170	180
		190	200	210	220	230	240
m506.pep	VKRM	IIRYFFRV	CFRHLDLV	HRPFRKLA	AFDGFXXV	ALMAFAVVG	DDFGGFFV
g506	VKRM	IRHFFGIG	FRHLDLVH	RPFRRLA	ALDGFVQV	ALMAFAVVG	DDFCSSFV
		190	200	210	220	230	240
		250	260	270	280	290	300
m506.pep	GAEM	EFHPKTL	ACFVPEAV	GMRTAVH	MAVAGGDA	AAVAHHDGN	LVQCFGQQR
g506	AAEM	EFHPKTF	ARFVPEAV	GMRTAVH	MAVAGGNT	AVAHHDGN	LVQFGGQQR
		250	260	270	280	290	300
		310	320	330	340	350	360
m506.pep	RAHI	GARVAFD	GFVQVGEL	TRVAQEEH	GRVVADHIP	VAFFGIKFQ	GKTADVAF
g506	GTHI	GARIAFD	GFVQVGEP	ARVAQEEH	GRVVADHIP	VAFFGIEFQ	RKTADVAF
		310	320	330	340	350	360
		370	380	390	400	410	420
m506.pep	ACHG	GETGEHL	GFFADFAE	DFGAGVFG	DVVRYGKR	TERARTFG	VHTAFGDD
g506	ACHG	GETGEHL	GFFADFAE	NFGAGVFG	DVVVCYGR	TERARTFG	VHTAFGDD
		370	380	390	400	410	420
		430	440	450	460	470	480
m506.pep	IQPQ	ILRQQRA	ARTGGQAV	LIVGNRR	AVVHVGQM	GYRAFGGS	SHRSCSFS
g506	IQPQ	ILRQQGA	ARAGGQAV	LIVGNRA	VVHVGQMG	YAFGGSHR	SCSFSQVG
		430	440	450	460	470	480
		490	500	510	520		
m506.pep	RFGG	KRIRNR	FLDCNK	FLESTFY	FPFVKTM	DATIRQD	FRY
g506	RFGG	KRIRNR	FLDCNK	FLESTFY	FPFAKTM	DAIRQD	FRY
		490	500	510	520		

a506.seq

1	ATGGCGGTAT	TTGATGAAGT	CGGGCGCGTC	GCCCATTGCG	GCGGCGGTGT
51	TGCCGAACAA	TGCTGTTC	TGCGGTCTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGTTTGGC	TGAATATGTC	GTCACTCGTCT	TGGCGGTAGT	CCCGATGCGC
151	CGCGTCGCCG	TTGATTTTCA	AAGGCGGTTT	GCGCAAGTCG	GCGTGTCTGT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAAGT	GCGGCAGGCT	GCCGTAGTTG
251	CCGTGCGCGC	GTCTTGTGCC	GTGCGCTGTG	TTGCTGTGAA	CAGGGCACAACG
301	CGGACGGTTG	ACAGGGATTT	GGCGGAAGTT	CACGCCCAAG	CGGTAGCGGT
351	GCGCGTCGCG	GTAATTTGAAC	AAACGCGCCT	GCAACATTTT	ACTTGGGCTG
401	GCGCGGACAC	CGGGAACGAG	TTGTGTCGGT	GCGAAGGCGG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CAACTCGAAT	TGCGCCACTT
501	CAATCAGCGG	ATATGCTTTT	TTGCGGCAAA	CTTTGGTCAA	GTCAAACGGA
551	TGATACGGCA	CTTTTTCGCG	ATCGGCTTCA	GGCATGACTT	GGATGTACAT
601	CGTCCATTTT	GGAACTCGC	CGCGCTCGAT	GGCTTCGTAC	AGGTGCGCCT

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651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTTG GGTGCGGAAA TGGAAATTCA CCAAAAACG
751 CTCGCCTGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCACTG CTTCCGGCAG CAGCGTCCAG AAGTCCAGT TGTTTGTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGCTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGCAA AACC CGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCTCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

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This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

a506.pep

```

1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHVQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFFQRRF GEVGLLLPLA EAVGVFVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGFRHDLVDH
201 RFFRKLALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICGCAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRKTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQOR AARTGGQAVL IVGNRRRAVH
451 GQMGYRAFPG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPFVKTM DATIRQDFRY *

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m506/a506 94.8% identity in 520 aa overlap

	10	20	30	40	50	60
m506.pep	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQVEQGARLAEIVVIVLAVVPVCRVAVDFFQRRF					
a506	MAVFDEVGRVAHCGGGVAEQCLFLRVVHVQVEQGARLAEIVVIVLAVVPVRRVAVDFFQRRF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m506.pep	GESGLLLPLAEAVGVFVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
a506	GEVGLLLPLAEAVGVFVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506.pep	VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
a506	VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506.pep	VKRMIRYFFRVCFRHDLDVHRPFRKLAAFDGFXVALMAFAVVGDDFGGFFVGQVFNALL					
a506	VKRMIRHFFRIGFRHDLDVHRPFRKLALDGFVQVALMAFTVVGDDFGGFFVGQVFNALL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506.pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVC					
a506	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDAVAHHHDGNLVQCFGQQRPEVPVVC					
	250	260	270	280	290	300



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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGLTRVAQEEHGRVVDHIPVAFFGIKFQKGTADVAFICIGCAAF					
a506	RAHIGARVAFDGFVQVGLTRVAQEEHGRVVDHIPVAFFGIELQKRTADVAFICIGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCFSQVGMGGKRLTV					
a506	IQPQILRQORAARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCFSQVGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
a506	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq  
 1 ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG  
 51 TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG  
 101 CCTTTGCGCT CTTCTGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG  
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT  
 201 GGGTTTGGAA GGCAGCGTTG AGCGTGGCTT GGACTTCTTC CAATTCGGGC  
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAATTCGGT  
 301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT  
 351 GCTGCTGCTC CTGCCGGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG  
 401 TCGCGTTCGA TCGGTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC  
 451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCGT  
 501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG  
 551 TTATTTAA

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep  
 1 MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNGLFGMGKL  
 51 LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG  
 101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF  
 151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq  
 1 ATGCTCTTGC TGA CT TTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG  
 51 TTTCGGCCTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTCAGACGA  
 101 CCTTTGCGCT CTTCTGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG  
 151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCTGCT  
 201 GGGTTTGGAA GCGCGCGTTG AGCGTGGCTT GGGCTTCTTC CAATTCGGGC  
 251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCGG CCAGCTCGGT  
 301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT  
 351 GCTGCTGCTC TTGATGAATG CGTTGTAACT GCGCCTGCGC TGCCTGCTTG  
 401 TCGCGTTCGA TCGGTGGTG CAGGTTTTCG TGATGCGGGA TTTGTTCTTC  
 451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTG CTCAATTCAT  
 501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG  
 551 TCGTTTAA

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep  
 1 MLLLTQQGG CFLRGGGFGF VGQVXGLVFL FQTFALFVL GNRLFGMGKL

51 ILLQRFQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLVFG NLHRPFRQLG  
 101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLFF  
 151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

m507/g507

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	:              :           :     :					
g507	MLLPALQGGGFLSGGGFGLVGVQVGLVFLQLTAFALFVLGNLFGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m507.pep	AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
	:             :             :             :					
g507	AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFDLQLVFLKLHADLLLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m507.pep	LMNALXLRRLCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
	:                      :                   :       :					
g507	LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
	130	140	150	160	170	180
m507.pep	VYFVV					
	:					
g507	VYFVI					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1385>:

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGCTTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTCTCTG	TTTCAGACGA
101	CCTTTGCGCT	CTTCGTGCTT	GGCAACGGTT	TGTTCCGGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	TCGTCCTGCT
201	GGGTTTGGA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTCCGGG
251	AGACGCTCTT	CGTGTTCGGC	AACCTGCATC	GCCATTCCG	CCAATTCCGT
301	TTGCTTTTCT	TCCGCCTGCA	ACTCGTTTTC	TTCAAGCTGC	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCCTGCGC	CGCCTGCTTG
401	TCGCGTTTCA	TGCGTTGGTG	CAGGTTTTTC	TGATGGCGGA	TTTGTTCCTC
451	CAAACGGGCA	ATCTGTTTCG	GCAACACGCC	GCGTTTGTTC	CCCAATTCTG
501	GCACCGCCTG	CTGCTGCGAC	TGTTCCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTAA				

This corresponds to the amino acid sequence <SEQ ID 1386; ORF 507.a>:

a507.pep

1	MLLLALQGG	SFLRGGGFGF	VRQIQGLVFL	FQTTFALFVL	GNLFGMGKL
51	LLLQRFQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	FKLHADLLLL	LMDALHLRLR	RLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLQG	VYFVV*	

m507/a507 89.7% identity in 185 aa overlap

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGFVGQVXGLVFLFQTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	:             :             :					
a507	MLLLALQGGGFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL
            |||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLHRPFRQFGLLFFRLQLVFFKLHADLLLL
            70      80      90      100     110     120

            130     140     150     160     170     180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
            |||||
a507       LMDALHLRLRLLVAFDALVQVLLMADLFFQTGNLFAQHAAFVAQFVHRLLLRLFGSLQG
            130     140     150     160     170     180

m507.pep  VYFVVX
            |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTTCAG GGTTCGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTGA ATCTGCGCA GTTTTCCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GCGGATTTGC TGCCGGTAGT TTTGTTTTTG CGGGTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFFL
51 HGVVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVLF L RVEFVDGDFG KPVLA VG FQ GKLR L FQTAL LLLA AVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51 TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTTCAG GGTTCGCACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTGA ATCTGCGCA GTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTGGA ACTCGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GCGGATTTGC TGCCGGTAGT TTTGTTTTTG CTGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51 HNNIFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVLF L LVEFVDGDFG KPVLA VG FQ GKLR L FQTAL LLLA AVRGGL
151 LLVFEFGGGF LQGNVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

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	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFFLLHNNIFFVQGL					
g508	MVAFGVDQGLLLQGGGLGGGLKLRQLGLQGLYAGVLLPALFLNLRFFLLHGDVFFVQVRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFEPGDLLPVVLFLLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGNDDV					
g508	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQSSDDV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```

a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGCAGCT TGGTTTGCAG GGTTTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCTCTG
151 TACGACAATA TATTCTTCGT CCAAACCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGG ACTCGGTTTC ATAGCGGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGT GTTCAAGCTG
301 GGCAATTTGC TGTGGTAGT TTTGTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAATG GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```

a508.pep
1  MVAFGVDQGF LLLQGGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLRFFLL
51  YDNIFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLAF LPIEGLLFKL
101 GNLLLVVLF LVELVDGDFG KPVLA VG FQ QG KLR L FQTALLLLAAVRGGL
151 LLVFEFGGGF LQNGDVV*

```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLRFFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLYAGVLFPTLLNLRFFLLYDNIFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFKLGDLLPVVLFLLVEFVDGDFG					
a508	YGFAQLFELD VLLVVLELGFIGEGKLLLAFLPIEGLLFKLGNNLLVVLFLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGNDDVVX					
a508	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQNGDVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

```

1  atggtcgctg tatgtgatga acgggctgta cagcggacgt tggaggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgctgttg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggccgaa gcataaggct cgagaaagcc gaatttgcag cccatgcccc
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggttcttc ggtgcgggag atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgctgcggta aaaacggaa
551 acgcgcatcg cgtggcgcg gaaggcaaa cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcgg cgccgccgat ccagccgccg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgttccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cagcggcttg ttgatttcgt cgttgacgct gagtttggg cggcgcgttt
801 cgctggtctg ccacaagccc agaagcacgg tgtcgatttc gcggcgagc
851 cgtgccagcg cgtcgccatt ggtgcagcgt tcgcgttgcg gcagcagcg
901 gcggatgcgg cgtttgaaat tcaaaacggc ttggcgttgc acttcggctg
951 ggtgcgcggc caaaacggcg gtaacggacg tattgtccaa ctgccgctgc
1001 accgatttgc cgtcggtttt ccccgctttg agcctgcgga cggtttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgtgg atttggcggc
1101 ggcttctgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtgc ggaagtggac aagagtttga
1251 ccgtttcgac aaccaacggc gaggcttctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtccgccgcc aaagccgcgt ccttcggatt
1351 gtccaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcc aaccgttcac actttaacca
1451 ctcattgtccc gaaatgccgt ctgaagtga acgcccgcgg acggcgcgct
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctcttctgtc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatat
1651 tttggtcgtc ggctgcggcg gattgggcgc cgcgcgccct gccctatctc
1701 gccgcctcgg ggtcgggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1  MVAVCDERAV QRTLVAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAFALRQOR
301 ADAAVEIQNG LALHFGRVVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMLHDFP LIAVNTVNVP QMPHPQTVH TLTHVPKCR LKLNAARRRR
501 YNRPLFFSE HHHDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1  ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTGCGCGAA CAGGGCGGTT TGTttttGCT CTTCGTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTtt
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGACGGCTG
251 CGTTGTTCGA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGCGGTT AGGGTTCTTC GCGCGGGGCG ATTTCTTCGT CGGCGGATTT
451 GTCGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGTTC CGCCGCGATA GAAGCGGAAC

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551  ACGGCATCGG  CGTGGCGGCG  GAAGGCAAAG  CGCAGGGTTT  CGGCAGAAAC
601  AAACGGATTG  CCGTCGCGGT  CGCCGCGGAT  CCAGCCGCCG  ATTTTGAGGA
651  TGTCGGGAAC  GCGGACGCCG  GGATAGGCCG  TCTGAAAGTC  GTGTTCCATC
701  TTGCGGTAGA  GCTTGGGCAG  GGCTTCGAAA  AAGCTCATCG  GGAAGATGGA
751  CACGCCGTG  TTGATTTCTG  CGTTGACGCT  GAGTTTGTGG  CGGCGGTTTT
801  CGCTGGTCTG  CCACAAGCCC  AGCAGGATAG  TGTCGATTtC  GCgCGCAGC
851  CGTGCCAGCG  CGTCGGCATT  GGTGCAGCGT  TCgCGTTGCG  GCAACAGTGC
901  GCGGATGCGG  CGGTGAAGC  TTAAGACGGT  TTGGCGTTGC  ACTTCGGTCG
951  GGTGCGCGGT  CAAAACGGCG  GTAACGGACG  TATTGTCCAA  CTGCCGCTGC
1001 ACCGATTTGC  CGTCGGCTTT  CCCCCTTTG  AGCCTGCGGA  CGGTTTCCGT
1051 CAGGCTGCCT  TCCGCGCCGC  CGCGTCCGGC  TTCTTCGTGG  ATTTGGCGGC
1101 GCGGTTCTGT  GTGCACGTCT  TCGGCGATGT  TCAAATCTG  GGCGAACAGG
1151 CCGCAGGCCA  AGGTTAAATC  GTGGGTTTGT  TGTCGTCCA  ATTGCGGCAA
1201 TACTTTTCA  ATCAATGCCG  CGCTGTCGTC  GGAAGTGGAC  AAGAGTTTGA
1251 CTGTTTCGAC  AACCAACGGC  GAGGCTTCTT  CGTGCAGGAG  GTTGAACAGG
1301 GATTGTTTCA  GAAATTCGCG  GTCCGCGGCC  AAAGCCGCGT  CCTTTGGATT
1351 GTTCAGAATA  TGCAAGTGCA  TGATTTTCT  CTCTCGTCTG  CCGTAAATAT
1401 TGTAATGTA  CCCCAAATGC  CGCATCCGTG  CCAAACCGTT  CACACTTTAA
1451 CCGCCCGTGT  CCCGAAATGC  CGTCTGAAGT  TGAACGCCGC  CCGACGGCAG
1501 CGTTACAATC  GCCCGCAACT  GTTTTtTCC  GAACATCATC  ATGACCACGA
1551 CCGAACACGA  CAACGACGAT  GCATTCCTGC  TCGGTACAG  CCGCCACATC
1601 CTCTTGGACG  AAATCGGCAT  CGAAGGGCAG  CAGAACTTT  CCGCCGCGCA
1651 TATTTTGGTC  GTCGGCTGCG  GCGGTTTGGG  TGCCGCCGCA  CT.GCCCTAC
1701 CTTGCCGCTT  CGGTGTGCG  CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

m509.pep

```

1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVUDA EFVAARFAGL PQAQDSVDF AAQPCQRVGI GAAPALRQQC
301 ADAAVEAXDG LALHFGVRVG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDCFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNARRQ
501 RYNRPQLFFS EHHHDHDTTR QRRCI PAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

m509/g509

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
g509	MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVFQACVLEKLGNHIGVFACVLAQVERH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLOFFQIIQKLLCRSIRLEKA EFAAHTQTER					
g509	HVEAEHGHGTDEVCQTAFGKQAAA VVDKGTLOFFQII EKFLGRSIRLEKA EFAAHTQTER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDGAAVGFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI					
g509	ARFAHSARHNVGNAAVRFVFFGAGDFFVRRREGQCHYVVVDFDAADGKRQFAVKFEFAAV					
	130	140	150	160	170	180

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIVAVAAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
	:::     :     :     :     :     :					
g509	KTEHGIGVAAEGKAQGFARNKRIVAVAAADPAADFDIRNADIGIGRLKVVFHLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQDSDVFAAQCQRVIGAAAFALRQQC					
	:     :     :     :     :     :					
g509	GFKKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQKHGVDFAAQCQRVIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADAAVEAXDGLALHFGRVGRQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG					
	:     :     :     :     :					
g509	ADAAVEIQNGLALHFGRVGRQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFCCVVAG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVFGDVQNLGEQAAGQGXIVGLLFVQLRQYFFNQCRVAVGSGQEFDCFD					
	:     :     :     :     :     :					
g509	IFVDLAAAFVHVFGDIQNLGEQPAQKRQIVGLPFVQLRQYFFNQCRVAVGSGQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPQCQTV					
	:     :     :     :     :					
g509	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLRIQDMQLHDFPLI-AVNTVNVNVPQMPHPQCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCRLKLNAARRQRYNRPQLFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH					
	:     :     :     :     :					
g509	HTLTTHVPKCRLKLNAARRRRYNRPQLFFSEHHHDDRTQRRTTAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTCPTLPLRV SAR					
	:     :					
g509	RRAAEAFRRAYFGRRLRRIGRRRCPISPGR SAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1   ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGCT TGTTTTGTCT CTTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTG GAAAAGCTCG GCAACCACAT CGGCGTGTG
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTGCGCAAG CAGGCGGCTG
251 CCGTTGTGCGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTGT CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GCGCGGGCG GTTCTTCGT CGGGCGATT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTCGAGT CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 GAACGGATTG CCGTCGCGGT CGCCGCGGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTGATTTC CGGCGCGCAG
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

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901 GCGGATGCGG CGGTTGAAAT TCAAGACGGT CTGGCGTTGC ACTTCGGTCCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTGTC CGTCGGCTTT CCCCCTTTG AGCCTGCCGA CGGTTTCCGT
1051 CAGGCTGCCT TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GGCCTTCGTG GTGCACGTCT TCGGCGATGT TCAAAATCTG GCGGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCGTCCA ATTGCGGCAA
1201 TACTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CCGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCGCG GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTCT CTCATTGCCG TAAATACTGT
1401 AAATGTACCT CAAATGCCGC ATCCGTGCCA AACCGTTCAC ACTTTAACCG
1451 CCCGTGTCCC GAAATGCCGT CTGAAGTTGA ACGCCGCCCG ACGGCAGCGT
1501 TACAATCGCC CACAACGTT TTT.TCCGAA CATCATCATG ACCACGACCG
1551 AACACGACAA CGACGATGCA TTCCTGCTGC GGTACAGCCG CCACATCCTC
1601 TTGGACGAAA TTGGCATCGA AGGGCAGCAG AAACCTTCCG CCGCGCATAT
1651 TTTGGTCGTC GGCTGCGGCG GTTTGGGTGC CGCCG.CCCT GCCTATCTC
1701 GCCGCTCCG GCATCGGCAC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1398; ORF 509.a>:

a509.pep

```

1  MVAVCDERTV QWTLMAQFAQ QGGLFLLFVE AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGYGT DEVCQTAFGK QAAAVVDKGM LQFFQIIIEKF
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGNGATVGFF GAGGFFVGRF
151 VQQRHHIAVD FDAADGERQF AVEFVEFATV KTEHGIGVAA EGKTQGFGRN
201 ERIAVALAAD PAADFEDVRN ADIGIGRLKV VFHLAVELGQ GFKAHRKDG
251 HAVVDFVDDA EFVAARFAGL PQAQDSDVDF AAQPCQRVGI GTAFALRQOR
301 ADAAVEIQDG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQG*I VGLLFVQLRQ
401 YFFNQCRVAV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LIAVNTVNVF QMPHPQTVH TLTARVPKCR LKLNAAARRQ
501 YNRPQLFXSE HHHHDHRTRO RRCIPAAVQP PHPLGRNWHR RAAETFRAY
551 FGRRLLRFGC RXPCPISPLP ASAR*

```

m509/a509 93.0% identity in 575 aa overlap

m509.pep	MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNHIGVFACVLAQVERH
a509	MVAVCDERTVQWTLMAQFAQQGGLFLLFVEAVVVVFQACVLEKLGNHIGVFACVLAQVERH
	10 20 30 40 50 60
m509.pep	HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
a509	HVEAEHGYGTDEVCQTAFGKQAAAVVDKGM LQFFQIIIEKF LCRSIRLEKAEFAAHTQTER
	70 80 90 100 110 120
m509.pep	ARFAHSARHNVDGAAVGFAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
a509	ARFAHSARHNVDGAAVGFAGDFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFATV
	130 140 150 160 170 180
m509.pep	EAEHGIGVAAEGKAQGFGRNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ
a509	KTEHGIGVAAEGKTQGFGRNERIAVAVAADPAADFEDVRNADIGIGRLKVVFHLAVELGQ
	190 200 210 220 230 240
m509.pep	GFEKAHREDGHAVVDFVDDAEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGIAAFALRQOC
a509	GFKAHRKDGHAVVDFVDDAEFVAARFAGLPQAQDSDVDFAAQPCQRVGIGIAAFALRQOR
	250 260 270 280 290 300
	310 320 330 340 350 360



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```

m509.pep      ADAAVEAXDGLALHFGRVVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          ADAAVEIQDGLALHFGRVVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG
              310      320      330      340      350      360

              370      380      390      400      410      420
m509.pep      FFVDLAAAFVHVFGDVQNLGEQAAGQGIXIVGLLFVQLRQYFFNQCRVAVGSGQEFDCFD
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          FFVDLAAAFVHVFGDVQNLGEQAAGQGIXIVGLLFVQLRQYFFNQCRVAVGSGQEFDRFD
              370      380      390      400      410      420

              430      440      450      460      470      480
m509.pep      NQRRGFFVQVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSAVNIVNVPQMPHPCQTV
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          NQRRGFFVQVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSI-AVNTVNVPQMPHPCQTV
              430      440      450      460      470

              490      500      510      520      530      540
m509.pep      HTLTARVPKCRLKLNAAARRQRYNRPQLFFSEHHHDHTRQRRICIPAAVQPPHPLGRNRH
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          HTLTARVPKCRLKLNAAARRQRYNRPQLFXSEHHHDHTRQRRICIPAAVQPPHPLGRNWH
              480      490      500      510      520      530

              550      560      570
m509.pep      RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
              |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
a509          RRAAETFRRAYFGRRLRRFGCRXPCFISPLPASARX
              540      550      560      570

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagcg
51  ggatagtgcc ttttggcagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggtcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgtccgcgac
201 gcggccgcct tcgcgcatgg ctccggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttggtc gatgttcac ctttaatcct
351 tattgtgctg tttcctgccg ttgggggagg cgcgctgccg gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTLAAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFDVLDF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGCT TTTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG TGTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 GCGGTGCAwG ACTTCAAtGT GGAATTGTTC GATGTTGATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCCA TTGGGGGAGG GCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTLAAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFXVDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA F WQALSISAILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
g510	MPSRTPQGKRGYSCPKRDSA F WQALSISVILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVXDFXVDLFDVHPLILIAA					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVHDFD VDLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

```

1  ATGCCTTCGC GGACACCGCA GGGAAAAAGG GGTTATTCCT GCGCCAAGCG
51  GGATAGTGCT TTTGGCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTTCA GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGC TGTCGCGCAC
201 GCGTCCGCCT TCGCGGATGG CTTTCGGCTT GCCGTTGAGC ATTCCGACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCCG GCGTGTGAC GGTGAGCCGG
301 G.CGTGCATG ACTTCGATGT GGACTTGTTG GATGTTGATC CTTTAATCCT
351 TATTGCTGCG TTTCTGCGG TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

```

1  MPSRTPQGKR GYSCAKRDSA F WQALSISAI LRAKSPIAKS PPFREVFNR
51  WTTLSAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLT VSR
101 XVHDFD VDLF DVHPLILIAA FPAVGGGALP VR*

```

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSA F WQALSISAILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
a510	MPSRTPQGKRGYSCAKRDSA F WQALSISAILRAKSPIAKSPPFREVFNRSWTTL SAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRGVXDFXVDLFDVHPLILIAA					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLT VSRXVHDFD VDLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

```

1  atgaaagtgc ttgttttagg tgcgggtgtt gccggcgat cctccgtgtg

```

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```

51  gtatctggca gaggccggac atgaagtaac ggtcatcgac cgcaccgagg
101  gtgtggcgat ggaaaccagt tttgccaatg caggccagct ttcttacggc
151  tataccacgc cttgggctgc acccggtatt ccgaccaaag cactgaaacg
201  gctgtttaaa agccatccgc ctttactgtt ccgccctgac ggcggcctgt
251  atcaaataca atggctgtgg cggatgtcgc aaaactgcac ggcaacgcgc
301  tatcaaataca ataaagagcg catggtcagg atttccgaat acagccgtga
351  aatgtttccgc cgttttgaag cgcaaaccga catgaatttt gagggacgca
401  aaaaagggac gttgcagatt ttccgccaaa ccgaagaagt cgaagcggca
451  aaacaagaca ttgccgtttt ggaacgctac ggcggtgccg accgccgtct
501  gaagcccga  gaatgcgcag aattcgagcc tgcgttgga  cgcgttaccg
551  caaaaattgt cggcggctct cacctgcctg cggatgcgac cggcgactgc
601  cgcctcttca ccgaaaacct gtacaaattg tgtcaagaga agggggtagc
651  gttctacttc aaccaaacca tcagccgcac cgaccacaac gggctgcgca
701  tcaaagccgt tgaaacgaaa cagggcggtt tgaacagat gccgttgtct
751  gcgcgctcgg ctgcttcagc aggactgtgt tggcgagtt ggatctcaat
801  ctgcccattt atcccgtcaa aggtatttcc ttga

```

This corresponds to the amino acid sequence <SEQ ID 1406; ORF 512.ng>:

g512.pep

```

1  MKVLVLGAGV AGVSSVWYLA EAGHEVTVID RTEGVAMETS FANAGQLSYG
51  YTTPWAAPGI PTKALKRLFK SHPPLLFRPD GGLYQIEWLW RMLQNCTATR
101  YQINKERMVR ISEYSREMFR RPEAQDTMNF EGRKKGTLOI FRQTEEVAAA
151  KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIVGGL HLPADATGDC
201  RLFTENLYKL CQEKGVRFYF NQTISRIDHN GLRIKAVETK QGGLKQMPLS
251  ARSAASAGLC WRSWISICPF IPSKAIP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1407>:

m512.seq (partial)

```

1  ..GTTTTGGAAC GCTACGGCGT GCCGTACCGC CGTCTGAAAC CCGAAGAATG
51  TGCAGAATTT GAGCCTGCGC TGGCACGCGT TACCGCCAAA ATTGCCGGCG
101  GCCTGCACCT GCCTGCAGAT GCGACCGGCG ACTggCGCCT CTTCACTGAA
151  AACCTATACA AATTGTGTCA GGAAAAGGGC GTACGGTTTC ATTCAACCA
201  AAACATCAGC CGCATCGACC ACAACGGGCT GCGCATCAAA ACCGTTGAAA
251  CCAAACAGGG CGGTTTGAAG CAGATGCCGT TGTCTGCGCG CTCGGTTGCT
301  TCAGCAGGAC GGTTTGGCG CAGTTGATC TCAATCTGCC CATTATCCC
351  GTCAAAGGCT ATTCCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1408; ORF 512>:

m512.pep (partial)

```

1  ..VLERYGVFYP RLKPEECAEF EPALARVTAK IAGGLHLPAD ATGDWRLFTE
51  NLYKLCQEKV VRFHFNQNIS RIDHNGRLIK TVETKQGLK QMPLSARVA
101  SAGRFWRWI SICPFIPSKA IP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 512 shows 93.4% identity over a 122 aa overlap with a predicted ORF (ORF 512.ng) from *N. gonorrhoeae*:

m512/g512

```

                                     10      20      30
m512.pep                               VLERYGVFYPYRRLKPEECAEFEPALARVTAK
g512      TDMNFEGRKKGTLOIFRQTEEVAAKQDIAVLERYGVFYPYRRLKPEECAEFEPALARVTAK
          130      140      150      160      170      180

          40      50      60      70      80      90
m512.pep  IAGGLHLPADATGDWRLFTEENLYKLQCEKGVRFHFNQNISRIDHNGRLIKTVETKQGGLK
g512      IVGGLHLPADATGDCRLFTENLYKLQCEKGVRFYFNQTISRIDHNGRLIKAVETKQGGLK
          190      200      210      220      230      240

          100      110      120
m512.pep  QMPLSARSVASAGRFWRWSWISICPFIPSKAIP
g512      QMPLSARSAASAGLCWRWSWISICPFIPSKAIP

```

763

250 260 270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTG GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACACAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCGTGCCGT ACCGCGGTCT
501 GAAGCCCGAA GAATGCGCAG AATTTCGAGC TCGCGTGGCA CGCGTTACCG
551 CCAAAATTGC CGGCGGCCTG CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAGGAAA AGGGCGTACG
651 GTTTCATTTT AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAAACCGT TGAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGTTTT TGGCGCAAGT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAPIGI PTKALKWLFK SHPPLLERPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMER RFEAQTMNMF EGRKKGTLLQI FRQTKEVEAA
151 KQDIAVLERY GVPYRRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK OGGLKQMPPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVPRRLKPEECAEFEPALARVTAK
a512      TGMNFEGRKKGTLLQIFRQTKEVEAAKQDIAVLERYGVPRRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

              40      50      60      70      80      90
m512.pep  IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNLRIKTVETKQGGGLK
              |||
a512      IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQISRIDHNLRIKTVETKQGGGLK
              190      200      210      220      230      240

              100      110      120
m512.pep  QMPLSARSVASAGRFWRKWSISICPFIPSKAIPX
              |||
a512      QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
              250      260      270
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGCAAGGT ATGATTCAAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGTTTCC TCGCGTTCAT CCTGTTTATG TTGCGCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTT GCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTGTCGCG CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

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501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT  
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTTGTCGAT ACCATCATCG  
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC  
 151 GATTGAGCG GTGCGGCGCT GACgcAGGCG GCGATTGTCA GCCAAGTGGG  
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT  
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC  
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTT CGTATGCTGG TTTGGCGTGG  
 351 GGTCTATTTT GCGCGCGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG  
 401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCTGCTG  
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA  
 501 AATGGGCAAA GACCCCGAGT TCAAACCTTc cgAACATCCG GGCCTGAAAC  
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQOPYG  
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI  
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL  
 151 LSPLAFMLLR DYTAKLMGK DPEFKLSEHP GLKRRIKSDV W\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQOPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQOPYGDLSGAALTQA					
	10	20	30	40	50	60
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHP					
	130	140	150	160	170	180
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

```

1 ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51 CGATCCGATG TGGTCATACT TGGTTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTG TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTGTTCGC CCTGAGCCTG ATTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT TCGGGCGTCC CCTGGTGTAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAAATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTGAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTACTCGGCG GTCTGATTTT
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CTGTATTCC AACGAGGCGG
851 GTATGGGTTT CCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTCT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCGTCC ATCCTGTTTA TGTTCGCTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTCGCGG
1201 TGGGTCTATT TCGGCGCGGT TGCCAAATGT CCTTTGGTCT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCGA GTTCAAACCT TCCGAACATC CGGGCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1 MNENFEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG FVQFRLFGRS
51 IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGGA
101 VFWMWVTALI GMSSAFVESS LAQLEKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGLVFALSL IFCFGVFEEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVEL MAVLYLFIAL FIILTNIPMI PDVFGQIFSG
251 AFKFDAAAGG LLGGLISQTM MMGIKRGlys NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VEVDTIIVCS CTAFIILYQ QPYGDLGAA LTQAAIVSQV
351 GQWAGFLAV ILEMFASFV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLSPALF MLLRDYAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||
a513
260 270 280 290 300 310
DAAAGGLLGLISQTM MMGIKRGlys NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIIVCSCTAFIILYQ QPYGDLGAA LTQAAIVSQV GQWAGFLAVILFMFAFSTVIGNY
|||||
a513
320 330 340 350 360 370
TIIIVCSCTAFIILYQ QPYGDLGAA LTQAAIVSQV GQWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
AYAESNVQFIKSHWLITAVFRMLVLAVVYFGAVANVPLVWDMADMMAMGIMAWINLVAILL
|||||
a513
380 390 400 410 420 430
AYAESNVQFIKSHWLITAVFRMLVLAVVYFGAVANVPLVWDMADMMAMGIMAWINLVAILL

160 170 180 190
LSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX
|||||

```

a51.3

LSPLAFMLLRDYTAKLKMKGKDFEFLSEHPGLKRRIKSDVWX

440

450

460

470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq

```

1   atggttcaaa tacaggttgt gcgcgcgcgc ggcgttgccc gtggtctgca
51  ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
101 ccgttttgaa tcacgaagcg cggcgcgcgc gcaacacctt ccgcatcaaa
151 atagctgctg cggaaagagc ggggatgtg cggttccttc cgcaggttga
201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
301 cccgcccga acggttgtat cgaagaggac ggggtagctg cctgtcggga
351 tgctgcggct gccgagtcgc cgcaaagtgc ggcgggcggc ggtttgaccg
401 atggtttcgg ggctgtccat atccggatgg cggcagcggc aatcgtacca
451 gtagtcgcgc tgcattccgt ttcgtcggc ggcgacgacg ctgcaggaaa
501 tgctgtggtg cgtgtcttgc cggtgtgcgc caaaaccgtg ggtgttgccg
551 taaacgtatt ggtactgtcc ggtttgacc gccgcgcctt cggagttttc
601 gatgcggctg tccgtgtcca acgctgcctg ttgcattgt tttgccaagc
651 cgacggcggc ttccgtatcc aaatccatt cgtggttaaag gtcggggtcg
701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
751 ttccgcgggtg tggcgggcga tgcggcggc ggcgcggacg gtgtcgcga
801 gggcttggtt ggagaagtcg gcggtgcgc cgcgcccttt gcgtttgccg
851 acgtaaacgg taatgtccag cgatttgtcc tgcgtgaact cgatttgttc
901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
951 cggcttcggc ggcggtcgcg cccgctgctt ttgccaagtc gacggtgcgc
1001 cggcagaggt cgaggagttc ggaagcgggt tgggtgaaca gcataacaat
1051 cttctcttgt ggagcgttgt ggcattttaa

```

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep

```

1   MVQIQVVRAA GVARGLHSEF ARAVTAEBIA FDNVLNHEA RRGNTFRIK
51  IAAERAGDV RFFAQVEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GDAAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAVEVEF GSGVVEQHNN
351 LSWWSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)

```

1   ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
51  GCACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
101 GCGCCGCCGG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCCGAAAC
151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCCGGATG CTGCGGCTGC
201 CGAGTCGGCG CAAAGTGC GGCGCGCGG TTTGACCGAT GGTTCGCGGG
251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
351 TGCCTTGCCG GTGTGCGGCA AAACCGTGGG TGTTGCCGTA AACGTATTGG
401 TAATGGCCGG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGCTCATC
451 CTCGTTTCAGG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGGCGGCTK
501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CCGCGGTGTG
601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
701 ATGTCCAGCG ACTTGTCTCG CTGGAACCTG ATTTGTTsGA TTsGCCAG
751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGCGGCG GCAGAGGTGC
851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
901 TGCTTGCGG CATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

```

1      .GKSGGCAFFA QVEBIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51     GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101    HAVFVGNDNA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151    LVQGGFLFALF CQADGGXRIQ IPFVVKVGA DVFCHQTGIG KSGATVPGGV
201    AGDVGDDGFDG VLQGFPGFEGV STGAAPAFAD VNGNVQRLVL LELDLDXDAQ
251    PHADALSQXF AEITGFGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301    CFAAF*

```

**Computer analysis of this amino acid sequence gave the following results:**

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

**m515/g515**

```

m515.pep                                10      20      30
                                         GKSGGCAFFAQVEEIQDFSADAVDQETALA
                                         ::|||
g515  AEEIAFDNAVNLNHEARRGGNTFRIKIAAAERAGDVRFFAQVEEIQDFFADAVDQETALA
      30      40      50      60      70      80

      40      50      60      70      80      90
m515.pep  VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGLTDGFGAVHIRMAA
          |||:|||||
g515  VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGLTDGFGAVHIRMAA
      90     100     110     120     130     140

      100     110     120     130     140     150
m515.pep  GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLVLMAGLHRRAFGVFDALIL
          |||:|||||
g515  GGIVPVVALHSVPVGGDDAAGNAVVRALPVCCKTVGVAVNVLVLSGLHRRAFGVFDAAVR
      150     160     170     180     190     200

      160     170     180     190     200     210
m515.pep  VQGGFLFALFCQADGGXRIQIPFVKVGVADVVFCHQTGIGKSGATVFGGVAGDVGDFDGV
          |||:|||||
g515  VQRCLFALFCQADGGFRIQIPFVKVGVADVLRHQLGVGKSGATVFGGVAGDVGCGADGV
      210     220     230     240     250     260

      220     230     240     250     260     270
m515.pep  LQGFGEVVGSTGAFAFADVNGNVQRLVLELDLXDQAQPHADALSQXFAEIGFGGGRAR
          |||:|||||
g515  AQGLFGEVVGAGAAFAFADVNGNVQRFVLELDLDFDAQAHADALSERFAEVGFGGGRAR
      270     280     290     300     310     320

      280     290     300
m515.pep  RFCQVERAAAEVEEFGSGVVEQHNNLSXXCFAAF
          |||:|
g515  CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF
      330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

```

a515.seq
  1  ATG GTT CAAA TAA AGT TGT GCG CGC CGC GCG GCG GTT GCCC GTGGT CTG CA
51  TTCCG AGT TTT GCG CGC GCG CTG TAA CTG CTGA GGA AAT AGCC TTC GAC AAT G
101 CCG TTT TGA TCACGA AGCG CGGTG CGCGGTG GCA AC GCCTT CCG CAT CAAA
151 ATAGCT GCTG CGGAA AGAGC GGGGG ATGTG CGG TTCTTCG CGC AGGT TGA
201 GGAAAT CGGG CAGGACT TTT TTGCC GATG TGT CGAT CAG GAA ACTGCTT
251 TGGCG GTAGA GCGCT CCGCC GGAGAGT GCG CCG AC GAGGT GTCCG ATAAG
301 ACCGCC CGAA ACGGT GGTAT CGA AGAGGAC GGG GTAGT TG CCTGTC GGGG
351 TGCTG CGGCT GCCGAGT CGG CGCAA AGTGC GCG CGGG CGCG GGT TTG ACCG
401 ATG GTTTCG GGTCT TCCAT ATCCGG ATGG CGG CAGGCG AATCGT ACCA
451 GTAGT CGCGC TGCAT GCCGT TTTCG TCGCG GCGAAC GACG CTGCAGG AAA
501 TGCTG TGGTG CGTGCT TTGCG CGGTGT GCGG CAAA ACCGTA GGTGTT GCCG

```



a515.pep

```

1  MVQIKVVRAA  GVARGLHSEF  ARAVTAEEIA  FDNAVLNHEA  RCGGNAFRIK
51  IAAAEAGDVG  RFFAQCVEEIG  QDFFADAVDQ  ETALAVERSA  GECAEDVSDK
101  TARNGGIEED  GVVACRDAAA  AESAQSAAGG  GLTDGFGAVH  IRMAAGGIVP
151  VVALHAVFVG  GNDAAAGNAV  DALPVCQKTV  GVAVNVLVMA  GLHRRAGVGF
201  DALILVQGGL  FALFCQADGG  FRIQIPFVVK  VGVADVLRHQ  LGVGKSGATV
251  FGGVAGDVXX  GADGVAQGLF  GEIGGAGAAF  AFADVNGNVQ  RIVLLKLDLF
301  DFAQPHADAL  SQ*FAEIGFG  GGCARRFCQV  ERAAAVEEFG  GSGVVEQHRN
351  LS**CFAAF*

```

```

a515      10      20      30
m515.pep      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                ::| | | | | | | | | | | | | | | |
a515      AEEIAFDNAVLNHEARCGGNAFRKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
                30      40      50      60      70      80

                40      50      60      70      80      90
m515.pep      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                90      100      110      120      130      140

                100      110      120      130      140      150
m515.pep      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGAVNVLMAGLHRRAFGVFDALIL
                || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGAVNVLMAGLHRRAFGVFDALIL
                150      160      170      180      190      200

                160      170      180      190      200      210
m515.pep      VQGGFLFALFCQADGGXRIQIPFVKVGVADVCHQGTIGKSGATVFGGVAGDVGDFDGV
                || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGFLFALFCQADGGFRIQIPFVKVGVADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
                210      220      230      240      250      260

                220      230      240      250      260      270
m515.pep      LQGGFFGEVGGSTGAFAFADVNGNVQRLVLLLELDLXDQAQPHADALSQXFAEIGFGGGCAR
                ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLDFDFAQPHADALSQXFAEIGFGGGCAR
                270      280      290      300      310      320

                280      290      300
m515.pep      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
                || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
                330      340      350      360

```

**g515-1.seq**

1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTGTA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGCGCGCGG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAGTGTCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGCG TCCGTATCC AAATCCCAT CGTGGTAAAG GTCGGGGTCG
701 CCATGTGTTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGCGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAGTCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTTGTCC TGCTGGAACG CGATTTGTTC
901 GATTTCGCCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CGGCTTCGGG GCGGGTCGGC CCCGCTGCTT TTGCCAAGTC GAGCGTGGCG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGGT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRRA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RRGNTFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGADVLRHQ LGVGKSGATV
251 FGGVAGVDVG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RVLLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQVQ ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCGGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTGTA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGCGCGCGG GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGATGCGCGT TTTCTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTTGCCG
551 TAAACGTATT GGTAAATGCC GGTTTGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGCG TCCGTATCC AAATCCCAT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTTGCA
801 GGGCTTTTTC GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGCTC TGCTGGAACG CGATTTGTTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRRA GVARGLHTEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADEVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGLL FALFCQADGG FRIQIPFVVK VGADVLFHQ TGIGKSGATV
251 FGGVAGVDVG GFDGLVQGF GEVGTGAAG AFADVNGNVQ RVLLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

          10      20      30      40      50      60
g515-1.pep  MVQIQVVRRAAGVARGLHSEFARAVTAEEIAFDNVNLNHEARRGNTFRIKIAAAERAGDV
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m515-1      MVQIQVVRRAAGVARGLHTEFARAVTAEEIAFDNVNLNHEARRCGGNAFRIKIAAAERAGDV
          10      20      30      40      50      60

```

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAACRDAAA					
	70	80	90	100	110	120
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAFVFGNDAAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVKVGVDVLRHQ					
m515-1	GVAVNVLMAGLHRRAFGVFDALILVQGGFLALFCQADGGFRIQIPFVVKVGVDVFCQ					
	190	200	210	220	230	240
g515-1.pep	LGVGKSGATVFGGVAGDVGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFVLLDLF					
m515-1	TGIGKSGATVFGGVAGDVGGFDGVLQGGFGEVGGSTGAFAFADVNGNVQRLVLLDLF					
	250	260	270	280	290	300
g515-1.pep	DFAQAHADALSERFAEVGFGGRARCFCQVERAAAEVEEFGSGVVEQHNNLSWSVVAFX					
m515-1	DFAQPHADALSQX					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATG GTTCAA TAAAGTTGT GCGCGCCGCC GCGCTGCCCC GTGGTCTGCA
51  TTCCGAGTTT CCGCGCGCTG TAACGTCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGA TACGAAGCG CGGTGCGGTG GCAACGCCCT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCCGTAGA CCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCCGGA
351 TGTGCGCGCT GCCGAGTCGG CGCAAAGTGC GGGCGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGTGTGGTGG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTGCCG
551 TAAACGTATT GGTAAATGGCC GGTTCGACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTGA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGCGCGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTGCGGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGTGAAACT CGATTGTTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTC TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAFVFG GNDAAGNAV RALPVCCKTV GVAVNVLMAG GLHRRAFGVF
201 DALILVQGG FLALFCQADGG FRIQIPFVVK VGVDVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					

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```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70      80      90      100     110     120

              130     140     150     160     170     180
a515-1.pep   AESAQSAAAGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              |||
m515-1      AESAQSAAAGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130     140     150     160     170     180

              190     200     210     220     230     240
a515-1.pep   GVAVNVLMAGLHRRRAFGVFDALILVQGGFLFCQADGGFRIQIPFVVKVGVDVLRHQ
              |||
m515-1      GVAVNVLMAGLHRRRAFGVFDALILVQGGFLFCQADGGFRIQIPFVVKVGVDVLRHQ
              190     200     210     220     230     240

              250     260     270     280     290     300
a515-1.pep   LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLDF
              |||
m515-1      TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKDLDF
              250     260     270     280     290     300

              310
a515-1.pep   DFAQPHADALSQX
              |||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1   atgttggtcc gtaaaacgac cgccgccggt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaagag ggcagcctgg tgatgatggg
201 cgggaaatac tgggtcgccg tcaatcccgga agattcggcg aagctgacgg
251 gccttttgaa ggcggggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcgcccgg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaa
451 ctcgacaatc ggaccattta cacgcgctgc gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagtg
551 tgcccgcgga tatttattat acggttactg aaaaacatac cgacaatacc
601 aagctgtttg gaaatatctt atatacgccc cccttgttga tattggatgc
651 ggcggccgcg gtgctgtgct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1   MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQITIRKRV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNIIYTP PLLILDAAA VLVLPALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1   ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GC CTTCCGTTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAGAG GGCAGCCTGG TGATGATGGG
201 CGGAAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCCGCG AAGCTGACGG
251 GCATTTTGAAG GGCAGGGCTG GACAAACCC TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAAC TCG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATCGCCAAG CTGAAACAGC TCGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

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501 CTACGCCACA CCGCAAAAC TGAACGCCGA TTACCATTT GAGCAAAGTG  
 551 TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC  
 601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC  
 651 GCGCGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGGTCGTGG  
 701 ATGCCGCCCG CAAATGA

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

m516.pep

1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV  
 51 VAEDNAQLEK GSLVMMGGKY WVVNPEDSA KLTGILKAGL DKPFQIVEDT  
 101 PSYARHQALP VKLESPGSON FSTEGCLLRY DTDKPADIAK LKQLGF EAVK  
 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEHTDKS  
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

m516/g516

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKQDQIRAFGVVAEDNAQLEK					
g516	MLFRKTTAAVLAATLILNGCTMLLRGMNPNVSQTITRKHVDKQDQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
m516.pep	GSLVMMGGKYWVFNPEDSA KLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSON					
g516	GSLVMMGGKYWFAVNPEDSA KLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSON					
	70	80	90	100	110	120
m516.pep	FSTEGCLLRYDTDKPADIAKLKQLGF EAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
g516	FSTGGLCLRYDTGRPDDIAKLQLEFKAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF					
	130	140	150	160	170	180
m516.pep	EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK					
g516	EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPAAALGAVVDAARK					
	190	200	210	220	230	239

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

a516.seq

1 ATGTTGTTCC GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT  
 51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA  
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTGCGGTGTG  
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG  
 201 CGGGAAATAC TGGTTCGTCG TCAATCCTGA AGATTCGGCG AAGCTGACGG  
 251 GCATTTTGAA GGCCGGGTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC  
 301 CCGCGCTTTG CCTACCAAGC CCTGCCGGTC AAATCGAAT CGCCCGCCAG  
 351 CCAGAATTTC AGTACCGAAG GCCTTGCCT GCGCTACGAT ACCGACAGAC  
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTGGAATC  
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA  
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTGAG CAAAGTGTGC  
 551 CTGCCGATAT TTATTACAG GTTACGAAAA AACATACCGA CAAATCCAAG  
 601 TTGTTTGAAA ATATTGCATA TACGCCACC ACGTTGATAC TGGATCGCGT  
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT  
 701 CCTCAGACAA ATGA

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

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1 MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDQIRAFGV  
 51 VAEDNAQLEK GSLVMMGGKY WFFVNPEDSA KLTGILKAGL DKQFQMVEPN  
 101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIACL KQLEFEAVEL  
 151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVFADIYYT VTKKHTDKSK  
 201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK\*

m516/a516 86.1% identity in 238 aa overlap

	10	20	30	40	50	60
m516.pep	MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDKQIRAFGVVAEDNAQLEK					
a516	MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDKDKQIRAFGVVAEDNAQLEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m516.pep	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN					
a516	GSLVMMGGKYWFFVNPEDSAKLTGILKAGLDKQFQMVEPNRFA-YQALPVKLESPASQN					
	70	80	90	100	110	
	130	140	150	160	170	180
m516.pep	FSTEGLCLRYDTPADIAKLKQLGFEAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF					
a516	FSTEGLCLRYDTPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF					
	120	130	140	150	160	170
	190	200	210	220	230	239
m516.pep	EQSVFADIYYTVTEEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX					
a516	EQSVFADIYYTVTKKHTDKSKLFENIAYTPTLILDAVGAVLALPVAALIAATNSSDKX					
	180	190	200	210	220	230

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

g517.seq  
 1 atgcatcggg ttccagacgg cattggagtg tcagtcgtgt tctgccgatt  
 51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg  
 101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg  
 151 tgcgtctttc aatccccgatt tgatgttttt gggcaggtcg atttggctgg  
 201 tgtcgccggg aatgacggct ttccgccgga agccgatgag ggtcaggaac  
 251 attttcattt gttcgggctt ggtgttttgc gcttcgtcga ggatgatgta  
 301 tgcgccgttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa  
 351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcaggtca  
 401 tagagggcat cataaagcgg acggaggtag gggtcgactt tttgggtcag  
 451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa  
 501 ctaa

This corresponds to the amino acid sequence &lt;SEQ ID 1436; ORF 517.ng&gt;:

g517.pep  
 1 MHRVSDGIGV SVVFCRFVGF DDFLHQMPD NVFAGEGMEI QSCHAVQFLT  
 51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
 101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLQG  
 151 VSGQEAQFLT GPDGRPN\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

m517.seq  
 1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT  
 51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG  
 101 CCGGTAAAGG TGTGGAAATA CAGCCCTTCC ACGTTGTGCA GTTCTCTCACG  
 151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCTG ATTTGGCTGG  
 201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTGAGGAAC  
 251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA  
 301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCGATTTCOA  
 351 TCAGGCCTTT TTCAATCAGC TTGTTTACAC GGTCAAAGCC CATCAGGTCA  
 401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep  
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVVOFLT  
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ  
151 VSGQEAQFLA GFDGWAH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVVOFLT RIFXSRFDVF					
	:     :     :     :     :     :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLT CVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :     :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	:     :     :     :     :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq  
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT  
51 CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGCTTCG  
101 CCGGTAAGG TGTGGAATA CAGCCCTTCC ACGCCGTGCA GTTCTCACG  
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG  
201 TGTGCGCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC  
251 ATTTTCATTG GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA  
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCAATCTCAA  
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTGGAAGCC CATCAGGTCA  
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG  
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA  
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep  
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVOFLT  
51 RIF\*SRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV  
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ  
151 VTGQRTQFLA GFDGRPH\*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVVOFLT RIFXSRFDVF					
	:     :     :     :     :     :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVOFLT RIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	:     :     :     :     :     :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF					

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	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

g518.seq

```

1 atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttggtgtct
51 ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac catTTTTTca gcataaatat tctgaccgca
151 agagcggcat ctccacgggc aaccgtgttc agactgcatac aggcggtagc
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cgggcggcaa cgttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

g518.pep

```

1 MTFSAAKLNI SALMLCLSAG MTVLLSAFL LRPEGSILFN HFFSINILTR
51 RAASPRATVF RLHQAVRFHK MPKTISKMR NYAVRITPPP RAATLHYNRL
101 PLKSDPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

m518.seq

```

1 ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTGCT
51 TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTGACCGGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTC AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

m518.pep

```

1 MTFSAAKLNI SARMLCLSAG MTVLLSAFL LRPEGSILFN HFFSINILTR
51 RAASPOATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRRERR RCAVILSNR KKSDPAFVAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

m518/g518

m518.pep	MTFSAAKLNI SARMLCLSAG MTVLLSAFL LRPEGSILFN HFFSINILTR RAASPOATVF
g518	MTFSAAKLNI SALMLCLSAG MTVLLSAFL LRPEGSILFN HFFSINILTR RAASPRATVF
	10 20 30 40 50 60
	70 80 90 100 110
m518.pep	RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSN
g518	RLHQAVRFHKMPKTISKMRNYAVRITPPRAATLHYNRLPL-----
	70 80 90 100
	120 130
m518.pep	GRKKSDPAFVAESEI
g518	--KKSDPAFVAESEI
	110



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATCAAC CATTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATTCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAAATCAGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC .....
351 ... ..AAAAAAT CAGACCCTGC TTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAA.SPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNI SARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQA-RFARCRITINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRRERRRCAVILSNG					
a518	RRHQA.VRFRKMPTINKRRRNYAVRITPSSXAATRHYNRLPS-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDFAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaat tttt tcattatctt gttggcagcc gtcgcccgtt tcggcttcaa
51  atcctttgtc gtcaccccc agcaggaagt ccacgttgtc gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatttt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcttc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgctgcgttc
351 cgttatcggg cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcggy ggcttggggt
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctgagggtgc
651 ggtcaatgcg tccaatgccg agaaaatcgc ccgcataaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgcgcgcct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcataaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDRVA YRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
```

m519.seq (partial)

1	TCGGTTATCG	GGCGTATGGA	GTTGGACAAA	ACGTTTGAAG	AACGCGACGA
51	AATCAACAGT	ACTGTTGTTG	CGGCTTTGGA	CGAGGCGGCC	GGGgCtTgGG
101	GTGTGAAGGT	TTTGCGTTAT	GAGATTAAAG	ACTTGGTTCC	GCCGCAAGAA
151	ATCCTTCGCT	CAATGCAGG	GCAAATTACT	GCCGAACGCG	AAAAACGCGC
201	CCGATCGCC	GAATCCGAAG	ATCGTAAAT	CGAACAAATC	AACCTTGC <del>CA</del>
251	GTGGTCAGCG	CGAAGCCGAA	ATCCAAACAT	CCGAAGGCGA	GGCTCAGGCT
301	GCGGTCAATG	CGTCAAATGC	CGAGAAAATC	GCCCGCATCA	ACCGCGCCAA
351	AGGTGAAGCG	GAATCCTTGC	GCCTTGTTCG	CGAAGCCAAT	GCCGAAGCCA
401	TCCGTCAAAT	TGCGCGCGCC	CTTCAAACCC	AAGGCGGTGC	GGATGCGGTC
451	AATCTGAAGA	TTGCGGAACA	ATACGTCGCT	GCGTTCAACA	ATCTTGCCAA
501	AGAAAGCAAT	ACGCTGATTA	TGCCCGCCAA	TGTTGCCGAC	ATCGGCGACC
551	TGATTTCTGC	CGGTATGAAA	ATTATCGACA	CGTGAACAAAC	CGCCAA <del>g</del> TAA

m519. pep (partial)

```

1  ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
51  ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLASGQREAE IQQSEGEAQA
101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGLISAGMK IIDSSKTAK*

```

### Homology with a predicted ORF from *N. gonorrhoeae*

m519/g519

```

m519.pep      10      20      30
               SVIGRMELDKTFEERDEINSTVVAALDEAA
               |||||
g519           YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
               90      100      110      120      130      140

               40      50      60      70      80      90
m519.pep      GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
               |||||
g519           GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
               150      160      170      180      190      200

               100      110      120      130      140      150
m519.pep      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
               |||||
g519           IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAANRQIAAALQTQSGADAV
               210      220      230      240      250      260

               160      170      180      190      200
m519.pep      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTA
               |||||
g519           NLKIAGQYVTAFAKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSPEAKTAK
               270      280      290      300      310

```

a519.seq

1	ATGGAATTTT	TCATTATCTT	GCTGGCAGCC	GTCGTTGTTT	TCGGCTTCAA
51	ATCCTTTGTT	GTCATCCAC	AGCAGGAAGT	CCACGTTGTC	GAAGGCGTCG
101	GGCGTTTCCA	TCGCGCCCTG	ACGGCCGGTT	TGAATATTTT	GATTCCCTTT
151	ATCGACCGCG	TCGCCTACCG	CCATTCGCTG	AAGAATAATC	CTTTAGACCT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTA TCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTC
301 AGC AACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGT TATCGGG CGTATGGAAT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TCGGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGT CAGCGCG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATG CCGCCGCCCT TCAAACCCAA GCGCGTGGCG ATGCGGTCAA
801 TCTGAAGATG GCGGAACAAT ACGTCGCGCG GTTCAACAAT CTGCCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATT TCTGCCG GTATGAAAT TATCGACAGC AGCAAACCG CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFGRKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF
51  IDR VAYRHS L KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNY IMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKV LRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQS EGEAQAVNA SNAEKIARIN RAKGEAESLR LVAEANA EAI
251 RQIAAALQTC GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

m519/a519 99.5% identity in 199 aa overlap

m519.pep
10 20 30
SVIGRMELDKTFEERDEINSTVVAALDEAA
|||||
a519 YFOVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
90 100 110 120 130 140

m519.pep
40 50 60 70 80 90
GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
|||||
a519 GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLASGQREAE
150 160 170 180 190 200

m519.pep
100 110 120 130 140 150
IQQSEGEAQAVNASNAEKIARINRAKGEAESLRLVAEANA EAIRQIAAALQTGGADAV
|||||
a519 IQQSEGEAQAVNASNAEKIARINRAKGEAESLRLVAEANA EAIRQIAAALQTGGADAV
210 220 230 240 250 260

m519.pep
160 170 180 190 200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDS SKTAKX
|||||
a519 NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDS SKTAKX
270 280 290 300 310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCCCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTC
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACCGC CGAAGCGGAA AAACGCGCCC
551 GTATTGCGCA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGT CAGCGTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCCTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATG CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

```

801 TC<sup>2</sup>TGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG  
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
 901 ATTTCTGCGG GCATGAAAAT TATCGACAGC AGCAAAACCG CCAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF  
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS  
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANABAI  
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
 301 ISAGMKIIDS SKTAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCGGTTT TCGGTTTCAA  
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG  
 101 GGCCTTTCCA TCGCGCCCTG ACGGCGGTT TGAATATTTT GATTCCCTTT  
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT  
 201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG  
 251 GCATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTG  
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC  
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA  
 401 TCAACAGTAC TGTGTGTGCG GCTTTGGACG AGGCGGCGGG GGCTTGGGGT  
 451 GTGAAGGTTT TGCCTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT  
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAAGCGGAA AAACGCGCCC  
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT  
 601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC  
 651 GGTCAATGCG TCAATGCGG AGAAATCGC CCGCATCAAC CGCGCCAAAG  
 701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCGG AAGCCAATGC CGAAGCCATC  
 751 CGTCAAAATG CCGCGCCCTT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA  
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG  
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG  
 901 ATTTCTGCGG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQEVHV V ERLGRFHRAL TAGLNILIPF  
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS  
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG  
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS  
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI  
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL  
 301 ISAGMKIIDS SKTAK\*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEG RKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						
m519-1						

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m519-1      KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1   ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GCGGTTTCCA TCGCGCCCTG ACGGCCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTCTG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGGTTATGA GATTAAAGAC TTGGTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTGAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCG CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTGTGTGCGG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCGCG GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCGG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1   MEFFFIILLAA VVVFQKSFV VIPQEVHV VRLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESG RKIEQINLAS
201 GQREAEIQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFFIILLAAVVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHS
              |||||
m519-1      MEFFFIILLVAVVFQKSFVVIPQEVHVVERLGRFHRALTAGLNILIPPIDRVAYRHS
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIIFYQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

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m519-1      KRARIAESEGRKIEQINLASGQREABIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240
              250      260      270      280      290      300
a519-1.pep  LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAPNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAIAIRQIAAALQTQGGADAVNLKIAEQYVAAPNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300
              310
a519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

### Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in *E. coli* as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in *E. coli*. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51  catttcggaa aggatgaagt tgctggtgcc gtaataatg ccggcgatgg
101 atttaatect gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttccttg
301 gcaatgcccc tgccgccgaa caattcgacc aagacatcga cgtcttttacg
351 cgcgaacagt tcgaacggat cttttgacaa gggcgggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa ataccgattt
451 cgcgccccaa gcggcgaggaa atttcctctg cgttgtcccg caacacggca
501 gccgcaccgc cgccgaccgt acctaagcct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILIFAA KPSRTALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP PSMAFNATSL
101 AMVPPNNST KTSTSLRANS SNGSFDKGGG RADFGGLFLR LSRTWQKYG
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCTTGC GC TTCTTTCA GT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51  CATTTTCG Gk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATC CT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCC G CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGG G AAGATTTCGT TGCCGTATTC GGCAGACAGT TTTTGTGTTG
251 CGGTAACGA T GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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782

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301 GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351 TCGGACCACT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
1  MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDLILFAA KPSRRALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151 RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

m520/g520

	10	20	30	40	50	60
m520.pep	MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDLILFAAKPSRRALMIGIPPATAASNW					
g520	MPALLSIRANALPFSRISERMKLLVPLIMPAMDLILFAAKPSRTALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
g520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
g520	SNGSFDKGGRRADFGGLFLRLSRWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKY					
g520	CLLASLCLLVSRKCKY					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
51  CATTTCCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTAAGTCCGC TTCAAATTGG ACGATGACGT TTGTTTTTC
201 CGCCAGCGGG AAGATTTTCGT TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301 GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351 TCGGACCACT TCGAACGGAT CTTTGACAAA GGCTG.CGG ACGGGCAGGT
401 TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATT
451 CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCCG CAACACGGCA
501 GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551 CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
1  MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDLILFAA KPSRRALMIG
51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```

1 51 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY\*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYPNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYPNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRKCKYX					
a520	CLLASLCLLVSRKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCGTGTC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTC
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCGTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSILTKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTTCGTGTC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTCGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTG GGGCTTTTTC
351 TTCCTCAAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTC CTCTGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFSASGK
51  ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```



101 NGSLLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
151 TVPKPKRPMF TGFIVSPCKP TEM\*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSLRATSSNGSLTKAADGQIWRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKRREISSALSRTAAAPPTVPKPKRPMFTGFIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSRTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT  
51 TGCCGCCCAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA  
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG  
151 ATTTTCGTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG  
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC  
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG  
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTC  
351 TTCACTCAA TCGCACACGG CAGAAATACG GATTTGCGCG CCCAAGCGAC  
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG  
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC  
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTCFSASGK  
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS  
101 NGSLLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP  
151 TVPKPKRPMF TGFIVSPCKP TEM\*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
m520-1	MKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNWTMTCFSASGKISLPYSASSF					
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
m520-1	LLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATSSNGSLTKAADGQVCRAFSSLK					
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKRREISSALSRTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
m520-1	SHTAEIRISRPKRREISSALSRTAAVPPPTVPKPKRPMFTGFIVSPCKPTEMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCTT AATCCTAATC AACCTTCCC TGATTTCAG  
51 CCCATTGGGT GCGAATGCGG CCAAATCTA TACCTGCACA ATCAACGGAG  
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

q521n . pep

1	MKSKLPLILI	NLSLISSPLG	ANAAKIYTC	INGETVYTTK	PSKSCHSTDL
51	PPIGNYSSER	YILPQTPEPA	PSPSNGGQAV	KYKAPVKTVS	KPAKSNTPPQ
101	QAPVNNRRS	ILEAELSNER	KALTEAQKML	SQARLAKGGN	INHQKINAL*
151	SNVLDROONI	QALORELGRM	*		

m521.seq

1	ATGAAATCAA	AACTCCTCTT	AATCTAATC	AACCTTTCCC	TGATTTCAAG
51	CCCATTGGGT	GCGAATGCGG	CCAAAATCTA	sACCTGCACA	ATCAACGGAG
101	AAACCGTTTA	CACCA <sub>s</sub> CAAG	CCGTCCAAAA	GCTGCCACTC	AACCGATTTG
151	CCCCAATCG	GCAACTACAG	CAGCGAACGC	TATATCCCGC	CCCAAACGCC
201	CGAACCGGTA	TCATACCCGT	CAAACGGCGG	ACwGGTTGTC	AAATATAAAG
251	CCCCGGTCAA	AACAGTATCC	AAGCCGGCAA	AATCCA <sub>r</sub> TAC	GCCGCCGCCG
301	CAACAAGCAC	CCTCAAACAA	CAGCAGACGC	TCCATTCTCG	AAACAGAATT
351	GAGCAACGAA	CGCAAAGCAT	TGGTTGAAGC	CCAAAAAATG	TTATCACAAG
401	CACGCTGGC	AAAGGCGCGC	AACATCAACC	ATCAAGAAAT	AAATGCATTA
451	CAAGCAATG	TATTGGACAG	GCAGCAAAAT	ATTCAAGCCC	TGCAAAAGGA
501	ACTGGGGCGT	ATGTAA			

m521.pcp

```

1  MKSKLLLLILI NFSLLSSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTDL
51  PPIGNYSSE YIPPOTPEPV SSPSNGGXV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNSRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDROON IOALORELGR M*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m521/q521

	10	20	30	40	50	60
m521.pep	MKS K L L L I L I N F S L I S S P L G A N A A K I X T C T I N G E T V Y T X K P S K S C H S T D L P P I G N Y S S E R					
	:           :           :           :           :					
g521	M K S K L P L I L I N L S L I S S P L G A N A A K I Y T C T I N G E T V Y T T K P S K S C H S T D L P P I G N Y S S E R					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	Y I P P Q T P E P V S S P S N G G X V V K Y K A P V K T V S K P A K S X T P P P Q Q A P S N N S R R S I L E T E L S N E					
	:           :           :           :           :					
g521	Y I L P Q T P E P A P S P S N G G Q A V K Y K A P V K T V S K P A K S N T P P - Q Q A P V N N S R R S I L E A E L S N E					
	70	80	90	100	110	
	130	140	150	160	170	
m521.pep	R K A L V E A Q K M L S Q A R L A K G G N I N H Q E I N A L Q S N V L D R Q O N I Q A L Q R E L G R M X					
	:           :           :           :           :					
g521	R K A L T E A Q K M L S Q A R L A K G G N I N H Q K I N A L X S N V L D R Q O N I Q A L Q R E L G R M X					
	120	130	140	150	160	170

a521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

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```

51 CCCATTGGGT GCGAATGCGG CCAAATCTA CACCTGCACA ATCAACGGAG
1 01 AAACCGTTTA CACCACCAAG CCGTCCAAA GCTGCCTCTC AACCGATTG
1 51 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAACATC
2 01 CGAACCGACA CCATCACCCT CAAACGGCGG ACAGGCTGTC AAATATAAAG
2 51 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCGCCG
3 01 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AACAGAATT
3 51 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
4 01 CACGTCTGGC AAAAGGCGGC AACATCAACC ATCAAGAAAT CAACGCATTG
4 51 CAAAGCAATG TATTGGACAG GCAGCAAAT ATCCAAGCAC TGCAAAGAGA
5 01 ATTGGGACGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1 MKSKLPLILI NFSLISSPLG ANAAKIYCT INGETVYTTK PSKSLSTDLD
51 PPIGNYSSE YIPPQTSEPT PPSNGGQAV KYKAPVKTVS KPAKSNTPPP
1 01 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
1 51 QSVLDRQON IQALQRELGR M*

```

m521/a521 94.2% identity in 171 aa overlap

```

m521.pep      10      20      30      40      50      60
MKSLLLLILINFSLISSPLGANAAXIXTCTINGETVYTXKPSKXSCHSTDLPPIGNYSSE
|||||
a521          10      20      30      40      50      60
MKSKLPLILINFSLISSPLGANAAXIYCTINGETVYTTKPSKSLSTDLPPIGNYSSE

m521.pep      70      80      90      100     110     120
YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE
||||| ||: ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
a521          70      80      90      100     110     120
YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRSILETELSNE

m521.pep      130     140     150     160     170
RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX
|||||
a521          130     140     150     160     170
RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1 atgactgagc cgaacacga aacgccgacg gaagagcagg ttgccgcgcg
51 caaaaaagca aaagccaaa tccgcacat ccgcatttgg gcgtgggtca
101 ttttgcggtt gctcgcttca accgccctgc tctccaatg cgcgatgtcc
151 aaaccgcagg caaacagaa aattgtcgag tcttgcatag aaaaatttcc
201 gtttgctgaa aaatggcaga acgatttgaa agcgcgcggc ttggatgcgg
251 acaatacccc tctcgccgtc gactactgca aatgtatgtg ggagcagcct
301 ttggacggat tgagcgagaa acagatcagc tccttcggca aactcgggtc
351 acaagaacag cttgacctgc tcggcgccgc aaacgcgttt gaaactcgag
401 acaacaatg tgtcgcgat ttgaaagccg attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1 MTEPKHETPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMs
51 KPQAKQKIVE SCMKNIPFAE KWQNDLKARG LDADNTRLAV DYCKCMWEQP
101 LDGLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1 ATGACTGAGC CGAAACACGA AATGCTGACG AAAGAGCAGG TTGCCGCGCG
51 CAAAAAAGCA AAAGCCAAA TCCGCACCAT CCGCATTGCG GCGTGGGTCA
101 TTTTGGCGTT GTCGCTTTA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
151 AAACCGCAGG CAAACAGAA AATTGTCGAG TCTTGCGTGA AGAATATTCC
201 GTTTGCCGAA AAATGGCAA ACGATTGCGG GGCCCCGGGT TTAGATTCAA
251 ACAATACCCG CCTCGCCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT

```

787

301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC  
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG  
 401 ACAAGCAGTG TGTGCGGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMSKPQAKQKIVE  
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKMWEQP  
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
	:     :     :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	:     :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCG  
 51 CAAAAAAGCA AAAGCCAAA TCCGCACCAT CCGCATTGG GCATGGGTCA  
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC  
 151 AAACCGCAGG CAAAACAGAA AATGTGCGAG TCTTGCGTGA AGAATATTCC  
 201 GTTTGCCGAA AAATGGCAA ACGATTGCG GGCCCGCGGT TTAGATTCAA  
 251 ACAATACCG CTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT  
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC  
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG  
 401 ACAAGCAGTG TGTGCGGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMSKPQAKQKIVE  
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKMWEQP  
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE\*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSDNNTRLAVDYCKMWEQPLDRLSEKQIRSFGLGAQEQ					
	:     :					
a522	SCVKNIPFAEKWQNDLRARGLDSDNNTRLVDYCKMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

```
g523.seq
  1  atgactgtat ggtttgttgc cgctgttgcc gtcttaatca tcgaattatt
 51  gacgggaacg gtttatcttt tggttgtcag cgcggtcttg gcgggttcgg
101  gcattgccta cgggctgact ggcagcacgc ctgccgcgt cttgaccgcc
151  gcactgcttt ccgcgctggg catttggttc gtacatgcc aaaccccgct
201  gggaaaagt gaaacggatt catatcagga ttggatacc ggaaaaatcg
251  ccgaaatcct ccgatacaca gcgggcaacc gttacgaagt tttttatcgc
301  ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351  aacgcgcgcc ctcatcgctc gcaaagaagg taaccttctt atcatcgcaa
401  acccttaa
```

g523.pep

1	MTVVFVAAVA	VLIIELLTGT	VYLLVVSAA	AGSGIAYGLT	GSTPAAVLTA
51	ALLSALGIWF	VHAKTAVGKV	ETDSYQDLDT	GKYAEILRYT	GGNRYEVFYY
101	GTHWQAQNTG	QEVFEPGTRA	LIVRKEGNLL	IIANP*	

```
m523.seq (partial)
  1  ..GCCGCTCTTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GnCGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTGGAT GGCGGACAAT ATGTCGAAAT CCTCCGACAC ACAGCGCGCA
251 ACCGTTACGA AGTTTtTtTAT CGCGGTACGc ACTGGCAGGC TCAAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTAA
```

```
m523.pep      (partial)
   1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
  51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RGTWQAQNT
 101  GQEELEPGTR ALIVRKEGNL LIITHP*
```

m523/g523

```

              10      20      30      40      50
m523.pep     AVLIIELLTGTVYLLVVS AALAGSGIAYGLTGSTPAAVLT XALLS ALGIXF
               |||||
g523          MTVFVA AVAVLIIELLTGTVYLLVVS AALAGSGIAYGLTGSTPAAVLTAA LLSA LGIW F
                10      20      30      40      50      60


           60       70       80       90      100      110
m523.pep    VHAKTAVRKVETDS YQDL DAG QYVEIL RHTGGNRYEVFYRGTHWQAONT GQEEL EPGTRA
             :||| |:::||:|||||:|||||:|||||:|||||:|||||: |||||
g523         VHAKTAVGVKETDS YQDLD T GKYA E I LR YTGGNRYEV FYRGT HW QA ON TG QE VF EP GTR A
                 70        80        90       100      110      120



            120
m523.pep    LIVRKEGNLL II THP
             ||||| |:|
```

g523

LIVRKEGNLLIIANPX  
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

```
a523.seq
1  ATGACTGTAT GGTTCGTTGC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51  GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

```
a523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVSAAL AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GOYAEILRHA GGNRYEVFYR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*
```

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVSAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFYRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

```
g525.seq
1  atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51  agcggcggtt gccgaaatgg ttcaaatacga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcctgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttccgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgccgaac tactgggggtg tttatgatat
551 gcacgggctg a
```

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

```
g525.pep
1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQKRLPTID EWEFAGLASA TQKKRLKRTR
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

m525.seq

**This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:**

m525.pcp

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng)

from *N. gonorrhoeae*:

m525/g525

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq

1	ATGAAGTTTA	CCCGTTACT	CTTCTCTGT	GCGGCACTCG	CCGGCACTCA
51	AGCGGCAGCT	GCCGAAATGG	TTCAAATCGA	AGGCGGCAGC	TACCGCCCGC
101	TTTATCTGAA	AAAAGATACC	GGCTGATTA	AAGTCAAACC	GTTCAAACTG
151	GATAAAATAC	CCGTTACCAA	TGCCGAGTTT	GCCGAATTTG	TCAACAGCCA
201	CCCCCAATGG	CAAAAAGCCA	GGATCGGTTT	CAACACGGCA	GAACCCGCTT
251	ACCTGAAGCA	TTGGATGAAA	AACGCGACGC	GCAGCTATGC	GCCGAAGGCG
301	GGCGATTTAA	AACAACCGGT	AACCAATGTT	TCCTGGTTCG	CCGCCAACGC
351	CTATTGCGCC	GCACAAGGCA	AACGCGTGCC	GACCATTGAC	GAATGGGAAT
401	TTGCCGGAAT	TGCTCCGCC	ACGCAG.AAA	AACGGCTCAA	ACGAACCCGG
451	CTACAACCCG	ACTATTCTCG	ACTGGTATGC	GGATGGCGAC	CGGAAAGACC
501	TGCACGATGT	GCGCAAG.G	TGCCCCGAAC	TACTGGGGCG	TTTATGATAT
551	GCACGGTCTG	A			

This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151 LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

      10      20      30      40      50      60
m525.pep  MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
a525      MKFTRLFLCAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
      10      20      30      40      50      60

      70      80      90     100     110     120
m525.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
a525      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
      70      80      90     100     110     120

      130     140     150     160     170     180
m525.pep  AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRTTERPARCRXKAARTTGA
a525      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCRQXVARTTGA
      130     140     150     160     170     180

m525.pep  FMICTGX
a525      FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
1  ATGAAGTACG TCCGGTTATT TTCTCTCGGC ACGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAGGCCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGCAATGTA AACAGCCGGT TACCAATATT TCCTGTTTGT CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCTGACC GACCATCGAC GAATGGGAAT
401 TTGCCGACT TGCTTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAGACC GCCCGAATA CTGGGGTGT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTCG AGCGGCGCAT CTGTCGGGGC
651 GAGCGACTCG TCCAATATG CCGCTTCTCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATACGTC CTGCACAACT TGGGCTTCCG CTGCGCAAGC
751 CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
1  MKYVRLFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKDRPNYGV YDMHGLIEW TEDFNSLLS
201 SGNANAQMFQ SGASVGASDS SNYAFLRYG IRTSLQSKYV LHNLFRCAS
251 R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
1  ATGAAGTATG TCCGGTTATT TTCTCTCGGC GCGGCACTCG CCGGCACTCA
51  AGCGGCGGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```



```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCC CAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCGAACTA CTGGGCGT TATGATATGC
551 ACGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWG YDMHGLIEW TDFNSSLLS
201 SGNANAQMF SCASIGSSDS SNYAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFKL DKYPVTNAEF					
g525-1	MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKDT GLIKVKPFKL DKYPVTNAEF					
	10	20	30	40	50	60
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
g525-1	AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKAGELKQPVTV SWFAANAYCA					
	70	80	90	100	110	120
m525-1.pep	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
g525-1	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
g525-1	AQGKRLPTID EWEFAGLASA TQKNGSNEPG YNRTILDWYADGGKRLHDV GKGRPNYWG					
	130	140	150	160	170	180
m525-1.pep	YDMHGLIEW TDFNSSLLS SGNANAQMF SCASIGSSDS SNYAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEW TDFNSSLLS SGNANAQMF SCASVGS DSSNYAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEW TDFNSSLLS SGNANAQMF SCASIGSSDS SNYAFLRYG IRTSLQSKYV					
g525-1	YDMHGLIEW TDFNSSLLS SGNANAQMF SCASVGS DSSNYAFLRYG IRTSLQSKYV					
	190	200	210	220	230	240
m525-1.pep	LHNLGFRCTSRX					
g525-1	LHNLGFRCA SRX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

m525-1.seq

```

1 ATGAAGTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCGCG
101 TTTATCTGAA AAAAGATACC GGCTTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCC CAATGG CAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTCCGCC ACGCAGAAA ACGGCTCAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCGAACTA CTGGGCGT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGCAATG CCAACGCGCA AATGTTTTC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAAC TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKF-TRLLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKDDT GLIKVKPFKL
51  DKY PVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GDL KQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNR TILDWYA DGRKDLHDV GKGRPNYGV YDMHGLIEWE TEDFNSSLLS
201 SGN ANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
a525-1      MKFTRLLFLCAALAGTQAAAEMVQIEGGSYRPLYLKDDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90      100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGELKQPVTNVSWFAANAYCA
a525-1      AEFVNSHPQWQKGRIGSKQAEPAYLKHWKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
              70      80      90      100     110     120

              130     140     150     160     170     180
m525-1.pep  AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYGV
a525-1      AQGKRLPTIDWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYGV
              130     140     150     160     170     180

              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWETEDFNSSLLSSGNANAMFCSGASIGSSDSNYYAAFLRYGIRTSLSQSKYV
a525-1      YDMHGLIEWETEDFNSSLLSSGNANAMFCSGASIGSSDSNYYAAFLRYGIRTSLSQSKYV
              190     200     210     220     230     240

              250
m525-1.pep  LHNLGFRCTSRX
a525-1      LHNLGFRCTSRX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51  gcttggtcgg tctgccgtcg ggatgggcgg aagtgatgcg gctgaattgg
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgccgggcg gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga agggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctacccagt tcgatatgct tttgcgcaag ggaacggggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatac gattttgttt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLVPSFFQP VOLAAVALGR SAVGMGGSDA AELVELFALF PQCCRFRVFF
51  IQKPRLLGCRA ALVVQTFNLD FMKGIERQV DNIADVYGFT VDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVOPHGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTTCG
51  GCTTGGTTCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGCTCTTTC CCTCAATGTT GCCGTTWTCG CGTCTCTTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

794

```

2 01 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGty GrTwATaTCG
2 51 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
3 01 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
3 51 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
4 01 TCTTTCATAC GATTTGTTT GAAATAATTG AATTGTTTC GAGTTAGCA
4 51 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

```

m527.pep
1 MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLf
51 IQKPRXGCRA ALVVQTFNxD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

```

m527/g527
      10      20      30      40      50      60
m527.pep MVLVPSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA
      |||||
g527      MVLVPSFFQPVQLAAVALGRSAVGMGSDAAELVELFALFPQCCRFRVFFIQKPRLGCR
      |||||
      10      20      30      40      50      60
m527.pep ALVVQTFNxDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP
      |||||
g527      ALVVQTFNLDfMGKIERQVDNIADVYGFTVFDLRAVYLNPTQFDMLLRKGTGLEKTCRP
      |||||
      70      80      90      100     110     120
m527.pep KPFVQPHGGRIVLVFHTILFEIIEFVSSLA
      |||||
g527      KPFVQPHGGRIVLVFHTILFEIIEFVSSLA
      |||||
      130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

```

a527.seq
1 ATGTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TCGGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTACTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTGTTT GAAATAATTG AATTGTTTC GAGTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

```

a527.pep
1 MVLVPSFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLf
51 IQKPRLGCRALVVQTFNLD FIGKIERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

```

      10      20      30      40      50      60
m527.pep MVLVPSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA
      |||||
a527      MVLVPSFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLFIQKPRLGCR
      |||||
      10      20      30      40      50      60

```

795

	70	80	90	100	110	120
m527.p ep	ALVVQTFNKFDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
a527	ALVVQTFNLDFIGKIERQVDNIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.p ep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLAX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1507>:

```

g528.seq
1  atggaattc  gggtaataaa  atatacggca  acggctgcgt  tgtttgcatt
51  tacggttgca  ggctgccggc  tggcgggggt  gtatgagtgt  ttgtccttgt
101 ccggtctggt  taagccgaga  aaacctgccg  ccatcgattt  ttgggatatt
151 ggcggcgaga  gtccgctgtc  tttagaggac  tacgagatac  cgctttcaga
201 cggcaatcgt  tccgtcaggg  caaacgaata  tgaatccgcg  caaaaatctt
251 acttttatag  gaaaataggg  aagtttgaag  cctgcggggt  ggattggcgt
301 acgcgtgacg  gcaaaccttt  ggttgagagg  ttcaaacagg  aaggtttcga
351 ctgtttggaa  aagcaggggt  tgcggcgcaa  cggcctgtcc  gagcgcgtcc
401 gatggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1508; ORF 528.ng>:

```

g528.pep
1  MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1509>:

```

m528.seq (partial)
1  ATGGAATTC  GGGCAATAAA  ATATACGGCA  ATGGCTGCGT  TGCTTGCATT
51  TACGCTTGCA  GGCTGCCGGC  TGGCGGGGTG  GTATGAGTGT  TCGTCCCTCA
101 CCGGCTGGTG  TAAGCCGAGA  AAACCGGCTG  CCATCGATT  TTGGGATATT
151 GCGGCGGAGA  GTCCGCCGTC  TTTAGGGGAC  TACGAGATAC  CGCTTTCAGA
201 CGGCAATAGT  TCCGTCAGGG  CAAACGAATA  TGAATCCGCA  CAACAATCTT
251 ACTTTTACAG  GAAAATAGGG  AAGTTTGAAG  C.TGCGGGCT  GGATTGGCGT
301 ACGCGTGACG  GCAACCTTT  GATTGAGACG  TTCAACAGG  GAGGATTTGA
351 CTGCTTGGA  AAG....

```

This corresponds to the amino acid sequence <SEQ ID 1510; ORF 528>:

```

m528.pep (partial)
1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE K....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

m528/g528

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
g528	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPLSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQKSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE					
g528	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE					
	70	80	90	100	110	120

796

m528.pep      K  
 |  
 g528          KQGLRRNGLSERVRW

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

a528.seq  
 1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT  
 51 TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT  
 1 01 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT  
 1 51 GGCGGCGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA  
 2 01 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT  
 2 51 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT  
 3 01 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTGA  
 3 51 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC  
 4 01 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

a528.pep  
 1 MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI  
 51 GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR  
 1 01 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW\*

m528/a528 95.0% identity in 121 aa overlap

	10	20	30	40	50	60
m528.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD					
a528	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED					
	10	20	30	40	50	60
	70	80	90	100	110	120
m528.pep	YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLK					
a528	YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK					
	70	80	90	100	110	120

m528.pep      K  
 |  
 a528          KQGLRRNGLSERVRWX  
 130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

g528-1.seq  
 1 ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT  
 51 TACGGTTGCA GGCTGCCGGC TGGCGGGTG GTATGAGTGT TCGTCCCTGT  
 101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATT TTGGGATATT  
 151 GGCGGCGAGA GTCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA  
 201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT  
 251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT  
 301 ACGCGTGACG GCAAACCTTT GGTGAGAGG TTCAAACAGG AAGGTTTCCA  
 351 CTGTTTGAA AAGCAGGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC  
 401 GATGGTAA

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

g528-1.pep  
 1 MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI  
 51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR  
 101 TRDGKPLIVER FKQEGFDCLK KQGLRRNGLS ERVRW\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

m528-1.seq  
 1 ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

797

```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGC GGC GAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAIDFWDI
51  GGESPPSLGD YEIPLSDG NR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCL E KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

	10	20	30	40	50	60
g528-1.pep	MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPLSLED					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
g528-1.pep	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCL E					
m528-1	YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCL E					
	70	80	90	100	110	120
g528-1.pep	YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCL E					
m528-1	YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCL E					
	70	80	90	100	110	120
g528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					
g528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGC GGC GAGA GTCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGTTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGCGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAIDFWDI
51  GGESPPSLED YEIPLSDG NR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCL KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

	10	20	30	40	50	60
a528-1.pep	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAIDFWDIGGESPPSLED					
m528-1	MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAIDFWDIGGESPPSLGD					
	10	20	30	40	50	60
a528-1.pep	YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCL K					
m528-1	YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCL E					
	70	80	90	100	110	120
a528-1.pep	YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCL K					
m528-1	YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCL E					
	70	80	90	100	110	120
a528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					
a528-1.pep	KQGLRRNGLSERVRWX					
m528-1	KQGLRRNGLSERVRWX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

```
g529.seq (partial)
1 atgacccata tcaaacccgt cattgccgcg ctgcactca tcgggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctggaagtcc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccagcggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgtcgt tgacggcaaa tccccgcgc aaatctccgc
351 cgctttctg.
```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

```
g529.pep (partial)
1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF..
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

```
m529.seq
1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGACCG CCTGATCAAA CTGAAGTCC CACCTGATT GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAAGCGTC AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTGA CGGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAAATC
451 CCCCAAGACA GCTTGCGCCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCGAGCGCG ACAAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGTTGGC
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCGCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAAACTGGC GGCGCACCGT GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAATTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTGCGCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAATC CATTCCGAAC TGCCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

```
m529.pep
1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PDAEVLKSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAIGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGGKDKDTTV WQSPSPDPNL EAAFLTRFMQ YLGVDGQAE NASAKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPGLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDASALLGKL HSELR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

          10      20      30      40      50      60
g529.pep  MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA
```

a529.seq

1	ATGACCCATA	TCAAACCCGT	CATTGCCGCG	CTCGCACTCA	TCGGGCTTGC
51	CGCCTGCTCC	GGCAGCAAAA	CGAACAGCC	CAAGCTCGAC	TACCAAAGCC
101	GGTCGACCCG	CCTGATCAAA	CTCGAAGTC	CAGCTGATT	GAACAACCCC
151	GACCAAGGCA	ACCTCTACCG	CCTGCCTGCC	GGTTGGGGT	CCGTCGCGCG
201	CAGCGATTGG	GAAAAACGCC	GCACACCCGC	CGTCCAACAG	CTCTCCGATG
251	CCGAAGTATT	GAAAAGCGTC	AAAGGTGTCC	GCCTCGAGCG	CGACGGCAGC
301	CAACGCTGGC	TCGTTTGTCA	CGGCAAGTCT	CATGCCGAAA	TCTGCCCGCT
351	CCTGAAAGCG	TTTTGGCAGG	AAAACGGCTT	CGACATCAAA	TCCGAAGAAC
401	CCGCCATCGG	ACAAATGGAA	ACCGATGGG	CGGAAACCG	TCCGAAATC
451	CCCCAAGACA	GCTTGCGCCG	CCTATTCGAC	ACAGTCGGTT	TGGCGCGCAT
501	CTACTCCACC	GGCGAGCGCG	ACAAATTCAT	CGTCCGTATC	GAACAGGGCA
551	AAAACGGCGT	TTCCGCATCA	TTCTTCGCCC	ACAAAGCCAT	GAAGAAGATG
601	TACGGCGCGA	AAGACAATA	CACGACCGTA	TGGCAGCCCT	CCCCGTCGGA
651	TCCCAACCTC	GAAGCGCTT	TCTTGACGCG	CTTTATGCAA	TATTTGGGCG
701	TTGACGGACA	GCAGGCGGAA	AACGCATCGG	CAAAAAAACC	TACCCTTCCC
751	GCCGCCAACG	AAATGGCGCG	TATCGAAGGC	AAAAGCCTGA	TTGTCTTTGG
801	CGACTACCGG	AGAAAGCTGC	GGCGCACCGC	GCTCGCCCTC	GACCGCATCG
851	GGCTGACCGT	CGTCGTCAA	AACACCGAAC	GCCACGCTTT	CTCTGTTCAA
901	AAAGCCCCGA	ACGAAAGCAA	TGCAGTTACC	GAACAAAAAC	CCGCGCTGTT
951	CAAACGCCTG	CTGGGCAAAG	GCAAAGCGGA	GAACCTGCC	GAACAGCCGG
1001	AACTGATTGT	CTATGCCGAG	CCTGTGCGCA	ACGGCTCGCG	CATCGTCTTG
1051	CTCAACAAAG	ACGGCAGCGC	ATATGCCGCG	AAAGACGCAT	CCGCATTATT
1101	GGGCAAACTC	CATTCCGAAC	TGCGTTAA		

a529.pep

1	<u>MTHIKPVIAA</u>	<u>LALIGLAACS</u>	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNNP
51	DQGNLYRLPA	GSGAVRASDL	EKRRTPAVQK	PADAEVLKSV	KGVRLERDGS
101	QRWLVDVGKS	HAIEIWPLLKA	FERQDGFVDIK	SEEPAGIGME	TWEAENRAKI
151	PQDLSRLRFD	TVGLGGIYST	GWQDKFIVRI	EQKGNGVSDI	FFAHAKMKEV
201	YGGKDKDTTV	WQPSPSDPNL	EAAFLTRFMQ	YLGVDGQQAE	NASAKKPTLP
251	AANEMARIEG	KSILVFGDYG	LRNRRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
301	KAPNESNAVY	EQKPGLLFKRL	GGKQKAEKPA	EQPELIVYAE	FPVANGSRIVL
351	LNKDGSAYAG	KDASALLGKL	HSELR*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDVGKSPAEIWPPLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAIEVLKSVKGVRLERDGSQRWLVDVGKSHAEIWPPLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180



800

```

m529.pep  FWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDKVLGGIYSTGERDKFIVRI
a529      FWQENGFDIKSEEPaIGOMETEWAENRAKIPQDSLRLRLFDTVLGGIYSTGERDKFIVRI
           130      140      150      160      170      180

           190      200      210      220      230      240
m529.pep  EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQPSDPNLEAAFLTRFMQYLGVGQQAE
a529      EQGKNGVSDIFFAHKAMKEVYGGKDKDITVWQPSDPNLEAAFLTRFMQYLGVGQQAE
           190      200      210      220      230      240

           250      260      270      280      290      300
m529.pep  NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFVQ
a529      NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFVQ
           250      260      270      280      290      300

           310      320      330      340      350      360
m529.pep  KAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
a529      KAPNESNAVTEQKPGLFKRLLGKGKAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
           310      320      330      340      350      360

           370
m529.pep  KDASALLGKLHSELRX
a529      KDASALLGKLHSELRX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgggcaat gacgggtttg atatgggtca tcgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgcgat gttatgccgt ccgaacggtt
101 cagacggcat ggctatatatt aaagtgtgcc tgaggctttc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgacgc
201 tgcggtccgc atccgcccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgtcgtaaat cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPPIS VRRDWVRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  wTGAGTGCGA GCGCGGCAAT GACGGGTyTG ATATGGGTCA TCGTGTcATC
51  sTGtGTGATG GATATTAAAG TGtYtGTTGC GwTATGCCGT CCGAACGGTt
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTkTTGC wTGTCGGTTT yCCGTCAGCG GAACGAGCGG CAGGCGGACG
201 TCGGTTTCG ATCTGCCCAg GCGGATACC GCCCATTTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep  XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA 60
          |||

```

```
g530      MSASAAMTGLIWVIVSSCVMDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA    60  
          10           20           30           40           50           60
```

---

```
m530 . pep ERAAGGRAVRICPGRIPPISVRRGWVRTWCKRSESVGR   99  
          |||::||| | ||||||| ||:|||::||  
g530      ERAAGARAVRI RPRRI PPI SVRD WVRTW CKRK SESAGR   99
```

```
a530.seq
1   ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTATC
51  CTGTGTGATG GATATTAAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCCGCCT TCCGTACGCG GAACAGCGCG CAGGCGGACG
201 TGCGGTTCGC ATCTCCCCAG GCCGATACC GCCCATTCG GTGCGCGCGG
251 GCTGGGTTCC CAGAACATGG TGTCTAATC CGGAATCAG CGGTCTGTGA
```

```
a530.pep
1  MSASAAMTGL IWVIVSSCVM DIKFVVALCR PNGSDGMAIF KVLRLSGRR
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRRTW CRKSESAGR*
```

```

              10      20      30      40      50      60
m530 . pep  XSASAAMTGLIWVIVSSCVM DIKVVAXCRPN GSDGMXIFKVVLR LSGRGLLXVRFPSA
              |||||
a530        MSASAAMTGLIWVIVSSCVM DIKVFVLCRPN GSDGMAIFKVVLR LSGRGLLPVRLPSA
              10      20      30      40      50      60

              70      80      90     100
m530 . pep  ERAAGGRAVRI CPGRIPPI SVRRGWVRR TWCRKSESVGRX
              |||||
a530        ERAAGGRAVRI CPGRIPPI SVRRGWVRR TWCRKSESAGR X
              70      80      90     100

```

```
g531.seq
  1  ATGACCGCCC TACTCGTCAT CCTCGCCCTC GCCCTGATAG CGGTCGGCAC
51  GGCAGGCATC GTCTATCCCG CCCTGCCCGG CTTGGCATTG ATGTTTGCCG
101 GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ATCAAATCTA CGGCGCAGGC
151 ATCTTGTGGA CGGTCGGACT CATCAGCCTT GGGCGCATAC TGGCGGACTA
201 TATGGCAGGC ATGTTGGGGG TAAAATACAC TGGGGCAGGC AAATCGCCG
251 TCCGAGGTGC ATTGGCCCGC AGCATCATCG GCATATTTT CTCCCTTCCC
301 GGACTAATAC TCGGCCCTT TATCGGCGCG CGGCAGGCG AACTGATCGA
351 TCGGCGCAAT ATGCTTCAGG CAGGTAAGC GGGCTTGGGT ACGCTGTTGG
401 GGCTTGTCTG CGGCACGGCG TTCAAATCG GCTGCGCCGT ATCCATCTTG
451 TTTATCCTGT TGGTGAAATA CATCGCATAC CTGTTTTAA
```

```

g531.pep
  1  MTALLVILAL ALIAVGTAGI VYPALPGLAL MFAGTWLLAY AGGYQIYGAG
51  ILWTVGLISL GGILADYMG MLGVKYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AGELIDRRN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY AF

```

```
m531.seq
  1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
 51  GGCGGGCATC GTTTaCCCCG CCCTGCCCGG ATTGGCATTG ATGTTTGCCG
101  GAACATGGCT GCTTGCCCTAT GCCGGCGGCT ACCAAATCTA CGGCGCGGGC
151  GTTTTGTTGA CGGTCGGACT CATCAGCCTT GCCGGCATA TGGCGGACTA
201  TTGCGCAGGC ATATGGGGGA CAAAATATAC CGGAGCGGGC AAGCTCGCCG
251  TTCGGCGCGC ATTGGCCGGC AGCATCATCG GCATATTTTT CTCCTTCCC
301  GGACTAATAC TCGGTCCCTT TATCGGCGCG CGCGCAGGCG AACTGATCGA
```



803

```

a531      |||||
          AGILADYVAGIWGKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERN
          70      80      90      100     110     120

          130      140      150      160
m531. pep MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||||
a531      MLQAGKAGLGTLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1 atggctgaaa caatgaaaa acagcgcat tcgectgatt tgggttacgg
51 tttggaagac aggcgcgctg tcgtaatgc gctcttgagc gcggttaccc
101 atcttttggc gattttcgtg ccgatgatta cgcgcgcgt gattgtgggc
151 ggcgcgctgg aattgcggtg ggagatgacg gcgtatctgg tgcgatggc
201 gatggttgcg tcgggtgctg gcacttattt gcaggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1 MAETMKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGSVGSGML SIQRYRHDC
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1 ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51 TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGCT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTCT GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CGGTGCGGTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GCGCGGTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTCT GCGGCGGCTT CGGCGCGAAG CCGGACGGCA
551 CGTTGCGGTC GATGGAACAA TTGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCCG CTGTGCGCA TGAGCGGCAT
651 TGCGGTGCGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCCCGTACCG
751 TTTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGGCGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTC CGACGAGCCG ATTGAAGGCG AGGAATACAC CAAACGCGCT
901 CGCGGCGGCG TGTTCGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTTCGCT CCGCTGACGA CGTTTGCGCA AAACAACGGC GTGATTCAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTGGT CGCGCGTTTA CGACGATTC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTTT GATGTTCCGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCG CCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCT CGTTTGAGCC
1251 GGAAGTGTTT AAAAACCTGC CCGTCTTGTT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTGG TCTTGCCCGA AGATAAAC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSVF GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

### Homology with a predicted ORF from *N. gonorrhoeae*

g532/m532

	10	20	30	40	50	60
g532.pep	MAETMKKQADSPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
m532	MSGQLGKGADAPDLVYGLEDPRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGVPVSGSMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

a532.seq

1	ATGAGCGGTC	AGTTGGGCAA	AGGTGCGGAT	GCGCCTGATT	TGGTGTACGG
51	TTTGGAGGAT	AGGCCGCCGT	TCGGTAATGC	GCTCTTGAGC	GCGGTTACCC
101	ATCTTTTGGC	GATTTTTTGTG	CCGATGATTA	CGCCCGCGCT	GATTGTGGGC
151	GGCGCGCTGG	AATTGCCCGGT	GGAGATGACG	GCGTATCTCG	TGTCGATGGC
201	GATGGTTGCG	TCGGGTGTCTG	GCACATTATT	GCGAGTCAAC	CGCTTCGGGC
251	CGGTGCGGTT	GGGGATGCTG	TCCATCCAGT	CGGTGAATTT	CTCGTTCGTT
301	ACCGTCATGA	TTGCGCCTCGG	CGCGGGGATG	AAAGAGGGCG	GTTTGACTAA
351	GGATGCGATG	ATTCGACGCG	TCTTGGGCGT	ATCGTTTGTC	GGCGCGTTTT
401	TGGTGTGTTT	TTCGGCGTGG	CTTCTGCCGT	ATTTGAAAAA	AGTGATTACG
451	CCGACGGTCA	GCGGTGTGGT	GGTGATGCTG	ATCGGCTTGA	GTTTGGTACA
501	CGTCGGTATT	ACCGATTTCG	GCGGCGGGCTT	CGGCGCAAAG	GCGGACGGCA
551	CGTTTCGGCT	CATGAAAAAC	TTGGGGCTGG	CATCGCTGGT	GCTGCTGATT
601	GTGCTGGTGT	TCAATTGCGAT	GAAAAACCCG	CTGCTGCGGA	TGAGCGGCAT
651	TGCGGTCGGT	CTGATTGCCG	GCTATATCGT	CGCGCTGTTT	TTGGGCAAGG
701	TGGATTTTTT	GGCACTGCAA	AACCTGCCGC	TGGTTACGCT	GCCCGTACCG
751	TTTAAATATG	GTTTTTGCTTT	TGACTGGCAC	GCATTTATTG	TGGCGGGTGC
801	GATTTTCTTG	TTGAGCGTGT	TTGAGGCGGT	CGGCGATTTG	ACGGCGACGG
851	CAATGGTGTC	CGACCAGCCG	ATTGAAGGCG	AGGAATACAC	CAAACGCTTG
901	CGCGGGCGCG	TGTTGGCGGA	CGGTTGGGTG	TCGGTGATTG	CGACGGCTTT
951	GGGTTTCGTC	CCGCTGACGA	CGTTTGACAA	AAACAACGCG	GTGATTGAGA
1001	TGACCGGCGT	GGCTTCGCGC	CATGTGGGCA	AATATATTGC	CGTGATTTTG
1051	GTGCTGTTGG	GTCTGTTCCC	CGTTGTGCGA	CGCGCGTTTA	CGACGATTCC
1101	GAGTCCGGTG	TTGGGCGGGC	CGATGGTTTT	GATGTTGCGC	TTGATTGCGA
1151	TTGCGGGCGT	GCGGATTTTG	GTCAGCCACG	GCATCCGCAG	GCGCGAAGCG
1201	GTAATTGCGG	CAACGTCGGT	CGGTTTGGGC	TTGGGTGTGC	CGTTTGAGCC
1251	GGAAGTGTTT	AAAAACCTGC	CCGCTCTGTT	CCTAAACTCT	ATTTCCGCCG
1301	GCGGCATTAC	GGCAGTCTTG	CTGAATTTGG	TCTTGCCCGA	AGATAAAACC
1351	GAGGCGGCGG	TCAAGTTTGA	TACCAATCCAC	TTGGAACACT	GA

a532.pep

1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG  
51 GALELPVEMT AYLVSAMMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLVPV
251 FKYGFAFDWH AFIVAGAI FL SVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATAGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKEDTDH LEH*

```

# m532/a532 100.0% identity in 463 aa overlap

m532.pep	MSGQLGKGADAPDLVYGLDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
a532	MSGQLGKGADAPDLVYGLDRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT
m532.pep	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
a532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRRMSGIAVGLIAGYIVALFLGKVDFSALQ
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRRMSGIAVGLIAGYIVALFLGKVDFSALQ
m532.pep	NLPLVTLVPVFKYGFADWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
a532	NLPLVTLVPVFKYGFADWHAFIVAGAI FLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL
m532.pep	RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG
a532	RGGVLADGLVSVIATAGSLPLTTFAQNNGVIQMTGVASRHVGKYIAVILVLLGLFPVVG
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREA VIAATSVGLGLGVAFEPEVF
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRREA VIAATSVGLGLGVAFEPEVF
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

g535.seq

```

1 atgccctttc ccggttttcag acaantat ttt gcttngtct tgcacggtt
51 ttttgccgta ggtcggattc tcgaatccga catttccaac agcgggtttt
101 cggaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaattaca tcgcttccaa ttgcgaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagtga tggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

806

```

3 51 catcgatgat tttgtcccgt tgtacggtgg tttggcgcgt gttgccgtag
4 01 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
4 51 gatttcttcg acgaagcggg atgcatgccc gaattggggtt tgtccgtgca
5 01 gcatgcggtt gtgtgccatg gtgatgtaga ggcgtttgcy ggcgcggggtg
5 51 atggcgacgt acatgaggcg gcgttcttct tcgaggccgc cgcgctcggc
6 01 aaggctcatt tcgctgggga aacgcccctc ttccataccg gtgaggaaga
6 51 cggcggtgaa ttccaagcct ttggcggcgt ggacggtcat cagttggacg
7 01 gctttttcgc ctgcccctgc ttggttttcg ccggattcga gggcggcggt
7 51 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
51 ACISNLHRFQ FRKLGIFQFH ALFAEVDGQS GGFVFCGID NHAGAEFGVT
1 01 DVLSDAEACV GLRLFEVIDD FVPLYGGLAR VAVAVEGGFF DQVQVYFWR
1 51 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
2 01 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
2 51 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 aTGCCCTTtC CCGTTTTTcAG ACGGCCTTTT GCTTTGTCTT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTTCACAC AGCGGTGTTT
1 01 CGGAAACAAT AGACGCGTCA AATGTTTTTG TCGGATACGA ATATCCGACC
1 51 TACATTTCAA ATTTACATCT CTTCCAATTT CGCAAATG GTGTCCAAC
2 01 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTGCGCT
2 51 TTATCTGCGG CATCGATAAT CACGCGGTG CCGAATTGG CGTGGCGGAC
3 01 GTTTTGTCGG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
3 51 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GCGCGGTGTT GCCGTAAC
4 01 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAACTACT CGGGTGGGAT
4 51 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
5 01 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTGCGGGC GCGGGTGATG
5 51 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
6 01 GCTCATTTTC CTGGGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
6 51 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGGTCATGAG TTGGACGGCC
7 01 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTGAGGG CGGCATTGCT
7 51 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRPF ALSLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDQSG GFVFCGIDN HAGAEEFGVAD
1 01 VLSDETTCVG LGLFVVVDDF IFGCGGLARV AVTVVGLRFD GQVQYFGWD
1 51 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFEAAAFGK
2 01 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
2 51 XEGENGEGGV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

	10	20	30	40	50	59	
m535.pep	MPFPVFRPFALSLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ						
	:            :              :            :						
g535	MPFPVFRQXFAXSLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ						
	10	20	30	40	50	60	
m535.pep	60	70	80	90	100	110	119
	FRKLGVLQFHALFAEIDQSGGFVFCGIDNHAGAEFGVADVLSDETTCVGLGLFVVDD						
	:      :      :      :      :      :      :      :      :						
g535	FRKLGIFQFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFEVIDD						
	70	80	90	100	110	120	

	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	:        :   :      :						
g535	FVPLYGGLARVAVAVEGGFFDGGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKQFQAFGGVDGHLDGLFACAC						
	:       : :  :       :       :   :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVVEFQAFGGVDGHLDGFFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIXEGENEGGGVV						
	:     :     :     :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

```

a535.seq (partial)
1 TTCAGACGGC CTTTTGCCTT GTCCTTGCTA CAGTTTTTTG CCATAGGTCG
51 GATTCTCGAA TCCGACATTT CCAACAGCGG TTTTTCGGAA ACGATAGACG
101 CGTCAAATAT TTTTTCGCGA TACGAGTATC CAGCCTGCAT TTCAAATTTA
151 CATCGCTTCC AATTTCGCAA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCCTTTATC TGCGGCATCG
251 ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGCTTT GTCCGATACG
301 GAAACCTGCG TAGGTTTGGG CTTGTTTGTG GTGTCGATG ATTTTGTCTT
351 TGGGCGCGGC GGTTTGGCGC GTGTTGCCAT AGCGGTCGTA GGCGGGTTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTCTT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCCGTG CAGCATCGGT TGTTGCGCCA
501 TGGTGATGTA GAGCGCTTTG CGGGCGCGGG TAGATGGCGAC GTACATCAGG
551 CGGCGTTCCT CTTCCAGGCC GCCCGTTTCG GCAAGGCTCA TTTGCTGGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATTCCAAGC
651 CTTTGGCGGC GTGCACGGTC ATGAGTTGTA CGGCTTTTTC GCCCGCGCCT
701 CTTTGGTTTT GCCTGGATTG GAGAGACGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGCGC GGGTCGTCG A

```

```
a535.pap (partial)
  1 FRFPFALSLL OFFAIGRILE SDISNSGFSE TIDASNIFVG YEYPACISNL
  51 HRFQFKRLGV QLFHALFAEI DQSGGGFAFT CGIDNHAGAE FGVADVLSDT
101 ETCVGLGLFV VVDDFVFGRG GLARVAIAVV GGFQDGQVVQ YFGRDFFDEA
151 GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEA AAFGKAHFAG
201 EAAFFHAGEE YGVKFQAFGG VHGHELYGFF ARACLVFAGF ESSIA*ESED
251 GEGGVV*
```

```

m535.pep      10      20      30      40      50      60
               MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASN VFVGYEYPTYISNLHLFQF
               |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a535          FRRFPFALSLLQFFAIGRILESDISNSGFSETIDASNIFVGYEYPACISNLHRFQF
               10      20      30      40      50

m535.pep      70      80      90      100     110     120
               RKLGVQLFHALFAEIDQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDFF
               |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a535          RKLGVQLFHALFAEIDQSGGFAFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDFF
               60      70      80      90      100     110

m535.pep      130     140     150     160     170     180
               IFGCGGLARVAVTVVGR LFDGQVVQYF G WDLFDEAGDDAELGLSVQHALLRHGDVEAFAG
               :||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a535          VFGRGGLARVAIVVGGFFD GQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG
               120     130     140     150     160     170

```



808

	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACACL					
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKFQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIXAEGENGEGGVVX					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa ctgtctatc
101 cgtccgcacc gcaaatcagg gacggcgcg atgcgtgca ctacctcaac
151 cgcattccga cacaaatcgg tttgcacg cgccgggttt
201 ggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacacct cccgacaatc cgactacac cgacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagt gacgcttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcagggtcgg catttgctgc
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcagc cggaagcagg acggaaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgcg
701 tgctttattt ttacggggaa cgtcccgacc cgtgcccga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgcgggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttgcgccttt tcccgtctaa acccttgga taccggcagc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcggcgag
1051 acacttgagg ttgaaaaagg cgaaaaatat ttcattccat ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg caggaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagcgg catcaggctt actccggaag acagcccgga
1251 acgcgggtga accctttatt tgcaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTOIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LINGVHENIS TEEEAESSD SDIRTQORQV DALMSAIYHR
151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RQPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDFVPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAHQ
301 FALFPLKPLE YGTLTYAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCCG CGGCAGGCGT
51  TTTTACCAT ACCCAAmCC AATCCCTGCC CGCGGGCGAA CTGTCTATC
101 CTTCCGCACC GCAAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT
201 GGAAACTCC GCCCGCAGGC ACGCAAGCTA CTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```

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3 01 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 3 51 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 4 01 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 4 51 CTTTCCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)  
 1 MKSLFIRLLL LGSAAGVFYH TOXQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK  
 101 LTERTRLAGY LYNVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTOXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRIQIGLHA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNVHENIS					
g537	LAHAPVLENSARRHARYLTLPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq

1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT  
 51 TTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC  
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC  
 151 CGCATCCGCG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGGTTTT  
 201 GGAAATTCG GCCCGCAGGC ACGCACGCTA TCTCACGCTC AATCCCGAAG  
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG  
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA  
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC  
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC  
 451 CTTTCCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCGG  
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGGCAAC GGCAGGTTTG  
 551 AGCGGCATTG CGCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT  
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACCG ACGAAGCCAT  
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC  
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC  
 751 ACGGGCAATC CTGCCAGCAT TGATTTTTCG GAGGCGGCAG GCAAAATTAC  
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCGTCA  
 851 GGGTTTTAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA  
 901 TTCGCGCTTT TCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC  
 951 GGTATTTCGAC TATGTCCGCA ACGGACGCGC CGCGCAGGCG AAATGGCAGT  
 1001 TTAGAACCCG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGGCGAG  
 1051 ACACTTGCGG TTAGAAAAGG CGAAAATAT TTCATCCACT GCGCGGACG  
 1101 CTGGTGTGTTG GAAGCGTGTA CCCGTTATAC CTACCGGCAG CGACCCGGCA

810

1 151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTCAGCGTT  
 1 201 GACGGAATGG CGGGCAGCCG CATCAGCGTT GCACCGGAAG GAGAAACGGA  
 1 251 ACGAGGCGTA ACCCTTTATT TACAGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep  
 1 MKSLFIRLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN  
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK  
 101 LTERTRLGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR  
 151 LSLDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY  
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDFVPEYEI  
 251 TGNPASIDFS EAAGKITMKS FKLYQKGNEI RFVRVLTAGN DPNRRLTAYQ  
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE  
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPGSRLSISR HKAGGIVFSV  
 401 DGMAGSRITL APEGETERGV TLYLQD\*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
a537	MKSLFIRLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASLYLTLPEDGHGEHHPDNPHYTAQKLTERTRLGALYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLPEDGHGEHHPDNPHYTAQKLTERTRLGALYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
a537	GRFERHCAQGRNQPEAGRKYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq  
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg  
 51 cgtcatgctg gtggcgctaa tgttgataa agatgatacg ggcagcaatg  
 101 ccgcccgtct gaacgggttt cagacggcat tggcggaagc cgtcgagctg  
 151 gtcaaaagcg cggcgggcga ttccgtacgc gtggagactg ccaaacgcga  
 201 ccgcccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt  
 251 cgaagcagt tgcgcagac ggcattgatt tggcgtatt caaccacgaa  
 301 cttactcca cgcaggaacg caatttgaa aaaatcctcc aatgcccggt  
 351 attggacaga gtggggctga ttctggcgat ttctgccgcg cgcggccgca  
 401 cgcaggaagg caggctgcaa gtcgagttgg cgcaattgag ccatttgagg  
 451 ggacgcttga tacgcgggta cggacatttg caaagccagc gcggcggtat  
 501 cggcatgaaa gggccgggca aaaccaaact ggaaaccgac cgccgatata  
 551 ccgcccacgc gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa  
 601 cagcgcgccc tgcgcgcaa gtcccgcgag tcgggcagaa tcaaacggtt  
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc  
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac  
 751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatctcgac  
 801 gataccgtc ggattcgta cgcattctgc gcacaaactg atttccgcct  
 851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgtc  
 901 gtcgatgctg ccgcccggaa cagcgggcag cagattgaag acgtggaaaa  
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcatc aaggtgtaca  
 1001 acaaaaccga cctgtgcgcg tctgaagaac aaaacacggg catatggcgc  
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaaaac

1	MSGRTGRNSA	TQAQPERVML	VGVM LDKDDT	GSNAARLNGF	OTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEA VAAD	GIDL VVFNHE
101	LTPTQERNLE	KILQCRVLDR	VGLILAI FAR	RARTQEGRLQ	VELAQLSHLA
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLEDT	RRLTAHRINA	LKKQLANLKK
201	QRALRRKSRE	SGRIKTFALV	GYTNVGKSSL	FNRLTSKGIE	AKDQLFATLD
251	TTARRLYISP	ACSIILTTDV	GFVSDLPKHL	ISAFSATLIE	TVQADVLLHV
301	VDAARNNSGQ	QIEDVENVLQ	EIHAHDIPCI	KVYNKTDLLP	SEEQNTGIWR
351	DAAGKIAAVR	ISVAENTGID	ALREAI AEYC	AAAPNTDETE	MP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

1	ATGACAGGCA	GAACAGGCGG	CAACGGCAGT	ACCCAAGCGC	AACCCGAACG
51	CGTCATGCTG	GTGGGCGTAA	TGTTGGACAA	AGATGGTACG	GGCAGTAGTG
101	CCGCCCGTCT	GAACGGTTTT	CAGACGGCAT	TGGCGGAAGC	TGTCGAGCTG
151	GTCAAAGCGG	CGGCGCGCGA	TTCCGTGCGC	TGGAGACATG	CCAAACCGCA
201	CCGTCCGCAC	ACCGCGCTGT	TTCTCGGCAC	GGGCAAGGCG	CGCGAGCTGT
251	CAGAAGCAGT	TGCCGCAGAC	GGCATCGATT	TGGTCGTATT	CAACCACGAA
301	CTCACGCCCA	CGCAGGAACG	CAACCTTGAA	AAAGAACTsA	AATGCCCGGT
351	ATTGGACAGG	GTAGGGCTGA	TTCTGGCGAT	TTTCGCTCGC	CGCGCCCGCA
401	CGCAGGAAGG	CAGGCTGCAA	GTCGAGTTGG	CGCAATTGAG	CCATTTGGCG
451	GGACGCTTGA	TACGCGGTTA	CGGCCATCTG	CAGAGCCAGC	CGCGCGGTAT
501	CGGCAATGAA	GGCCCCGGCG	AAACCAAACT	GGAAACCGAC	CGCCGATTGA
551	TCGCCCATCG	GATCAATGCC	TTGATAAAAC	AGCTTGCCAA	CCTCAAAAAA
601	CAGCGCGCCC	TGCGCCGCAA	GTCnCGCGAA	TCGGGCACAA	TCAAAACGTT
651	TGCGCTGGTC	GGCTATACAA	ATGTCGGAAA	ATCCAGCCTG	TTCAACCGGC
701	TGACAAAGAT	GGGCATATAT	GCAAAGGACA	AGCTTAGTCC	CGAATGCAGC
751	ATTATCTTGA	CCGATACCGT	CGGATTCGTn	AGCATTCTGC	CGCAcAAACT
801	GATTTCGGCC	TTTTGgCC .A	CGCTGGAAGA	AACCGCGCAA	GCCGATGTGC
851	TGCTGCACGT	CGTCGATGCC	GCCGCTCCGA	ACAGCGGACA	GCAGATTGAA
901	GACGTGGAAG	ACGTACTGCA	AGAAATCCAT	GCCGGCGATA	TTCCGTGCAT
951	cAAGGTGTAC	AACAAAACCG	ACCTGCTGCC	GTCTGAAGAA	CAAAACACGG
1001	GCATATGGCG	CGACGCTGCG	GGAAAAATTG	CCGCGCTCCG	CATTTCCGTT
1051	GCTGAAAAAT	CCGGTATAGA	CGCACTGCGC	GAAGCCATTG	CCGAGTCTTG
1101	TGCCGCCGCA	CCAAACACAG	ACGAAACCGA	AATGCCATGA	

**This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:**

1	MTGRTGGNGS	TQAQPERVML	VGVM LDKDGT	GSSAARLNGF	QTALAEAVEL
51	VKAAGGDSVR	VETAKRDRPH	TALFVGTGKA	AELSEA AAD	GIDL VVFNHE
101	LTP TQERNLE	KELKCRVLDR	VLGLAIFAR	RARTQEGRLQ	VELAQLSHLA
151	GRLIRGYGHL	QSQRGGIGMK	GPGETKLETD	RRLIAHRINA	LIKQLANLKK
201	QALRRKSRE	SGTIKTFALV	GYTNVGKSSL	FNRLTKSGIY	AKDKLSPECS
251	IILTDTVGVF	SDLPHKLISA	FSXTLEETAQ	ADVL LHV VDA	AAPNSGQQIE
301	DVENVLQEIH	AGDPICIKVY	NKTDLLPSEE	QNTGIWRDAA	GKIAAVRISV
351	AENTGIDALR	EAI A E S C A A A	PNTDETSE*		

**Computer analysis of this amino acid sequence gave the following results:**

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m538.pep	MTGRTGGNGSTQAQPERVMLGVVMLDKDGTGSAAARLNGFQTALAEAVELVKAAGDSVR					
	:	::		:		
g538	MSGRTGRNSATQAQPERVMLGVVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGDSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m538.pep	VETAKRDRPHTALFVG TGKAAELSEAVAADGIDL VVFNH ELTPTQERNLEKELKCRVLDR					
q538	VETAKRDRPHTALFVG TGKAAELSEAVAADGIDL VVFNH ELTPTQERNLEKILOC RVLDR					

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	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQRALRRKSRESGTIKTFALVGTYNVGKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQRALRRKSRESGRIKTFALVGTYNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGFVSDLPKHLISAFSXTLEETAQADVLLHV					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGFVSDLPKHLISAFSATLEETVQADVLLHV					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQQIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGTCT GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTGCCCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAAC TGGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCCGCAA GTCCCGCGAA TCGGGCACAA TCAAAACGTT
651 TGGCTGGTGC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGGCG GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCGTCA GCGATCTGCC GCACAACTG ATTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGAAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCGCG ATTTCCGTTG CTGAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDLVVFNHE
101 LTPTQERNLE KILQCRVLDR VGLILAI FAR RTQEGRLQ VELAQLSHLA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

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813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD  
 251 TTARRLYISP ECSIILTDV GFVSDLPKLI ISAFSATLEE TAQADVLLHV  
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR  
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP\*

m538/a538 94.6% identity in 392 aa overlap

	10	20	30	40	50	60
m538 . pep	MTGRTGGNGSTQAQPERVMLVGVM LDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR					
a538	MTGRTGRNGSTQAQPERVMLVGVM LDKDGTGSSATRLNGFQTALAEAVELVKAAGGDSVR					
	10	20	30	40	50	60
m538 . pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLD R					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRVLD R					
	70	80	90	100	110	120
m538 . pep	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKELKCRVLD R					
a538	VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPTQERNLEKILQCRVLD R					
	70	80	90	100	110	120
m538 . pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538 . pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
a538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	130	140	150	160	170	180
m538 . pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538 . pep	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
a538	RRLIAHRINALIKQLANLKKQALRRKSRESGTIKTFALVGYTNVGKSSLFNRLTKSGIY					
	190	200	210	220	230	240
m538 . pep	AKDKL-----SPECSIILTDVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPECSIILTDVGFVSDLPKLI SAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538 . pep	AKDKL-----SPECSIILTDVGFVSDLPKLI SAFSXTLEETAQADVLLHV					
a538	AKDQLFATLDTTARRLYISPECSIILTDVGFVSDLPKLI SAFSATLEETAQADVLLHV					
	250	260	270	280	290	300
m538 . pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538 . pep	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
a538	VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
m538 . pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
a538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539 . seq

```

1  atggaggatc tgcaggaaat cgggttcgat gtcgccgccg taaaggtagg
51  tcggcagcgc gaacatcatc gtctgcatca taccagtcgc ggcaacggca
101 aggcggacga tgtattgttt gcgttctttt tggttggcgg cttcgatttt
151 ttgcgcgtca tagggtgcgg cgggttagcc tgtctgccgg attttcaaca
201 gaatgtcggg gaggcggatt ttgccgtcgt cccagacgac gcggcagcgg
251 tgcgtgctgt aattgaggtc gatgcggacg atgccgtctg tgcgcaaaag
301 ctgctgttcg atcagccaga cgcaggcggc gcaggtaatg ccgctgagca
351 tcagcactgc ttcgtgcgtg ccattatggg tttccacaaa gtcggatttg
401 acttcgggca ggtcgtagc gcggatttgg tcgaggattt cttggggcgg
451 cagttcgggt tttttcgcgt cggcggtgcg tcgtttgtaa taactgcccc
501 agccggaatc gatgatgctt tgtgcgactg cctgacagcc gacgcagcag
551 gtttcgcggt cttcgccttc gtagcggacg gtcagatgca gggtttcggg
601 aacgtccagc ccgcagtgga aacaggtttt tttcatggca ttcgggttc

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651 gtctgtgttt ggtgcgggcg cacaatactc ggcaatggct tcgcgcagtg
701 cgtctatacc ggtatttttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcgggtttg ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccgggag
901 ccagcatcga cgacgtgcag cagcacatcg gcttgacagg tttcttccaa
951 ggtggcgga aagggcgaaa tcagtttgg cggcagatcg ctgacgaate
1001 cgacggtatc ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgcggtcg tgcgagagtg ggcgaaaagc tgggtctttc catatatgcc
1101 cgacttggtc agccgggtga acaggctgga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

g539.pep

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQONVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGPHK VGLDFGQVVQ ADLVEDFLGR
151 QGFFFRVGGA SFVITAQAGI DDALCDCLTA DAAGFAVFAP VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAQAYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICCPFLFA
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPTVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

m539.seq (partial)

```

1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGC GGTTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCaGCGG
251 TGCGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTTC ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGCACTGG
401 ACTTCGGGCA GGTCTGACAG GCGGATTTGG TCGAGGATTT CTGGGGCGG
451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GCGGCaAGG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTTCATGGA TTTCTGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCGCGT CGCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 CTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATT
851 GTTGCACTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCAG
951 CGTGGCG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CtnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

m539.pep (partial)

```

1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQONVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFRLRVGGA LFVITAQARV NNALCDRLTA GAQGFVAVFV VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLFA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPTVSVRI MLHSG....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

m539/g539

```

          10      20      30      40      50      60
m539.pep  MEDLQEIGFDVAAVKVGRQREHHRLHHPQPGNGEADDVLF AFFLVGGFDFLRVIGCGGVA
          |||||
g539      MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```

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	10	20	30	40	50	60
m539 . pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
g539	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
	70	80	90	100	110	120
m539 . pep	130	140	150	160	170	180
	LARAAVGFHKVGLDFGQVVQADLVEDFLGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	FVRAIMGFHKVGLDFGQVVQADLVEDFLGRQFGFRVGGASFVITAQAGIDDALCDCLTA					
	130	140	150	160	170	180
m539 . pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS					
g539	DAAGFAVFAFVADGQMVFQVFNQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
m539 . pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISPAWISCSTFTSSICCPFLGA					
g539	ATEMRTAAIFPAASRHPVFCSSDGSRSVLLYTLMHGISWAWISCSTFTSSICCPFLRA					
	250	260	270	280	290	300
m539 . pep	310	320	330	340		
	AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	AASTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGIMYSRRVVSRAVKS					
	310	320	330	340	350	360
g539	WSFAYMEDLVSRNLRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539 . seq
1  ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTCTCTTT TGGTTGGCGG CTTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TCGGTGCTGT AATTGAGTTC GATGCGGACG ATGCCGCTCTG TACGCCAAAAG
301 CTGCTGTTCG ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCGTACAG GCGGATTGG TCGAGGATTT CTTGGGGCGG
451 CAGCTCGGTT TTTTGC GCGT GCGGCGTGCG TTGTTGTAA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCGCGAGCGT CGCGCCATAT GCCCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TGATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGC GCGG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTGAGGATA ATGCTGCATT CCGGACTGAT GTACAGCCGC
1051 CCGCGCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTTTC CATATATGCC
1101 CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539 . pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGGDF

```



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```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAVRAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVO ADLVEDFLGR
151 QLGLRVGGA LFVITAQARV NNALCDCLTT GAAGFAVEVF VTDGQMQVFG
201 NVQPAVETGF FHGISVSSVF GAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPFLGA
301 AASTCSSTS ACAVSSSVAE KAEISLCGRS LTNPTVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

```

m539.pep      10      20      30      40      50      60
MEDLQEIGFDVA AVKVG RQREHRLHHPQPGNGEADDVLFAFFLVGGFDLRLVIGCGGVA
|||||
a539          10      20      30      40      50      60
MEDLQEIGFDVA AVKVG RQREHRLHHPQPGNGEADDVLFAFFLVGGFDLRLVIGCGGVA

m539.pep      70      80      90      100     110     120
YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR
|||||
a539          70      80      90      100     110     120
YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR

m539.pep     130     140     150     160     170     180
LARAAGVFHKVGLDFGQVVOADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDRLTA
|||||
a539         130     140     150     160     170     180
LARAAGVFHKVGLDFGQVVOADLVEDFLGRQLGLRVGGALFVITAQARVNNALCDCLTT

m539.pep     190     200     210     220     230     240
GAQGFAVVFVTD SQVEVFGNIQTAVETGFFHGISVSSVFGAAQDSAMASRSASIPVFS
|||
a539         190     200     210     220     230     240
GAAGFAVVFVTDGQMQVFGNVQPAVETGFFHGISVSSVFGAAQYSAMASRSASIPVFS

m539.pep     250     260     270     280     290     300
ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA
|||||
a539         250     260     270     280     290     300
ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPFLGA

m539.pep     310     320     330     340
AASTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG
|||||
a539         310     320     330     340     350     360
AASTCSSTSACAVSSSVAEKAELSLCGRSLTNPTVSVRIMLHSGMLYSRRRAVVSSVAKS

a539         370     380
WSFAYMPDLVSRLNRLDLPTLVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgccct cccgacgcgg caacgggggtg tttatcaaa acggcaaact
51 tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101 tgccggtgcc gaaccgatg ccgtctgaac cttcagacgg catcgggtgt
151 ttatttgtcc actcggacgg gtgcaggttc gtattgtgtc gattcgctgc
201 cgtaatacag cagccgaggt ttgacgggga tgcgtccctg cgatttgagg
251 tggcggttgg aatcgcgcaa ggaatacgcg cagccgcagt attcctgctg
301 gtagaagttt tcgctgttgc tgatttcaat catacgcgcg ccgcccgcgc
351 ctttgcccca gttgaagtc caataggcca catcatcgta aggcgcggcg
401 gcacggtgtc cgcagtcgtt gatttgcgcc atattttcc agcgtga

```

This corresponds to the amino acid sequence &lt;SEQ ID 1568; ORF 540.ng&gt;:

g540.pep

```

1  MPPSRRGNGV FYQNGKLANA VSACRLPNRQ TFPVPVPNPM PSEPSDGIGC

```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

Computer analysis of this amino acid sequence gave the following results:

**Homology with a predicted ORF from *N. gonorrhoeae***

ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

m542/g542

```

      10      20      30      40      50      60
m542.pep  MPKWSRIRRCSVLSLMFSASVSRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g542      MPKWSRIRRCSVLSLMFSAAVSRLTWCAPPNAAFRVRLKSSDGIASASAVCPAAGSMPS
          10      20      30      40      50      60

          70      80      90     100     110
m542.pep  ETVSHKSDSSRNTSASXRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX

```

q542

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

a542. seq

**This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:**

a542.ppt

**m542/a542 94.6% identity in 111 aa overlap**

m542.ppt

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

q543.seq

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

g543.pcp

m543.seq

1	ATGTTTGTGC	GGTTATTTCG	CGCCGTTTTT	GGCTTTCAAC	TCGGCAATCA
51	GTCCGTCCAC	GCCTTTTCGT	TTGATAATTT	CGCCGAATTG	GTTGCGGTAC
101	ACGGTAACCA	GGCTCGCGCC	TTCCGATGGC	ACGTTGTAGG	TACGGTATTT
151	ACCGCCGCTT	TGGTAGGTGC	TGAAGTCCAT	GTTGACGGGT	TTTTGCCCGT
201	GTAGCGCGAC	TTCCGCGCGG	ACGATGATTT	GTTTCCCGCC	TTTTATTGACG
251	ATGGGATTGT	CTTTGACGTT	GACGTTGGCG	TTTTTTAATT	TCAGCATCGT
301	GCCGGAATAG	GTGCGGATCA	GCAGGGTTTG	AAATCTTTTG	GCCAACGCTT
351	GTTTTTTCGC	GTCGGACGCG	GTGCCCAAG	GGTTGCCGAC	CGCCAATGCG
401	GTCATACGTT	GGAAATCGAA	ATAGGGAATC	GCATAGGCTT	CGGCTTTTTG
451	GCGAGCGGTG	TGGCATCTGC	CGTTTTTTAA	GATGCTCAAT	ACTTGATGGG
501	CGTTTTTGAC	GATTTGGCTT	ACCGGTCGCG	CAGGGGCGCG	AAATGCCATG
551	CGGATGCTCA	AAATACCGAT	GCCCAATGCG	CTGATGAGGG	AGGATTTTTT
601	CATGATTAAG	TGTCTTAGTT	TGAATATGAT	GGCATAAGTT	TATTCGGCGG
651	CTTTTTCCGC	ATTGCCGCGC	TCGGCATTTT	TCTCGGCAAA	ACTCGTCATG
701	AATTTGCCGA	TAAGGTTTTT	CAGAACCATT	GCAGAATCTG	TTACGGAGAT
751	GGTGTCGCCG	GCAGCAAGGT	TTTCCGTGTC	GCCGCCCTGC	TGCACGCCGA
801	TGTACTGCTC	GCCCAAAAGT	CCCGAAGTCA	GGATTTCGCG	GGAAACGTCG
851	CTGCTGAACT	GATACTTGCC	GTCCAAATCG	AGGCGCACCC	TCGCCTGATA
901	GGATTTCCGG	TCAAGTCCGA	TAGCGCCGAC	GCGCCCGACC	AATACGCCTG
951	CGGATTTGAC	GGGGGCATTG	ACCTTCAAAC	CGCCGATGTC	GCCGAAATCG
1001	GCATAAACGG	CGTAAGTTTT	GTCCGAACCG	CCGACGACCG	CACCGCCGGC
1051	CACGCGGAAA	GCAGAGAAAG	CAACCCGCGC	CGCCCAATC	AGGACGAACA
1101	GTCCGACCCA	AAATTCCAAT	ATGTTCTTCT	TCATTAA	

m543 . pep

1	MVCRLFAAVF	GFQLGNQSVH	AFRFDNFAEL	VAVHGNQARA	FDGDVVGTVF
51	TAALVGGEVH	VDGFLPGYAD	FGADDDFFAA	FIDDGIVFDV	DVGVFXXFQHR
101	AGIGADQQGL	KFFGQRLFLR	VGRGAPRVAD	RQCGHTLEIE	IGNRIGFGFL
151	ASGVGIAVFX	DAQYLSGVL	DLAYRVGRGG	KCHADAQNTD	AQCADEGGFF
201	HDXVSXFEYD	GIRLFGGFFR	IAAQGISFLGK	TRHEFADKVF	QNHCRGTGYD
251	GVAGSKVFSV	AALLQPDVLL	AGKSRQDLR	GNVAELILA	VQIEAHPRLI
301	GFRVKSDFSAD	APDQYACGFD	GGIDLTQADV	AEIGINGVSF	VRTAERRTAG
351	HAESEKGNRR	RANQDEQSDP	KFQYVLLH*		

from *N. gonorrhoeae*:

m543/g543

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNF	AELVAVHGNQARAFDGDVVGTVFTAALVGGEVH				
		:		:	:	
g543	MVCRLFAAVFGFQLGNQPVD	AFGFDDFAELVAVHGNQARAFDGDVVGTVFAAALVG	GKVH			
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDGFLPGYADFGADDDFFAA	FIDDGIVFDVDVGVF	FXFOHRAGIGADQQGLKFFGQRLFLR			
	:     :       :       :					
g543	IDGLLTGDADFGTDDD	FLAALIDDGIVFDVDGRVF	EFQOHRAGIGADQQGLKFFGQRLFLR			
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

m543 . pep      VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
g543            VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
                  130      140      150      160      170      180

                  190      200      210      220      230      239
m543 . pep      KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIAAGVIFLGKTRHEFADKV
g543            KCHADAQNTDAQCADEGGFFHDXV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
                  190      200      210      220      230

                  240      250      260      270      280      290      299
m543 . pep      FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
g543            FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
                  240      250      260      270      280      290

                  300      310      320      330      340      350      359
m543 . pep      IGFRVKSDSADAPDQYACGFDGGIDLTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
g543            IGFRVKSDSADAPDQYACGFDGGIDLTADVAEIGINGVSFVRTAERRTAGHAESEKGNR
                  300      310      320      330      340      350

                  360      370      379
m543 . pep      RRANQDEQSDPKFQYVLLHX
g543            RRADQDEQSDPKFQYVLFHX
                  360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543 . seq
1   ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNNGATTGT CTTTGACGTT GACGTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 CGGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTGAGTGG
501 CGTTTTCACG GATTGTTT ACCGCGTCGG CAGGGCGGCG AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCGCG ATTGCCGCG TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTGCCGA TAAGGTTTTC CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTCGCG GGAAACGTCG
851 CTGCTGAAT GATACTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCGGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTCGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCGC CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAG CAACCGCCG CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543 . pep
1   MAYGLLAAXV SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGVTF
51  TAALVGGEVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQQGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITAF* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRITGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLTADV AEIGINGVSF VRTAERRTAG

```

[illegible]

g544.seq

**This corresponds to the amino acid sequence <SEQ ID 1586; ORF 544.ng>:**

**g544.pcp**

```

1  MKKILTAAAV ALIGILLATV LIPDSKTAPA FSLPDLHGKT VSNADLQGV
5  TLINFWFPSC PGCVSEMPKV TKTANDYKNK DFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV IYDADKAVGQ AFGTQVYPTS VLIGKKGEIL KTYVGEPDFG

```





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151 KLYQEIDTAL AQ\*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544.pep	MXKILTA	AVVALIG	ILLAI	VLXPDS	KTAPAF	SXPDLHGKTVSNADLQ
a544	MKKILTA	AVVALIG	ILLAI	VLIPDS	KTAPAF	SLSXLHGKXVXNADLQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m544.pep	PGCVS	XMFKI	IKTAND	YKXKN	FQVLAV	AQPIDP
a544	PGCVSE	MXI	IKTAND	YKXKN	FQVLAV	AQPIDP
	70	80	90	100	110	120
	130	140	150	160		
m544.pep	AFGTQ	VYPTSV	LIGKX	GKGEI	FKTYV	GEPDFG
a544	AFGTQ	VYPTSV	LIGKK	GKGEI	LKTYV	GEPDFG
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547.seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgcccgaat
51  cgtcgaaact ttcgacgtat tcttccttag gaacgattgc gcctttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggg atatctcggt
151 gatataatta caagatgcgg cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcca gatggatgcc cattacttcc ccttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgctt ccaaaccgaa
401 aaaagcggtt tgttttttgt tggttaa

```

This corresponds to the amino acid sequence &lt;SEQ ID 1592; ORF 547.ng&gt;:

g547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKEGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLS PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547.seq

```

1  ATGTTCTG TAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCGCT CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
251 CCGAAGTCCA GATGGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTATATA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTTG TCTCCAAACG
401 GAAAAAAGCG GTTTGTTTTT TGTTGTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1594; ORF 547&gt;:

m547.pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKEGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXVCVKE ELLTILVKNL SPNGKKRFVF CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547 . pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547 . pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIVTNIRVF-CVCK					
	70	80	90	100	110	
	130	140				
m547 . pep	ELLTILVKNLSPNGKKRFVFCCK					
g547	ELLTILVKNLSPNGKKRFVFCCK					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547 . seq
1  ATGTCGTAG ATAACGATT TAATAAACG GTAGCGAGTT TTGCCAAAT
51  CGTCGAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GTCGTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG CTTGAGATT CCGAACCGCT CCTTTAAGA
201 CCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATAGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547 . pep
1  MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYL
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRLYL
101 KFIHLHIFTN IKVFXCVCK ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547 . pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNCTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547 . pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYFPLLRLKYLKFIMLHIFTNFKVFXCVCK					
	70	80	90	100	110	120
	130	140				
m547 . pep	ELLTILVKNLSPNGKKRFVFCCK					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548 . seq
1  atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
51  gcttgccgcc tgcaaacctc aagacaacag tgcggcgcaa gccgcttctt
101 caagtgcata cgcgcggctt gcggaaaatg cggcaaagcc gcaaacgcgc
151 ggtacggata tgcgtaagga agacatcggc ggcgatttca cactgaccga
201 cggcgaagga aagcctttca gcctgagcga ttgaaaggc aaggtcgtga
251 ttctgtcttt cggctttaag cactgtcccg atgtctgccc gacagggtct
```

```

301 ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351 gaaagtgggtg ttgctcagca tcgatccgga acgcgacacg cctgaaatca
401 tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451 acgggcgggc aaaacctgcc ggtcatcaag cagcaatacc gcgtgggttc
501 tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551 cttccggtgc gtatcttata gataaaaacg gtgaggttgc cattttctcg
601 ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651 ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1 MFSVPRSFPLGVFVLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51 GTDMRKEDIG GDFTLTDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGOAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1 ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51 GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGCGCAA GTGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TGCCTAAGGA AGACATCGGC GCGGATTCA CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGGCGAG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAATATTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAACG GTGAGGTTGC CATTTTCTCG
601 CTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1 MFSVPRSFPLGVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51 GTDMRKEDIG GDFTLTDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSIDLKQL GGOAKDVVV FVSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFPLPGVFVLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
g548	MFSVPRSFPLPGVFVLAALAAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m548.pep	GDFTLTDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSIDLKQLGGQAKDVVV					
g548	GDFTLTDGEGKPFSLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVVV					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m548.pep	FVSIDPERDTPETIIGKYAKQFNPDFIXLTATGGQNLPIVKQYRVVSAKVNQKDDSENYL					
g548	FVSIDPERDTPETIIGKYAKQFNPDFIGLTATGGQNLPIVKQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

827

	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```
a548.seq
1  ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CCGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GCGGATTTCG CGCTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCG GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AACTATTGTC GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```
a548.pep
1  MFSVPRSFPLGVFVLAALAA CKPDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV FVSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIK QYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*
```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFPLGVFVLAALAAACKPDNSAAQVASSSASASAAENAAKQXTRGTDMRKEDIG					
a548	MFSVPRSFPLGVFVLAALAAACKPDNSAAQVASSSASASAAENAAKPQTRGTDMRKEDIG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
a548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELLTYSDTLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m548.pep	FVSIDPERDTP EIIGKYAKQFNPDFIXLTATGGQNLPIKQYRVVSAKVNQXDDSENYL					
a548	FVSIDPERDTP EIIGKYAKQFNPDFIGLTATGDQNLPIKQYRVVSAKVNQKDDSENYL					
	130	140	150	160	170	180
	190	200	210			
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```
g550.seq
1  atgataacgg acagggttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcattttta
101 ccacaaacgg cttacagctt ccattcgccc aacttgccag cgtaagcttc
```

828

```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgctttgg
201 cggcagccgt agcgacgcga ggcagcaggc gggaaatcgaa cggagtagga
251 atcaggtatt ccgcgcgaa ttcgaaatttc ttaccgtaag cggcaaccac
301 ttcttcggtt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcgttg atggtggttg cgcgcacatc caacgcgccc
401 cgggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcggcgg gtaccgataa ccacgtccgg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatgggtttt
551 tcgttcacatg tggtcaacat ttcaggcgtc agcagggttg cgcggagag
601 gcccaagaag atgtctttgc ctttaaccgc atcggcaagt acgcgccggc
651 cggtgtcttc aacggcgtag aattttttgg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cacgcctttg gaggttgaaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801 cggcacctgc gccggagcac accaaagtgc cttcttcgat tttacggcgg
851 gtataacgca gggcgttcaa tacggcgggc gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

g550.pep

```

1 MITDRFHLFH FVPSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGSVSF
51 QICNRTGCHA AFHRCFGSR SDARQQAGIE RSRNQVFRAE FEFLT VSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVHLVREV
151 GAAGTDNHVR TGFFRQRRQD FRIRVGHGEH DGFFVHRVQH FRRQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

m550.seq (partial)

```

1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCAGC
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGWTC AAGCAGGCAA TCGCGGCCGC ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAKGGC GTTCAATACG
251 GCGCGGCCGG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

m550.pep (partial)

```

1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VQYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

m550/g550

				10	20	30
m550.pep				DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN		
				:       : : : : : :		
g550	DGFFVHRVQHFRROQVCAGEAQEDVFAFNRI	IGKYAPAVVFNGVEFFGFVHAVFVFAGLVN				
	190	200	210	220	230	240
	40	50	60	70	80	90
m550.pep	HAFGVANGHVFAFQAQIQQLXQAGNRGR	TCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA				
	: : : : : : : : : : : : : : :					
g550	HAFGVANGYVFTFQAQIQQLVQAGNRGGT	CAGAHQSRFFDFTAGITQGVQYGGGGNDGRA				
	250	260	270	280	290	300
	100					
m550.pep	VLVVVEYGDFAAFAX					
	: : : : : :					
g550	VLVIMKYGDFAAFAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1 CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51 TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAG ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCGG GATTCCGGTT GGCCATAGCG AACACGATGG
501 GTTTTTCGTT CATGGTGTT AGTATTTCAG GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCCTTG ACGGCATCGG CAAGCACGGC
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGAATCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTTCG GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTGTCGTG GAATACGGGG ATTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1 LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51 FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFR
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVVFV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYSGSG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

```

                                10      20      30
m550.pep                      DGIGKHALAVVFNGVELFGLVHTVVFVAGL
                                |||||
a550      EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVVFVAGL
              170      180      190      200      210      220

              40      50      60      70      80      90
m550.pep    VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG
              |||||
a550      VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYSGGGNDG
              230      240      250      260      270      280

              100
m550.pep    RAVLVVVEYGDFAAFAX
              |||||
a550      RAVLVVVEYGDFAAFAX
              290      300
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1 atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51 caacgcattt gccgccccgc ccggcgacgc gtcgttgga cgttggtgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgccgtga aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtc gtccgtcgtt gccaaaaatc
401 cgcgcttaat caagaaatcg atgagtgaat tagcgggtatc ttggactgca
```

830

451 ttgtcagga aaatcgcgcg acatcatctg cccgagttta cggaagagtt  
 501 acggcgcatc atctcgggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF  
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT  
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKS MSEIAVSWTA  
 151 LSGKIARHHL PEFTEELRRI ICGGIVD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
 151 AATGCCGGAT TTAAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA  
 201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG  
 251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT  
 301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT  
 351 GATTGCCTTT TACGGTTCGC CTGTGCGTCA GTCCGTCGTT GCCAAAAATC  
 401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAG TAGCGGTATC TTGGACTGCA  
 451 TTGTGAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT  
 501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG  
 551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF  
 51 NAGFKPYADK ALAEMPEAKK DQAAEFNRY RENVLKDLIT PEVKQAVRNT  
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKS MSEIAVSWTA  
 151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEFNRYRENVKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEFNRYRENVKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEFNRYRENVKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEFNRYRENVKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
g552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
g552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC  
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG  
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT  
 151 AATGCCGGAT TTAAACCGTA TGCGGACAAA GCCCTTGCCG AAATGCCGGA

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTCGC CTGTCCGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAAG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552 . pep
1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWDLTQNFDR DIEKNMIEGF
51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGGKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552 . pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDLTQNFDRDIEKNMIEGFNAGFKPYADK					
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDLTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m552 . pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
a552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m552 . pep	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
a552	YGSPVGQSVVAKNPRLIKKS MSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPDAG					
	130	140	150	160	170	180
	190					
m552 . pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1 . seq
1 TTGAATATTA AACTGAAAC CTGTATTG CCCTTCGCCA CGCTGGCATT
51 GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTGT TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAT CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1 . pep
1 LNIKLKTL L PFATLALCTN AFAAPPSDAS LARWLDLTQNF DRDIEKNMIE
51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLKNAREIY TQEEIDGMI AFYSPVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1 . seq



```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCACTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCGG ACAGGTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEFN RYRENVLKDL ITPEVQAVR
101 NTLKKNAREI YTQEEIDGMI AFYGSFVGQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
m552-1	LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE GFNAGFKPYA					
	10	20	30	40	50	60
a552-1.pep	DKALAEMPEAKKDQAAEFN RYRENVLKDL ITPEVQAVRNTLLKNAREIYTQEEIDGMI					
m552-1	DKALAEMPEAKKDQAAEFN RYRENVLKDL ITPEVQAVRNTLLKNAREIYTQEEIDGMI					
	70	80	90	100	110	120
a552-1.pep	AFYGSFVGQSVVAKNPRLIK KSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
m552-1	AFYGSFVGQSVVAKNPRLIK KSMSEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKNPD					
	130	140	150	160	170	180
a552-1.pep	AGCKQAGQVGKRHQKX					
m552-1	AGCKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaacct gtctttgggc ttgacaaaa agctgcccg
51  tatactgcaa acagaagtag cggagtgtgg cttggcatgt ctageggctg
101 tggccggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatt gggctgacgg gacgggcgtt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtgggtgctg aatcggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcgggacga cgaaagtca agacggagga aatatcgcg aagtttacgg
401 gaattgcttt ggaactgtgg ccaaacacgc gtctcgaggc aggggaagaa
451 aagcaggaaa tccgcatcct acccatgttg cgcgggattt ctgggctggg
501 gcggaatttg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaactggac gatcgggctg cggtaaatcg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaat catgataaat gggcacgaca
701 tttacagctt accgccacct tttattccgc aatttgagtg cgatgggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaaccggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

m553.seq (partial)

1	ATGGATTATT	TATCAAGACT	GTCCTTTGGA	TTTAACAAAA	AGCTACCTGT
51	CATTCTGCAA	ACAGAAGTTG	CTGAATGTGG	TTTAGCATGC	CTGACATCCA
101	TCTTGTCTTA	TTATGGCTTT	CACACTGATT	TAAGAACGTT	ACGCCAAAAA
151	TACACCCTGT	CATTTAAAGGG	CGCAAATCTT	GCAGACATCA	TGAGATTTTGG
201	CAATGAAATG	AAATTTAACGC	CACGAGCTTT	CGCTTTTAGAG	TTAGATTGAGC
251	TGTCAAATTT	ACAACCTACC	TGCATTCTCC	ATTGGAACCT	AAACCATTTT
301	GTTGTACTTT	GTTCCATTTC	CAAAGACAGT	ATCGTCATTA	TGGACCCTGC
351	TGTCGGTATG	CGAAAAATCA	AAATGGACGA	AGTTTCACAA	AAATTCACAG
401	GGATTGCCCT	AGAATTATTC	CCCAATACCC	ATTTTGAAGA	GAAAAAAGAA
451	ACAAAGAAAA	TCAAAATATT	ATCTCTATTA	AGGGGGGG . T	CAGGCTTAAA
501	ACGCTCTTTA	ATTCAAATGC	TTATATTAGC	TATTTCTTTG	GAAGTCTTTG
551	CATTG...				

m553.ppe (partial)

```

1 MDYLSRLSFG FNNKLPVILQ TEVAECGLAC LTSILSYGYF HTDLRTLROK
51 YTLSLKGANL ADIMRFGNEM NLTPRALRLE LDELSNLQLP CILHWNLNHF
101 VVLCSISKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEKKKE
151 TTKIKILSL LRGXSGLKRS L IOMLILAISL EVFAL...

```

### Homology with a predicted ORF from *N. gonorrhoeae*

m553/g553

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1623>:

a553.seq

1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT  
51 TATCCTGCAA ACAGAAATAT CAGAAATGCGG CTTGGCATGT CTGGCGGCTG  
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA  
151 TAC

**m553/a553 62.7% identity in 51 aa overlap**

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

1	MTAHKILPVL	LPIILGVSHA	TAASPAPNRP	TVHAAPTLOT	PETLTAAHIV
51	IDLQSRQTLS	AKNTNTFPVEP	AALTLQLMTAY	LVFKNMKSGN	IQSEENLKIP
101	ESAWASEGSR	MFVRPGDTVS	TDKLLKGMI	LCANDAALTL	ADRLNGSIE
151	NFVQQMKEA	RRLGMKNTVF	KNPTGLGREG	QVSTAKDLSL	LSEALMRDFP
201	EYYPLFSIKS	FKFENIEQNN	RNILLYRDNN	VNGLKAGHTE	SGGYNLAVSY
251	SGNRHILVI	TLGSESAETR	ASDNSKLLNR	EQAFDTPKI	YPKGKTVAQI
301	QISGGSKTV	RAGFLKEAYI	LDPHKEAKMA	ALQILETIQPI	PAPVKKQOIL
351	GKIKIRONHG	TIAEKEIVAL	ENVEKRSRWQ	RLWTRLTGQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

1	ATGACAGCAC	ATAAAATCCT	GCCCGTCTCTG	CTTTCATCA	TCTTAGGCGT
51	TTCTCAGCA	ACGGCTGCAT	CGCCGCGCC	CAACAGACCG	ACGGTACACG
101	CCGCCCCAC	GTTCCAAACA	CCCGAAACCC	TCACAGCGGC	ACACATCGTT
151	ATCGACCTTC	AAAGCAAAAC	GATTTTATCC	GCCAAAAAAC	TCAATACCCC
201	TGTTGAACCG	CGCGCATAA	CCCAACTGAT	GACCGCATAT	CTGTGTTTCA
251	AAAACATGAA	ATCGGGCAAT	ATCCAACTGT	AAGAAAACCT	AAAAATACCC

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301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCTG CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCTATC
751 TCCGGCAACG GCAGGCACAT CTTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACCTG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGCGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IQSEENLKIP
101 ESAWASEGSR MFVRPGDTSV TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFWQMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDN VNLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRONGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

m554.pep	10	20	30	40	50	60
	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSKQILS					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIVIDLQSRQTL					
	10	20	30	40	50	60
m554.pep	70	80	90	100	110	120
	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTSV					
g554	AKNINTPVEPAALTQLMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDTSV					
	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
	TDKLLKGMIALSANDAALTLAGRLNGSIEFVQMNKEARRLGMKNTVFKNPTGLSREG					
g554	TDKLLKGMIALCANDAALTADRLNGSIEFVQMNKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
	SGGYNLAVSYSGNRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLAQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300

           310      320      330      340      350      360
m554 .pep  QISGGSKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKQILGKIKIRONGY
           |||||
g554      QISGGSKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKQILGKIKIRONGH
           310      320      330      340      350      360

           370      380      390
m554 .pep  TIAEKEIVALENVKRSRWQRLWACLGTGX
           |||||
g554      TIAEKEIVALENVKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554.seq
1  ATGACAGCAC ATAAATCCT GCCCGTCCTG CTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
201 TGTCGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTCA
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAACTT AAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTGTAC GTCCCGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTT GCCGGCCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCAG CTGTCTGAAG CATTGATGCG CGACTTCCG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCCG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCAATC
751 TCCGGCAACG GCAGGCACAT CCTGTGCATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAAGTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCTACATC ACTCTGCCAC ATAAGGAAGC GAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAATGTAA AAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554.pep
1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAAHIV
51  IDLQSKQILS AKNINTPVEP AALTQMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGDVS TDKLLKGMIA LSANDAALTL AGRLNGNSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFNIEQNN RNILLYRDNV VNLKAGHTE SGGYNLAVSY
251 SGNRHLVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKQIL
351 GKIKIRONGY TIAEKEIVAL ENVKRSRWQ RLWACLGTQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554.pep  MTAHKILPVL LSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           |||||
a554      MTAHKILPVL LSIILGVSHATAASPAPNRPVHAAPTFTQ PETLTAAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554.pep  AKNINTPVEPAALTQMTAYLVFKNMKSNGIQSEENLKIPESAWASEGSRMFVRPGDVS
           |||||
a554      AKNINTPVEPAALTQMTAYLVFKNMKSNGIRSEENLKIPESAWASEGSRMFVRPGDVS

```

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	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
a554	TDKLLKGMIALSANDAALTLAGRLNGSGIENFVQOMNKEARRLGKNTVFKNPTGLSREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
a554	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
a554	SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	250	260	270	280	290	300
m554.pep	310	320	330	340	350	360
a554	QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQIPAPVKKGQILGKIKIRONGY					
	310	320	330	340	350	360
m554.pep	370	380	390			
a554	TIAEKEIVALENVKKRSRWQRLWACL TGQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattccc tggccgcttg
101 ccatcctgct tgccgcccgc atcgctgcgc cgcgtgcggg cggctttgtt
151 tggacatccc gccgacagca acgccagttt atcgaacgtc tgaaaaaatt
201 cgacatcgat ccgaaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcggacaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cacgctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaattgc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKRPRTR QEINQMAAKQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC TCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATT TCGTATTGAT TGTGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTAACACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCGCAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

838

101 LSQKCSVDEA HAMFKRPTR QEINQMAAQ SRGQKRPHR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT <del>KLRLG</del> LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
g556	MDNKT <del>KLRLG</del> LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
g556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAQSRGQKRPHRX					
g556	QEINQMAAQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATGGACAATA	AGACCAA	ACT	GCGCTTGGGC	GGCCTGATTT	TACTGACCAC
51	CGCCGTTT	AGCCTCATTA	TCGTATTGAT	TGTCGATTCC	TGGCCGCTTG	
101	CCATCCTGCT	TGCCGCCGTC	ATCGTCGCCG	CCGCTGCGGG	CGGCTTTGTT	
151	TGGACATCCC	GCCGACAGCA	ACGCCAGTTT	ATCGAACGTC	TGAAAAAATT	
201	CGACATCGAT	CCCGAAAAAG	GCAGAATCAA	CGAGGCAAAC	CTGCGCCGTA	
251	TGTACCACAG	CGGCGGACAA	CACCAAAAAG	ATGCGATTAC	CCTGATCTGC	
301	CTGTCGCAA	AATGTTCTGGT	GGACGAGGCG	CACGCTATGT	TCAAAAAACG	
351	CCCGACACGT	CAGGAAATCA	ATCAAATGGC	GGCAAAACAG	TCGCGCGGTC	
401	AGAAACGTCC	GCACCGTTAA				

This corresponds to the amino acid sequence &lt;SEQ ID 1636; ORF 556.a&gt;:

a556.pep

1	MDNKT <del>KLRLG</del>	GLILLTTAVL	SLIIVLIVDS	WPLAILLAAV	IVAAAAGGFV
51	WTSRRQQRQF	IERLKKFDID	PEKGRINEAN	LRRMYHSGGQ	HQKDAITLIC
101	LSQKCSVDEA	HAMFKRPTR	QEINQMAAQ	SRGQKRPHR*	

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT <del>KLRLG</del> LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
a556	MDNKT <del>KLRLG</del> LILLTTAVLSLIIVLIVDSWPLAILLAAVIVAAAAGGFVWTSRRQQRQF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
a556	IERLKKFDIDPEKGRINEANLRRMYHSGGQHOKDAITLICLSQKCSVDEAHAMFKRPTR					
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQMAAQSRGQKRPHRX					
a556	QEINQMAAQSRGQKRPHRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq. .

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pap. -

**Computer analysis of this amino acid sequence gave the following results:**

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1641>:



840

a557.seq  
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG  
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA  
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG  
 151 CTGTATCAGG CTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC  
 201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC  
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG  
 301 GTATTGAAAC GCGGCGAGCC GGTCGCAGAA CCGATGACCG GTGCCGTCCG  
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG  
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC  
 451 CGCCGCCTGA CCTTCTGAA GGCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep  
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA  
 51 LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRA AVINE YLLILTVEAQ  
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAAEQIV  
 151 RRLTFLKAE\*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA AV LMLGACGFHLKGADGISPPLTYRSWHIEGGQALRFFLETALYQASGRVDD					
a557						
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLRIDSVSQNKETYTVTRA AVINEYLLILTVEAQVLKRGE PVGKPMTVSVRRVL					
a557						
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAE MRQDAAEQIVRRLTFLKAEX					
a557						
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq..  
 1 ATGGATGCTT GTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA  
 101 TGCCCTTATA TACTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG  
 201 ATTCTATCGC TATAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep..  
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPLYTFS ELYMLQQGTA  
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSENQSP  
 101 LSDGIV\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq..  
 1 ATGAATGCTT GTTTTTCGT CATTCCCA CA CAGGCGGGAA TTCGGAGATT  
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA  
 101 TGCCCTTATA TACTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA  
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG  
 201 ATTCTATCGC CATAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA  
 251 AGTCCATTTC CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA  
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/g558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYTFSELYMQOGTAHQAPHCVLPE   :   :					
g558	MDACFFVIPAQAQAGIRRFGIVFKRSGRILAGAGMMPLYTFSELYMLQOGTAHQAPHCVLPE					
	10	20	30	40	50	60
m558.pep	RDYPPPIFYRHKQTGFNRKGMIKSISDIXRAMPSENQSPLSDGIVX 					
g558	RGCFFPIFYRYKQTGFNRKGMIKSISDTSRAMPSENQSPLSDGIVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1647>:

```
a558.seq
1  ATGAATGCTT  GTTTTTTCGT  CATTCCCACA  CAGGCGGGAA  TTCGGAGATT
51  CGGGATTGTT  TTCAAACGTT  CGGGTCGGAT  TCTTGCCGGT  GCGGGAATGA
101 TGCCCTTATA  TATAGTGGAT  TAAATTTAA  TCAGGACAAG  GCGCAGGAAC
151 CGCAGACAGT  ACAAATAGTA  CGGCAAGCG  AGGCAACGCC  GTACTGTGTT
201 AAATTTAATC  CACTATACTT  TCTCCGAGCT  TTATATGTTT  CAACAGAGGA
251 CGGCACATCA  AGCACCGCAC  TCGGTGTTGC  CCGAACGAGA  CTGCCCTCCG
301 ATTAGATTCT  ATCGCTATAA  ACAGACGGGT  TTCACCCGAA  AAGGAATGGG
351 AATGAAGTCC  GTTTCGCACA  CCTCTCGGG  GATGCCGTCT  GAAACCAAT
401 CTCCACTTTC  AGACGGCATT  GTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

a558.pap

1	MNACFFVIPT	QAGIRRFQIV	FKRSGRILAG	AGMMPYIVD	*I*IRTRRS
51	RRQYK*YGKA	RQRRTGLNLI	HYTFSELYMF	QORTAHQAPH	CVLPERDCPP
101	IRFYRYKOTG	FNRKGMGMKS	VSDTSRAMP	ENOSPLSDGI	V*

**m558/a558 70.2% identity in 141 aa overlap**

```

      10      20      30
m558.pep  MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLY-----
          |||
a558      MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRQYKXYGKA
          10      20      30      40      50      60

      40      50      60      70      80
m558.pep  -----TFSELYMFOOGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGMGIKS
          |||
a558      RQRRTGLNLIHYTFSELYMFOORTAQAPHCVLPERDCPPIRFYRYKQTGFNRKGMGMKS
          70      80      90      100     110     120

      90      100
m558.pep  ISDIXRAMPSENQSPLSDGIVX
          :||
a558      VSDTSRAMPSENQSPLSDGIVX
          130     140

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEO ID 1649>:

g560.seq  
1 atgctcatca tccgcaacct gatttactgg ctgatactct qttccaqccct

```

51  gattttcttc tttcccttta tgctgctcgc ctgccttttc cgggacgggg
101 cgcacaagat ggcgcggttc tgggtcggca tcctcaactg gtcgctcaaa
151 cacatcgctg ggctcaaata ccgcatcatc ggcgcggaac acattccgga
201 ccgcccctcc gtcattctcg ccaaaccacca aagcggtctg gaaacgctcg
251 cgctccaaga gatttttccg ccgcaggttt acgttgccaa gcgcgagttg
301 tcaaaaatcc cctttttcgg ctggggcttg aaactggtca aaaccatagg
351 catagaccgc aacaaccgcc gcgaagccaa cgaacagctc ataaaacagg
401 gtttggcgcg caaaaacgaa gggtattgga ttaccatttt ccccgaggc
451 acgcgccttg cgcccggaac acgcggcaaa taaaactcgc gcggcgcgcg
501 catggcgaaa atgtttgaga tggacatcgt ccccgctgcc ctcaacagcg
551 gcgaattttg gccgaaaaat tcctttctga aatatccggg ggaaatcacc
601 gtcacatctt gtccgacatc ccgcacgca agcggcagcg aagccgaatt
651 gatggaaaaa tgcgaacacc tcattgaaac gcaacaaccg cttatttccg
701 gcgcaggccc gtttgccgcc gaaatgccgt ctgaaaccgc atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTACTGCG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGCGCGGGTC TGGGTGCGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTCCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATACC CCTTTTCCG CTGGGGCTTG AAAGTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAACAGG
401 GGTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCCAGAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCCCCTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTATCTT GTCCGACCAT CCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTTCCG
701 GCGCAGGCCC GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKRK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

              10      20      30      40      50      60
m560.pep      MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560           MLIIRNLIYWLILCSSLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
              10      20      30      40      50      60

              70      80      90      100     110     120
m560.pep      GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
              |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560           GAENIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR

```

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

a560.seq	1	ATGCTCATCA	TCCGCAACCT	GATTTACTGG	CTGATACTCT	GTTCCACCCT
	51	GATTTTCCTC	TTTCCCTTTA	TGCTGCTCGC	CTCGCCTTTC	CGAGACGGGG
	101	CGCACAAAGAT	GGCGCGGGTC	TGGGTCAAAA	TCCTCAACCT	CTCGTCAAA
	151	CACATCGTCG	GGCTCAAATA	CCGCATCATC	GGCGCGGAAA	ACATCCCCGA
	201	CGCCCCCGCC	GTCATCTGCG	CCAAACACCA	AAGCGGCTGG	GAAACGCTCG
	251	CCCTTCAGGA	CATTTTTCGG	CCGCAGGTTT	ACGTTGCCAA	ACGCGAGTTG
	301	TTCAAATCC	CCTTTTTCGG	CTGGGGCTTG	AAACTGGTCA	AAACCATAGG
	351	CATAGACCGC	AACAACCGCC	GCGAAGCCAA	CGAGCAGCTC	ATAAAACAGG
	401	GGTTGGCGCG	CAAAAACGAA	GGCTATTGGA	TTACCATTTT	CCCCGAAGGC
	451	ACACGCCTTG	CGCCCCGAAA	ACGCGGCAAA	TACAACTCG	GCGGCGCGCG
	501	CATGGCGAAA	ATGTTTGAGA	TGGACATCGT	CCCCGTCGCC	CTCAACAGCG
	551	GCGAATTTTG	GCCGAAAAAC	TCCTTTCTGA	AATATCCGGG	GGAAATCACC
	601	GTCGTCATCT	GTCCGACCAT	CCCGCACGCA	AGCGGCAGCG	AAGCCGAATT
	651	GATGGGAAAA	TGCGAACACC	TCATCGAAAC	GCAGCAGCCG	CTCATTTCCG
	701	GCGCAGGCC	GTTTGCCGCC	AAAATGCCGT	CTGAAACCGC	ATGA

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

a560.pep	1	MLIIRNLIYW	LILCSTLIFL	FPFMLLASPF	RDGAHKMARV	WVKILNLSLK
	51	HIVGLKYRII	GAENIPDRPA	VICAKHQSGW	ETLALQDIFP	PQVYVAKREL
	101	FKIPFFGWGL	KLVKITIGIDR	NNRREANEQL	IKQGLARKNE	GYWITIFPEG
	151	TRLAPGKRK	YKLGARMAM	MFEMDIVPVA	LNSGEFWPKN	SFLKYPGEIT
	201	VVICPTIPHA	SGSEAELEMGK	CEHLIETQQP	LISGAGPFAA	KMPSETA*

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
a560	MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK HIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

844

	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMGKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

m561.seq.

```

1  ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GCGGCATTG TCTGTCGTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGC GC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCCT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAATATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTGCTC TGTACTGATG CTGTTTTGGC
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTTCAA TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGGAGTACC ATGAGGAAAT CTTCCTCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCAAACGG CATTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCTTTTGC
1251 CGAAACAAA CGGGAGGAAG CCGCAGAAA CATCAGCTTT ATCAAAACAG
1301 GCGTGCAGGA ATGTTATGAA GATGTCCGCG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GCAATAAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTCGC
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAAACG
1451 GTTCGTTTCT GCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAAGCC TGTCCAACAT CCGCAAACAC GCGGCGGCCA CCCATGTAAA
1551 ATTCACCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGAAGTC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

m561.pep

```

1  MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFELSLKRIA QSDAIHFLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRFFQWAIM LMTLVSSVLM LFVHQIWWIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYQTTDLHQ SYIPQAAEH FLNRILPAVG ADGRVCLDG
301 GSDVYVSIH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQ LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFAENK REEAENISF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFARFT QQTGTVETA WENGSELPPO EAQLQMIFIL

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501 QESLSNIRKH ARATHVKFTL SEHGGRFTMT IQDNGQGFD T EKIGEPTGSH  
 551 VGLHIMQERA KRIHAVLEIR SQAQGGTTVS LTVASEESLK \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSRLLENAASVIEEAGNLRMQAY					
	:      :     :     :     :     :     :     :					
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALS SVVLTLLLSRLENAASVIEEAGNLRMQAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
	:     :     :     :     :     :     :     :					
g561	RLAYMAGEGSPRAQIDNQIAEFEKSLKRISQSDAIHPLIPSDNPLAYDLIQSMLIIDWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVIM					
	:     :     :     :     :     :     :     :     :					
g561	NILPPLQAYRRPTQIELYRFAGNIELFLQALENAGEKNTWWLRRFQWVIMLMTLVSSVIM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKLKILYDDL					
	:     :     :     :     :     :     :					
g561	LFWHQIWVIRPLQALREGAERIGRRHFDIPVPEDVRENSNRSGGVSTKWRSGX					
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNQNLTLTYQTTTRDLHQSYIPQQA AEHFLNRILPAVGADSGRVC L DG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

```

1  ATGATACTGC CAGCCCCTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAA TGCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCGTGGCG AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCTT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCTCC CCCCGCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAAATG CCAACGAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCGTC TGTA CTGATG CTGTTTGGG
551 ACCAGATTG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTGTTTCAA TCAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACAAA CTACACGGGA
801 TCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTT CATTCATCAT GCGGATTGCG GCACAGCAGC
951 TTCGGATTG GGAAGTACC ATGAGGAAAT CTTCCCATC GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCAAACGG CATTTCTCTT
1051 GATGAAGACG ACCGCATCCT GCTTCAACA CTAGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GCGCAAAAAC AGGAGGAAGA AAAACGCCTG CTGTCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAA CCGCCTTTGC
1251 CGAAAACAAA CGGGAGGAAG CCGCAGAAAA CATCGGCTTC ATCAAAACAG
1301 CCGTGCAGGA ATGTTATGAA GATGTCGCG AACTGCTGCT CAACTTCCGT
1351 ACCAAAATCA GTAATAAAGA ATTTCCCGAA GCCGTGCGG ACCTATTCTC

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAG TGA

```

This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFWHQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRLKILYDDL EGQVAEQTRS
251 LEKQONLTL LYQTTRDLHQ SYIPQAAEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRLLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLIAQGLHDSIAQ
401 ALTFLNLQVQ MLETAFENK REEAAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKFRL LKQDGSFTMT IQDNGQFDT ENIGEPGSGH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTSV LTVASEESLK *

```

m561/a561 96.9% identity in 590 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY					
a561	MILPARFSDGISLSRLKLLTGLWVGLAALS SVVLTLLLSL RLENAASVIEEAGNLRMQAY					
	10	20	30	40	50	60
m561.pep	70	80	90	100	110	120
a561	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
a561	RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
	70	80	90	100	110	120
m561.pep	130	140	150	160	170	180
a561	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
a561	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM					
	130	140	150	160	170	180
m561.pep	190	200	210	220	230	240
a561	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
a561	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
	190	200	210	220	230	240
m561.pep	250	260	270	280	290	300
a561	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQONLTLTYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG					
a561	EGQVAEQTRSLEKQONLTLTYQTTRDLHQSYIPQAAEHFLNRILPAVGADSGRVCLDG					
	250	260	270	280	290	300
m561.pep	310	320	330	340	350	360
a561	310	320	330	340	350	360
m561.pep	GSDVYVSIHHADCCTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT					
a561	GSDVYVSIHHADCCTAASDLGKYHEEIFPIEYQNETLGRLLLSFPNGISLDEDDRILLQT					
	310	320	330	340	350	360
m561.pep	370	380	390	400	410	420
a561	370	380	390	400	410	420
m561.pep	LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK					
a561	LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK					

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	370	380	390	400	410	420
	430	440	450	460	470	480
m561. pep	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561. pep	WENGSLFPPEAQLQMIFILQESLSNIRK HARATHV KFTLSEHGGRFTMTIQDNGQGFD T					
a561	WENGTHLPTQDEQLQMIFILQESLSNIRK HAATHIKFRLLKQDGSFTMTIQDNGQGFD T					
	490	500	510	520	530	540
	550	560	570	580	590	
m561. pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKX					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQGGTTVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562. seq..

```

1  atggcaagcc cgtcgagtct gcctttcaat tcgggcaaga ccaaaccgac
51  ggcttttgcc gcgccggttt tggtcggaat catgttttcc acgccgctgc
101 gggcgcgccg caggtctttg tggcgcacgt cggtaacggt ttggtcgttg
151 gtcagtgcgt ggatggtggt cattgcgcct ttgacgatgc cgacgctttc
201 gctcaacact ttggcaaccg gcgagaggca gttggtggtg caggaagcgt
251 tggaacgac ggtcatgtcg gcggtcagga cgctgtcgtt caccgcgtac
301 acgacggtt catcgacatc gtcgccgcc gccgcgaaa tgaggacttt
351 tttcgcgccg ctttcgaggt ggattttggc tttttctttg ctggtgaacg
401 cgccggtgca ttccatgacc aaatcgacac cgagttcttt ccacggcagt
451 tcggcagggg tgccgggtcga gaagaagggg attttgtcgc cgttgacgat
501 gaggttgccg ccgtcgtggg atacgtcggc ttcaaagcgt ccgtgtacgg
551 tgtcgaattt ggtcagatgg gcgttggttt caaggctgcc gctggcggtg
601 acggcgacga tttggagttg gtcttga

```

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562. pep

```

1  MASPSSLPFN SGKTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEALTTVMS AVRTLSTFPY
101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLAL
201 TATIWSWS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562. seq

```

1  ATGGCAAGCC CGTCGAGCCT GCCTTTCAAT TCGGGCAGTA CCAAACCGAC
51  GGCTTTTGCC GCGCCGTTT TGGTCGGAAT CATGTTTTC ACGCCGCTGC
101 GGGCGCGCCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGTTGTT CATCGCGCCT TTGACGATGC CGACGTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAACGAC GGTGATGTCG GCGGTGAGGA CGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCGCGCCG CTTTCGAGGT GGATTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TGCCGGTCTGA GAAGAAGGGG ATTTGTGCGC CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTGCGC TTCAAAGCGT CCGTGCACGG
551 TGTGCAATTG GGTGAGATGG GCCTTGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA GTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562. pep

```

1  MASPSSLPFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51  VSAWMVVIAP LTMP TSLNLT LATGERQLVV QEALTTVMS AVRTLSTFPY

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848

1 01 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSMT KSTPSSFHGS  
 1 51 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL  
 2 01 TATSWSWS\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
g562	MASPSSLPFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m562.pep	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
g562	LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562.pep	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
g562	LSRWILAFSLLVNAPVHSMTKSTPSSFHGSAGLRVEKKGILSPLTMLRPPSWDTASAKR					
	130	140	150	160	170	180
	190	200	209			
m562.pep	PCTVSNLVRWALVSRLPLALTATSWSWSX					
g562	PCTVSNLVRWALVSRLPLALTATSWSWSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

a562.seq  
 1 ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC  
 51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC  
 101 GGGCGCGCG CAGGTCTTTG TGGCGCACGT CGGTAACGGT TTGGTCGTG  
 151 GTCAGCGCGT GGATGGTGGT CATCGGCCT TTAGCATGC CGACGCTTC  
 201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT  
 251 TGGAAACGAC GGTGATGTCG GCGGTCAGGA TGCTGTCGT CACGCCGTAC  
 301 ACGACGGTTG CATCGACATC GTCGCGGCC GGTGCGGAAA TGAGGACTTT  
 351 TTTCGCGCCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG  
 401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTCTTT CCACGGCAGT  
 451 TCGGCAGGGT TCGCGGTGCA GAAGAANGG ATTTTGTGCG CGTTGACGAT  
 501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACCG  
 551 TGTCGAATTT GGTGAGGTGG GCGTTGTTT CAAGGCTGCC GCTGGCGTTG  
 601 ACGGCGACGA TTTGGAGTTG GTCTTGA

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

a562.pep  
 1 MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL  
 51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFTPY  
 101 TTVASTSSPP GAEMRTFFAP LSR\*TLAFSL LVNAPVHSMT KSTPSSFHGS  
 151 SAGLRVXXKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRLPLAL  
 201 TATIWSWS\*

m562/a562 96.6% identity in 208 aa overlap

	10	20	30	40	50	60
m562.pep	MASPSSLPFNSGSKPTAFAPVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
a562	MASPSSLSFN SGSTKPTAFA APVLVGIMFSTPLRARRRSLWRTSVTVWSLVSAWMVVIAP					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m562. Pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562. Pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
	190	200	209			
m562. Pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562.	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563.seq

```

1  ATGAACAAAA CCCTCTATCG TGTGATTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTCTTTTAT GTTTGGCTTT
201 GGGTACCGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCGATTT GATGTGGGTA ATcgcGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTTGGA TTCAAGGCAA TCCTTGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTGTAAC CAAATCAACA GCAGCCATCC
501 TTCACAACTG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAAGATAA GGCAAGGCAA TGCTGTAATC GCCGACACG
701 GTTTGGATGC CCGTGATACC GATTTCACAC GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCACGATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACCTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCG CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACCTTGC AAGCAGGAAA ACGCATTTCG
1351 ATTAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGACA ACAAAACAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TTAAATAACC GTGAAAACAG TCTGATTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAACGT CGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GCGCGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA  
2151 AACCTTTTGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAAC  
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA  
2251 AATTATACTT TGCCGAGGA AATCACACGC GACATTTTAC TGGGTTTATT  
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG  
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGGAAAAGC  
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG  
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA  
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG TGACTATATG  
2551 CTGGGCAGCC TCAAACTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA  
2601 TGGTATTATC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG  
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC  
2701 TTAATGGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG  
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT  
2801 GGTGGGTACA AAAAGAAGTT AAACCTCCTG ATGGCGGCAC ACAAACCGTA  
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA  
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC  
2951 TGAAAAAATC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC  
3001 GATACGCTAG ACAATATCGG TGGGCGTATT CATGCGCAAA AATCAGCGGT  
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC  
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC  
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC  
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG  
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 1951 AHAVLGAAVA AAXGNAPAG ALGAGGSEAA APIIGKWLK KDGGSLSNAE  
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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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 651 QOSTAVIDNT NGTIQSGRDV AIQAKSLSN GTLAADNKLD IALQDDFYVE  
 701 RNIVAGNELS LSTRGSLKNS HTLQAGKRIR IKANNLDNAA QGNIQSGGTT  
 751 DIGTQHNLTN RGLIDGQOTK IQAGQMNNIG TGRIYGDNIA IAATRLDNQD  
 801 ENGTGAAIAA RENLNLGIGQ LNNRENSLIY SGNDMAVGGA LDTNGQATGK  
 851 AQRIHNAGAT IEAAGKMLG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG  
 901 RHELLREGTO HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV  
 951 TOTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG  
 1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSPAYE  
 1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSL YIINPVNKGY  
 1101 LVETDPRFAN YRQLGSDYM LDSLKLDPN LHKRLGDGY EQRLINEQIA  
 1151 ELTGHRRLDG YQNDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAQLTS  
 1201 DIVLVQKEV KLPDGGTQTV LVPQVYVRVK NGDIDKGAL LSGSNTQINV  
 1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQSAVTAT QDINNIGGML  
 1301 SAEQTLILLNA GNNINSQSTT ASSQNTQGS TYLDRMAGIY ITGKEKGVLA  
 1351 AQAGKDINII AQQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN  
 1401 HVIRAGSTNEV GSSIQTGKDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI  
 1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV  
 1501 VLQAGNDANI LGSNVISDNG TQIQAGNHVR IGTTQTQSQS EYHQTQKSG



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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGS LKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLSNT TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVSISITY GEQONRQTTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSN
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKSG WNAAGAVSFG
1801 QGGWSLGVTA GGNVGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKGK
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKLKADKE AAETAAREAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGKV ILNMLASGLA APTQSGAGIA AATASPAVS Y AIGQHFKDLA
2201 GQNANGKLTA SQETAHVLAH AVLGA AVAAV GDNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTATNVL GTATGA AVGN SATDAAQSSL
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHKDPGSTLE PNISTIASTF
2351 QLNLFNPSEF GEGGVGNF RHLVWQATIT REFGKDI AVK VGNSHESGEK
2401 INYSIRRLS LDKADEMIDQ LNNEIGREIA LNTNRLNTKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563.pep      MNKTLYRVIFNRKRGAVVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563.pep      MNKTLYRVIFNRKRGAVVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563.pep      FSALGFS LCLALGTVNIAFADGIIITDKAAPKTQQTILQTGNGIPQVNIQTPTSAGVSVN
              |||||
m563.pep      FSLLGFS LCLAVGTANIAFADGIIADKAAPKTQQTILQTGNGIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563.pep      QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVVIAGHGL
              |||||
m563.pep      VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVVIAGHGL
              190     200     210     220     230     240

              240
g563.pep      DARDTDFTRIL-----
              |||||
m563.pep      DARDTDFTRILSYHSKIDAPVWGQDVRVVAGQNDVVATGNAHSPI LNNA AANTSNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563.pep      -----LYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGMT
              :|||
m563.pep      GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQQLFASSGNVAIDANGRLVNSGMT
              310     320     330     340     350     360

```



856

	300	310	320	330	340
g563.pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
	:  :          :				
m563.pep	AAANAKDTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG				
	370	380	390	400	410 420
-----					
g563.pep					
m563.pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTGSQKLHIDAQGKMDNRGRMGLQDTAPTAS				
	430	440	450	460	470 480
-----					
g563.pep					
m563.pep	NGSSNQTGNSYNASPHSSTTTPTTATGTGTATVSISNITAPTADGTIRTHGALDNSGSI				
	490	500	510	520	530 540
-----					
g563.pep					
m563.pep	IANGQTDVSAQQGLNNAQQIDIHQLNAGKSAFDNHNGTIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590 600
-----					
g563.pep	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
m563.pep	RQOLEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650 660
-----					
g563.pep	390	400	410	420	430 440
	NGTIQSGRDVAIQAKSLSNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS				
m563.pep	NGTIQSGRDVAIQAKSLSNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS				
	670	680	690	700	710 720
-----					
g563.pep	450	460	470	480	490 500
	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG				
m563.pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQIQAGQMNNIG				
	730	740	750	760	770 780
-----					
g563.pep	510	520	530	540	550 560
	TGRIYGDNIAIAATRLDNQDENGTTGAIAAARENLNLGIEQLNNRENSLIYSGNDMAVGGA				
m563.pep	TGRIYGDNIAIAATRLDNQDENGTTGAIAAARENLNLGIGQLNNRENSLIYSGNDMAVGGA				
	790	800	810	820	830 840
-----					
g563.pep	570	580	590	600	610 620
	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG				
m563.pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG				
	850	860	870	880	890 900
-----					
g563.pep	630	640	650	660	670 680
	RHELLREGTQHELGWVYNNESDHLRTPDGAHENWHKYDYEKVTQETQVTGTAPAKIIA				
m563.pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAHENWHKYDYEKVTQKTQVTGTAPAKIIS				
	910	920	930	940	950 960
-----					
	690	700	710	720	730 740





859

	1950	1960	1970	1980	1990	2000
g563 . pep	TASQETAHVLAHAVLGA AVAAAXGNNAPAGALGAGGSEAAAPIIGKWLYGKGDGGS LNAE					
m563 . pep	TASQETAHVLAHAVLGA AVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGS DLTAE					
	2210	2220	2230	2240	2250	2260
	2010	2020	2030	2040	2049	
g563 . pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFQTASDFASSFSYPINMX					
m563 . pep	EKETVTAITNVLG TATGA AVGNSATDAAQGS LNQAQSAVENNDTVEQVKFALRHPRIAIAI					
	2270	2280	2290	2300	2310	2320
m563 . pep	GSVHKDPGSTLEPNISTIASTFQLNLFNPFSEFGGEGGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

```

m564 . seq
1  ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAATATGATA TTGCGGGCTT TCGCGGTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTC
201 TGCCCTTATC CTGACTTCTT CTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTG GTTG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAAC TGAAGTGGGC GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTATCG
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACAG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCCT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAATGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCACTTCAT GCCCGCAATG TTCATAATAG CCGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAAATCCG TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAAATGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACAG ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATAA CCGTGAACGT
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTGCGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGGA
1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACCACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTTAACATC CAAAGTCAGC AACTGACTAA CCAAGCGGCG
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAAACGGC AAACCTCTAT CTGCAAACCA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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2251 ATTCACGATA AAAATCAAAA CACTTTGGCG TTAAACAATG CGGATGGCAC  
2301 GATTCAATCT GCCGGTAATG TATCGCTACA AGCCAAATCA CTCGCCAACA  
2351 ATGGCACATT AACAGCCGGT AACAACTGG ATATTGCTTT GACGGACGAT  
2401 TTCGTGCTAG AGCGCGACCT CACTGCAGGC AAACAATTAA ATCTAAGCAT  
2451 AAAAGGCCGT CTGAAAAATA CCCATACCCT ACAAGCAGGC CATACGCTCA  
2501 AACTCAATGC CGGCAATATA GATAACCAAG TTACAGGCAA AATTATTGGT  
2551 GGAGAACAAA CGGACATCAC ATCCGAACAG CATGTTGACA ACAGGGGCTT  
2601 GATCAACAGC GACGGTTTGA CCCACATCGG TGCAGGTCAA ACCCTGACCA  
2651 ACACCGGGAC AGGCAAAATC TATGGCAACC ATATTGCCCT GGACGCGCAA  
2701 ATACTGCTTA ACCGGGAAGA AACGACGGAA GGCAGTACCA AAGCGGGGCG  
2751 AATAGCTGCA AGGAAACGTT TGGATATTGG AGCGAAAGAG ATTCATAACC  
2801 AAGAAGGTGC CCTACTATCC AGCGAAGGTA TTTTGGCCGT AgGTAATCGA  
2851 CTGGATGAAC AACATCATGC GGCAGGCATG GCCGATACCT TTGTTAATGG  
2901 CAGTGCCGGT TTGGAAGTAC AAGGTGATGC ATTGATGTCC GTTCGGAATA  
2951 TGCAGAATAT CAATAATCAC TTTAAAACAG AGACATACTT AGCCAAAGCG  
3001 GAAAAGCAAG TCCGCGACTA CACCGTACTG GGGCAAAATA CCTACTATCA  
3051 GCGGGGAAAA GACGGTTTAT TCGACAACCT GCAAGGACAA AAAGACCAAA  
3101 CTAATGCTAC GTTCCATTTA AAAATGGTT CTCGTATTGA GGCCAACCAA  
3151 TGGCATGTCC GAGACTACCA CATCGAGACT TATAAAGAAC GCATCATCGA  
3201 AAACCGGCCG GCACACATTA CTGTGGGCGG TGATTGACT GCCTCAGGTC  
3251 AAAATTGGCT GAACAAAGAC AGCCGGATTG TAGTAGGCGG GCGTATTATC  
3301 ACTGATGATT TAAACCAGAA AGAAATTACC AATCAAAGTA CAACAGGCAA  
3351 AGGTGCGACA GATGCTGTGC GCACACAGTG GGATTCAAGT ACAAAAAAAG  
3401 GATGGTACAG CGGTAGAAAA AGACAACGCC GACTGAAAG AAACCATACT  
3451 CCTTACCATG ATACCCAAT ATTTACCCAC GACTTCGACA CGCTGTATC  
3501 GCTCATCCAA CAGAATGCCG CCTCCCCTTC CTTTCAACCC GCCGCATCTG  
3551 CAATCAAATC GATTGACGGA GTATCCACGG CAGCCGTCOA TGGTCAGCGC  
3601 ATCCATACCG GTAATGTGGT CTCGTAAAT AACGCTACTG TTACTCTGCC  
3651 TAACAGCAGC CTCTATACCA CCCATCCTGA CAATAAAGGC TGGTTGGTTG  
3701 AAACCGATCC TCAATTTGCA GACTACCGCC GCTGGTTGGG CAGCGACTAC  
3751 ATGTTGCAAC AACTGCAATT GGACACCAAT CATCTACACA AACGGCTTGG  
3801 CGACGGCTAC TACGAACAAA AACTTGTTAA TGAACAAATC CATCAGTTAA  
3851 CAGGCTACCG CCGACTCGAC GGCTACAGGA GTGATGAAGA ACAATTCAAA  
3901 GCTCTGATGG ACAACGGCCT TACTGCTGCC AAAACATTGG GTCTCACCCC  
3951 AGGTATCGCC TTGAGTGCAG AGCAAGTTGC CCGCTTAATC TCAGATATCG  
4001 TTTGGATGGA AAATCAAACC GTCACCCTGT CTGACGGTTC GACTCAAACC  
4051 GTAATGGTTC CTAAAGTCTA TGCCCTGGCG CGCAAAGGTG ATCTCAATAC  
4101 CTCCGGTGGC CTGATTAGTG CCGAACAAGT CTTACTTAAA CTGCAAAACG  
4151 GCAACCTGAC TAACAGCGGT ACCATTGCGG GCGCAGAGGC CGTACTCATC  
4201 CAGGCACGGA ATATTAACAG CAACGGTAAC ATTCAAGCCG ACCAAATCGG  
4251 CTTAAAAGCT GAAAAAAGTA TCAATATCGA CGGCGGGCAG GTACAAGCAG  
4301 GCAGACTGCT GACTGCCCAA GCGCAAAATA TCAACCTTAA CGGTACAACC  
4351 CAAACTTCCG GTAATGAACG TAACGGCAAT ACCGCCATCG ATCGTATGGC  
4401 CGGCATTAACT GTGGTCGGAA GCCATACCTGA ACAAGTAGAT AACAGAACTT  
4451 CAGACGGCAT CCTATCCCTG CATGCCAGCA ACGATATCAA CCTCAATGCG  
4501 GCCACCGTCT CTAACCAAGT TAAAGACGGC ACTACCCAAA TTACCGCCGG  
4551 CAATAATCTC AACCTCGGCA CCATCCGTAC CGAACATCGC GAAGCCTATG  
4601 GTACATTAGA TGACGAGAAC CATCGCCATG TCCGCCAAAG TACCGAAGTC  
4651 GGCAGCAGTA TCCGCACGCA AAACGGCGCA CTGCTTAGAG CCGGTAACGA  
4701 CTTAAAAATC CGCCAAGGCG AACTGGAGGC CGAAGAAGGC AAAACCGTCC  
4751 TTGCCGAGG ACGTGATGTC ACTATCAGCG AAGGACGCCA AATAACCGAA  
4801 CTGGATACCT CGGTAAGCGG AAAAAGCAAA GGCATCCTTT CCAGTACCAA  
4851 AACACACGAC CGCTACCGCT TCAGTCATGA TGAAGCAGTC GGCAGCAACA  
4901 TCGGCGGCGG CAAAATGATT GTTGCAGCCG GGCAGGATAT CAATGTACCG  
4951 GGCAGCAACC TTATTTCTGA TAAGGGCATT GTTTTAAAAG CAGGACACGA  
5001 CATCGATATT TCTACTGCCC ATAATCGCTA TACCGGCAAT GAATACCAGC  
5051 AGAGCAAAAA ATCAGGCGTC ATGGGTACTG GCGGATTGGG CTTTACTATC  
5101 GGTAAACCGA AAATACCGA TGACACTGAT CGTACCAATA TTGTCCATAC  
5151 AGGCAGCATT ATAGGCAGCC TGAATGGAGA CACCGTTACA GTTGCAGGAA  
5201 ACCGCTACCG ACAAAACGGC AGTACCGTCT CCAGCCCCGA GGGGCGCAAT  
5251 ACCGTCACAG CCAAAAGCAT AGATGTAGAG TTCGCAACA ACCGGTATGC  
5301 CACTGACTAC GCCCATACCC AGGAACAAAA AGGCCTTACC GTCGCCCCA  
5351 ATGTCCCGGT TGTCCAAGCT GCACAAAATC TCATACAAGC AGCCCAAAT  
5401 TGGGCAAAA GTAAAAATA ACGCGTTAAT GCCATGGCTG CAGCCAAATGC  
5451 TGCAATGGCAG AGTTATCAAG CAACCCAACA AATGCAACAA TTTGCTCAA  
5501 GCAGCAGTGC GGGACAAGGT CAAAACAACA ATCAAGCCCC CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAGG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
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5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGGG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
6051 TGAAACCTAT CAGAGCAAAC AGCAAAACGG CAATGTCCAA GTTACTGTCTG
6101 GTTACGGATT CAGTGCAGG GGCAGTTACC GCCAAAGCAA AGTCAAAGCA
6151 GACCATGCCT CCGTAACCGG GCAAAGCGGT ATTTATGCCG GAGAAGACGG
6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCCAG AGCCGCTACG AAGGCAGAAG
6351 CTTCCGCATA GCGCGCAGTT TCGACCTGAA CGGCGGCTGG GACGGCACGG
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6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
6601 GAAACTGCGG ATCAACACTC AGGCCATCTG AAAACAGCT TCGACAAAGA
6651 CGCGGTGCGC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 AAGCGCAACG CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGCGCGC GGCACCTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGCGGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAACTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGATTG AACAAATAGG
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACGCG AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAAGTACGA GCCTTGTCAG CCCCATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1 MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51 IHSISVISFS LSLLLSALI LTSSSATAQG IVADKSAPAQ QOPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIOGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGG
201 FINASRATLT TAQPQYQAGD LSGFKIROGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWFAAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNGT IQAARLDMST GGLDNTGNIT QTGSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNSVIPQ IPSTATSGS STSVSVSKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NNAKLRVSGD SFNNTVKGL QAHDLAVNTQ TAKNSGHLT QTGKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIRAA HLQDLTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

```

### Homology with $\mathbb{F}_2$

SCORES      Init1: 190 Initn: 524 Opt: 594  
Smith-Waterman score: 866;      21.7% identity in 2427 aa overlap

		10	20	30	40	50	60	
m564	.pep	MNRTLYKVVFNKHRCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS						
		:  : : :  :  :  : :  :    :  :  :  :  :  :						
fhab_borpe		MNTNLYRLVFSHVGRMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA						
		10	20	30	40	50		
		70	80	90	100	110	119	
m564	.pep	LSLLLG-SALILTSSSATAQGIVADKSAPAAQQPTILQTNGGIPQVNIQTPTSAGVSVNQ						
		: : :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :						
fhab_borpe		WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK						
		60	70	80	90	100		
		120	130	140	150	160	170	179
m564	.pep	YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINS SHSSQLNGYIEV						
		: : : :  : : : :  :  :  :  :  :  :  :  :  :  :  :  :						
fhab_borpe		FQQFNVANPGVVFNNGLTGDSVRIGGALTKNPNLTR-QASAILAEVTDTPSPRLAGTLEV						
		110	120	130	140	150	160	

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	180	190	200	210	220	230	239
m564 .pep	GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLSGFKIRQGNVVIAGHGLD						
fhab_borpe	YKKGADLIIANPNGISVNGSLTLNASNLTLTTGRPSVNGGRI-GLDVQQTVTIERGGVN						
	170	180	190	200	210	220	
	240	250	260	270	280	290	
m564 .pep	ARDTDYTRILSYHSKIDAPV---WGQ---DVRVAVAGQNDVAATGDAHSPILNNAANTSN						
fhab_borpe	ATGLGYFDVVARLVKLGAVSSKQKPLADIADVAGANRYDHATRRATPI----AAGARG						
	230	240	250	260	270	280	
	300	310	320	330	340	350	
m564 .pep	NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWFFASAGNVAVNAEGKLV						
fhab_borpe	AAAGA-----YRIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA						
	290	300	310	320	330		
	360	370	380	390	400	410	
m564 .pep	NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSGTVLSSGRLTVRNIGRL						
fhab_borpe	---LGDATVQRGPLSLKGAGVVSAGKLAGGGGAV---NVAGGGAVKIA---SASSVGNL						
	340	350	360	370	380		
	420	430	440	450	460	470	
m564 .pep	KNQNNGTIQAARLDMSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP						
fhab_borpe	AVQGGGKQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVAAGKADKLSA						
	390	400	410	420	430		
	480	490	500	510	520	530	
m564 .pep	NPSV-IPQIPSTATGSGSSTVSVKPGSNNPVSPAPAKNYAVGRIQTGAFD-NAGSIN						
fhab_borpe	TRRVDVDGKQAVALSASSNALSVRAGGA-----LKAGKLSATGRDLVDGKQAVTLGSA						
	440	450	460	470	480	490	
	540	550	560	570	579		
m564 .pep	AGGQIDIAAQNGLGNSGSLNAAKLTVSG-----DSFNNT-----VKGKLQAHDLAVNT						
fhab_borpe	SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAARNLQSKG						
	500	510	520	530	540	550	
	580	590	600	610	620	630	
m564 .pep	QTAKNSGHLTQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKGNIRAAHLQDLTA						
fhab_borpe	AIGVQGGGAVSVANANSDAELVRGRGQVDLHDLAARGADISGEGRVNIGRARSDDVK						
	560	570	580	590	600	610	
	640	650	660	670	680	690	
m564 .pep	GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTGQTLDNTRGRIEATVNIQSQQLTN						
fhab_borpe	-VSAHGALSIDSMTALGAIGVQAGGSVSADMRSGAVTVSGGG-----AVNLGDVQ---						
	620	630	640	650	660		
	700	710	720	730	740	750	
m564 .pep	QSGHITATEQLTINSRNVNDNQKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ						
fhab_borpe	SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV						
	670	680	690	700	710		



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m564	.pep	760	770	780	790	800	810
		TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDFVVERDLTAGKQL-NLS					
fhab_borpe		RL-----DGA-HAGGQLRVSSDGOALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
		720	730	740	750	760	
m564	.pep	820	830	840	850	860	870
		IKGRLLK-NTHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVNDNRGLNSDGLT					
fhab_borpe		VTGGERVSVQSVNSASRVAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
		770	780	790	800	810	
m564	.pep	880	890	900	910	920	930
		HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETEGSTKAGATAARKRLDI-GAKEIHN					
fhab_borpe		--GSDGAISVSGRDAVRVDQARSLADISLG---AEGGATLGAVEAAGSIDVRGGSTV--					
		820	830	840	850	860	
m564	.pep	940	950	960	970	980	990
		QEGALLSSEGI FAVGNRLDEQHHAGMADTFVNGSAGLEVQGDALMSVRNMQINNHFKT					
fhab_borpe		AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
		870	880	890	900	910	920
m564	.pep	1000	1010	1020	1030	1040	1050
		ETYLAKAEK--QVRDYTVLGQNTYYQAGKDGLFDNSQGQKDOTTATFHLKNGSRIEANQ-					
fhab_borpe		ALQSAKASGTLHVQGGHELDLGTAAVGAVDV---NGTGDVVRVAKLVSDAGADLQAGRS					
		930	940	950	960	970	
m564	.pep	1060	1070	1080	1090	1100	
		--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRITDDLNQKE					
fhab_borpe		MTLGIVDTTGDQLQARAQQKLELGSVKSDGGQLQAAAGGALSAAAEVAGALELS---GQGV					
		980	990	1000	1010	1020	1030
m564	.pep	1110	1120	1130	1140	1150	1160
		ITNQSTTGKGRDVAVGTDQWDSVTKKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
fhab_borpe		TVDRASASRARIDSTGSGVIGALKAGAVEAASPRRARRALR-----QDFFTPG					
		1040	1050	1060	1070	1080	
m564	.pep	1170	1180	1190	1200	1210	1220
		SVI---QQNAASPSFQPAASAIKLIDGVSTAAVNGQRIHTGNVSVSLNNATVTLPNSSLYT					
fhab_borpe		SVVVRAQGNVTVGRGDPHQGVLAQGGDIIMDA--KGGTLLLNDALTENGTVTISADSAVL					
		1090	1100	1110	1120	1130	1140
m564	.pep	1230	1240	1250	1260	1270	1280
		THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQDLTNHLHKRLGDGYEQKLVNEQIHQ					
fhab_borpe		EHSTIESKISQSVLAAKGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
		1150	1160	1170	1180	1190	
m564	.pep	1290	1300	1310	1320	1330	1340
		LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFLGTPG-IALSAEQVARLTSDIVWMENQTV					
fhab_borpe		VDGRPQI-----TDAVTGEARKDES VVSDAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
		1200	1210	1220	1230	1240	1250

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m564	.pep	1350	1360	1370	1380	1390	1400
		TLSDGSTQTVLVPKVVYALARKGDLNTSGGLISAEQVLLKLQNGNLNSGTIAGROAVLIQ					
		: ::  :		: ::  :	: ::  :	: ::  :	: ::  :
fhab_borpe		--ENGASVTVRTT-----	GNLVNKGYSAGKQGVLEV--	GGALTNEFLVGS	SDGTORIE		
		1260	1270	1280	1290	1300	
m564	.pep	1410	1420	1430	1440	1450	
		ARNINSNGNIQ-----	ADQIGLKAESINIDGGQVQAGRLLTAQ----	AQNINLNGTT			
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
m564	.pep	1460	1470	1480	1490	1500	
		QTSGNERNGNTAI--	DRMAGINVV--	GSHTQVDNRTSD--	GILSLHASNDINLNAATVSNQV		
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADATLAAQV					
		1370	1380	1390	1400	1410	1420
m564	.pep	1510	1520	1530	1540	1550	
		--KDGTQTITAGNNLNLGT--	IRTE---	HREAYGTLDDENHRHVRQST-----	EVGS		
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNVTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
m564	.pep	1560	1570	1580	1590	1600	
		SIRTQNGALLRAGNDLKIRQGELEAEKGKTVLAAGRDV--	TISEGRQITELDTS---	VSG			
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		EVMAKSATLTTSAGAARN--	AGKMVQKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG				
		1490	1500	1510	1520	1530	
m564	.pep	1610	1620	1630	1640	1650	1660
		K---SKGILSSTKTHDRYR---	SHDEAV--	GSNIGGGKMIVAAGQDINVRGNSNLISDKGI			
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--	DNSG				
		1540	1550	1560	1570	1580	1590
m564	.pep	1670	1680	1690	1700	1710	
		VLKAGHDIDISTAHNRYTG-----	NEYHESKSGVMGTGGLGFTIGNRKTDDTDRTNIV				
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		TMAAGHDATLKAPHLRNTGQVVAGHDIHIINSAKLENTGRV--	DARNIDIALDVADFTN--				
		1600	1610	1620	1630	1640	1650
m564	.pep	1720	1730	1740	1750	1760	1770
		HTGSIIGSLNGDVTTVAGNRYRQT---	GSTVSSPEGRNTVTA	SIDVEFANNRYATDYA			
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQORDLVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGSLIA					
		1660	1670	1680	1690	1700	1710
m564	.pep	1780	1790	1800	1810	1820	1830
		HTQEOKGLTVALNVPVQAAQNFIAQAAQNVGKSKNKRVNAMAAANAA--	WQSYQATQQMQQ				
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		EVQE-----	NIDNKQA----	IVVGKDLTSL--	SAHGNVANEANALLWAAGELTVKAQN		
		1720	1730	1740	1750		
m564	.pep	1840	1850	1860	1870	1880	1890
		FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKGQTTLAATGSG					
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		ITNKRAALIEAGGNARLTA	AAVALLNKLGRIRAGEDMHLD---	APRI----	ENTAKLSGEV		
		1760	1770	1780	1790	1800	1810
m564	.pep	1900	1910	1920	1930	1940	1950
		EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGSEQSKNKS	SGWNAGVAVKIGNGIRF				
		: ::  :	: ::  :	: ::  :	: ::  :	: ::  :	
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----	IAAPWYGGDLTAEQSLIEV				
		1820	1830	1840	1850	1860	

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHVVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
		:		: :   :	:	: :   :	
fhab_borpe		GKDLYLNAGARKDE-----HRHL-----LNEGVIQAGGHGIGG-----DVDNRSV-					
		1870	1880	1890	1900		
		2020	2030	2040	2050	2060	
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE					
		: :   :	: :	: :	:	:	:
fhab_borpe		VRTVSAMEYFKTLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY					
		1910	1920	1930	1940	1950	1960
		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
		: : : :		:	:	: :   :	:   :
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	
		2130	2140	2150	2160	2170	
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGS D GDSKNSTTRSGVNTNHIHITDEAG					
		: :   : :	: :   :	:	: : : :   : : : :	: : : :	
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRRVHDQLG-----QRYGKALGGMDAETKEVDGIIQ					
		2020	2030	2040	2050	2060	2070
		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGLKNSFDKDAVAKEINLQREVTKFGRNAA					
		: :	:	:	: : :   : :	:	: :   : :
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPRVT--LAKALS					
		2080	2090	2100	2110	2120	
		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		: :	:	: :   : :	: :	:	:
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180
		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDWTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGSLSLAAPYLDKAAENLGPAGK					
		: :   : :	:	: : : :	:	:	:
fhab_borpe		AQNRGRPEGLKIGAHSA TSVSGSFDALRDVGLEKRLDIDDALAAVLVNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accattttcg cccgtcccag accggcggct tccaatactt
101 ccctgcgttt cgcctcgccg aacgacaccg gctcgcctgc acttctggct
151 acctgcacgc gtgcgatgtc caagtcgagc gcgaaatacg gaatatcctc
201 ttggggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gtcctatcgt tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASF NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

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```

251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTGCG CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCG
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTECFIL KAMANTTSF NTSSIAN SIN
 201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

	10	20	30	40	50	60
m565.pep	MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS					
g565	MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m565.pep	AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP					
g565	AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
  51 CGTAACCAACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
 101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
 151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
 201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCTGCGC AAGCCGACAA
 251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
 301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
 351 ATCGCTGCCG CCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
 401 CCGCCGTGCG CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCG
 451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
 501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
 551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
 601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
  51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
 101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
 151 AMASITKPNS PPCARYKAVL RLSPTECFIL KAMANTTSF NTSSIAN SIN
 201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

	10	20	30	40	50	60
m565.pep	MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS					

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```

a565      MDSTLSKTCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSPALLATCTRAMSKSS
           10      20      30      40      50      60

           70      80      90      100     110     120
m565.pep  AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           |||
a565      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120

           130     140     150     160     170     180
m565.pep  PKRKGAIIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||
a565      PKRKGAIIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180

           190     200     210
m565.pep  KAMANTTSAFNTSSIANSENTCRQPPINAX
           |||
a565      KAMANTTSAFNTSSIANSENTCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct ttccagacgg cattttgtat ggggggtaac
51  ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggct
151 gccggtttg tgggtgattt ccacgcgttc gccgtcgggt gccaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacgggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAHSA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACCG GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAHSA*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDNCGADGTGGKGHAAAGLVGDFHAL
           |||

```

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```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10      20      30      40      50      60
           70      80      90      100     110
m566 . pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g566      AVGGEEGGVVADYVACADGGKADGRRISVAFAAVNGALFEVAAERAGDDFAHSX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566 . seq
1  ATGCCGTCTG  ACAATATCT  TTTCAGACGG  CATTGTGTAT  GGGGGTTAAC
51  GGTTGTTTCTG  CCCGAGTACG  TCCTGCATAT  CGTACAAACC  CGTTTTACCG
101 TTTACCCAAA  CTGCGGCGCG  GACGGCGCGG  GCGGCAAAGG  TCATGCGGGT
151 GCTTGCCTTG  TGGGTGATT  CCACGCGCTC  GCCGTCGGTG  GCGAAGAGGG
201 CCGTGTGGTC  GCCGACGATG  TCGCCCGCGC  GGACGGTGGC  AAAGCCGATG
251 GTGGACGGAT  CGCGCGGGCC  GGTGTGGCCT  TCGCGCCCGT  AAACGGCGCA
301 TTGTTTGAGG  TCTCTGCCGA  GCGCGCCGGC  GATGACTTCG  CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566 . pep
1  MPSEQYLFRR  HFVWGLTVVQ  PEYVLHIVQT  RFTVYPNCGA  DGAGGKGHAA
51  ACLVGDFHAL  AVGGEEGGVV  ADDVARADGG  KADGGRIARA  GVAFVAVNGA
101 LFEVSAERAG  DDFAHA*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566 . pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10      20      30      40      50      60
           70      80      90      100     110
m566 . pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a566      AVGGEEGGVVADDVARADGGKADGRRIRAGVAFVAVNGALFEVSAERAGDDFAHAX
           70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567 . seq..
1  atgcgacgac  gggcagcggc  atcgacaagg  cgggtttgca  gtccggcggt
51  tatcaggtct  tattggcgga  tgcggacgtg  cagtcggcgg  cggtacgcag
101 caaagagggc  ggatacggcg  tgttgggtgc  gaacgcgcgc  gcttgccggc
151 gcggaaatcg  agctggtgca  ggaaatcgcc  cggaagtgc  gtttgaaaaa
201 cgcgctcaag  gcagtgccgg  aagattacga  cttatcctg  atcgactgtc
251 cgccttcgct  gacgctgtg  acgcttaacg  gcttggtggc  ggcggggcgc
301 gtgattgtgc  cgatgttggt  cgaatattac  gcgctggaag  ggatttccga
351 ttgattgctg  accgtgcgca  aaatccgtca  ggcggtcaat  cccgatttgg
401 acatcacggg  catcgtgcgt  acgatgtacg  acagccgcag  caggctgggt
451 gccgaagtca  gcgaacagtt  gcgcagccat  ttcggggatt  tgctttttga
501 aaccgccatc  ccgcgcaata  tccgccttgc  ggaagcgccg  agccacggta
551 tgccggtgat  ggcttacgac  gcgcaggcaa  aggggtgcaa  ggcgtatctt
601 gccttggcgg  acgaactggc  ggcgaggggtg  tcggggaaat  ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567 . pep
1  MRRRAAATR  RVCSPAFIRS  YWAMRTCSRR  RYAAKRADTA  CWVRTRALAG
51  AEIELVQEIA  REVR LKNALK  AVAEDYDFIL  IDCPPSLTLL  TLNGLVAAGG
101 VIVPMLCEYY  ALEGISDLIA  TVRKIRQAVN  PDLDITGIVR  TMYDSRSRLV
151 AEVSEQLRSH  FGDLLFETAI  PRNIRLAEAP  SHGMPVMAYD  AQAKGAKAYL
201 ALADELAARV  SGK*

```

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

m567.seq..

```

1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GCGCGATACG
251 CTGTGTTGGG TCGGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTT GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTGCTTTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

m567.pep..

```

1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAEEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSFGLDLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m567/g567 98.2% identity in 168 aa overlap

	60	70	80	90	100	110	119
m567.pep	GVYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAEEED						
g567	AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAEEED						
	20	30	40	50	60	70	
m567.pep	120	130	140	150	160	170	179
	YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI						
g567	YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI						
	80	90	100	110	120	130	
m567.pep	180	190	200	210	220	230	239
	TGIVRTMYDSRSLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG						
g567	TGIVRTMYDSRSLVAEVSEQLRSHFGDLLFETAIIPRNIRLAEAPSHGMPVMAYDAQAKG						
	140	150	160	170	180	190	
m567.pep	240	250					
	TKAYLALADELAARVSGKX						
g567	AKAYLALADELAARVSGKX						
	200	210					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

a567.seq

```

1  ATGAGTGCGA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTGCGATTG GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GCGCGATACG

```

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```

251 GCGTGTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTGTATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGTGCC AAGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
  1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
 51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GGYVGLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

```

m567/a567 97.7% identity in 257 aa overlap

```

          10      20      30      40      50      60
m567.pep  MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKAGLQSG
          |||||
a567      MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
          10      20      30      40      50      60

          70      80      90      100     110     120
m567.pep  VYQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEEDY
          |||||
a567      VYQVLLGDADVQSAAVRSKEGGYVGLGANRALAGAEIELVQEIAREVRLKNALKAVAEDY
          70      80      90      100     110     120

          130     140     150     160     170     180
m567.pep  DFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
          |||||
a567      DFILIDCPPSLTLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
          130     140     150     160     170     180

          190     200     210     220     230     240
m567.pep  GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAGT
          |||||
a567      GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
          190     200     210     220     230     240

          250
m567.pep  KAYLALADELAARVSGKX
          |||||
a567      KAYLALADELMARVSGKX
          250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
  1 atgtctaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
 51 gataccttgc agaactctgc gattaaagcg ttcgcggtcg cccaatattt
101 tcaggcgcat attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gcccatcag gaacgaaact tcgtcttcg ggcgacgcca
201 gttttcggtt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggccgt tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggt gtgttccaaa atggtctgcg

```



401 tgctgctctt catatctgcc tttcgcggtt cggcggtcaa atgccgtctg  
451 aacgccgcgc cgtga

This corresponds to the amino acid sequence <SEQ ID 1690; ORF 568.ng>:

g568.pep

1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL  
151 NAAP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1691>:

m568.seq

1 ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAACGCTT CCGCCTCTTC  
51 GATGCCCTGC AGAATCTGCC GGTGAAGCG TTCGCGGCTG CCCAATATCT  
101 TCAGGCGCAT ATTGTTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC  
151 TGTA AAAACA GCCCCATCAG GAACGAAACT TCGTCTTCGG GCGGCGGCCA  
201 GTTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCAGTTTGG  
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC  
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT  
351 AATCACGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG  
401 TGCTGCTTT CATGTCTGCC TTTGCGGTT CGGCATTCAA ATGCCGCTCTG  
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG  
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC  
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG  
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CCGATAGAGA  
651 CCGGCGCTTC TTCCGCTTCG CCGCGTACGA CTTAATCAG GTCTTTGCGG  
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC  
751 TGCCGGGTT AGTCCCAAGT TTGA

This corresponds to the amino acid sequence <SEQ ID 1692; ORF 568>:

m568.pep..

1 MLRVRPVLFA VNASASSMPC RICRLKRSRL PNIFRRILFS CRRRTCFCCKA  
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP  
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL  
151 NAEPCRLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE  
201 EFFDVVVGIA AHVADRDAAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS  
251 CRVQSQV\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m568/g568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
g568	MLRVRPVLFAVKASASSIPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
g568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIIRGRKRFFAQRPLPSIITA					
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMFAFRGSAFKCRLNAEPCRLNCHQIFFFGSQEFVGFGNVFVGQ					
g568	MCLGMAVCSKMVCVLLFISAFRGSAFKCRLNAAPX					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAAFFRFAAYDFNQVFAAFLGQHG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568 . seq
1  ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CGCCTCTTC
51  GATGCCCTTC AGGATTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATT
101 TCAGGCGCAT ATTGTTTCG TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGGCCA
201 GTTTCGGTT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCACGGCG ATATGCTTGG GAATGGCGGT GTGTTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTCGCGGTT CCGCATTCAA ATGCCGTCTG
451 AACCCGAAC CGTGCAGGT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CGGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568 . pep
1  MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCTIF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSFAFKRL
151 NAEPCLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568 . pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSCRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSCRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568 . pep	70	80	90	100	110	120
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNASKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568 . pep	130	140	150	160	170	180
a568	ICLGMVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLRNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568 . pep	190	200	210	220	230	240
a568	FLNRFFAATCLVFGNFFVFEEFFDVVVGIAAHVADRDAFFRFAAYDFNQVFAAFLQHG					
	190	200	210	220	230	240
m568 . pep	250	HRHADQVADSCRVSQVX				
a568	250	HRHADQVADSCRVSQVX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569 . seq..
1  atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgtgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgogggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

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```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa ttgggttgg tatgttgtt
251 tggcattttg gctcgccgtt atgcctttgt ggttgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgtc ggctggcttt tgctcatgcc
351 gttttggttc gcgctcgat ccctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

```

g569.pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51  KIETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

```

m569.seq..
1  ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51  GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCTT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTITG GCTCGCGGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTCACACGCG GTTGGCAGGT TTATGCGGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGTTTC GCGCTCGTAT CCCTGCGCCC GCATCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCGGATAT TTGCGCGTAT
451 TTCAGCGCGA AGGCGTTCCG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTGGTGTCTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGGACAC GGCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

```

m569.pep..
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIKPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRDTSI
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
m569.pep	TLVFGVVAYAGGWMLPNLVVYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF					
g569	TLVFGVVAYAGGWMLPNLVVYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
m569.pep	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

```

a569.seq
1  ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51  GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGGCGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

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875

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151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGCTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTGG TATGTTGTTT
251 TGGCATTGTT GCTCGCCGTT ATGCCTTTAT GGTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGCGCG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGGTGT TCGACCGCAC CGACAGCTG
751 ATTGCCGTTA TCAGCGTCTA TGCAGCGATG ATGTCGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569 . pep
1  MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51  KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGWQVYAV GWLLVMPFWE ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

```

m569/a569 99.6% identity in 265 aa overlap

	10	20	30	40	50	60
m569 . pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
a569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA					
	10	20	30	40	50	60
m569 . pep	70	80	90	100	110	120
	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWE					
a569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWE					
	70	80	90	100	110	120
m569 . pep	130	140	150	160	170	180
	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
a569	ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKSWEAIGGAVC					
	130	140	150	160	170	180
m569 . pep	190	200	210	220	230	240
	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSKLLPGH					
a569	VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGH					
	190	200	210	220	230	240
m569 . pep	250	260				
	GGVFDRTDSLIAVISVYAAMMSVLNX					
a569	GGVFDRTDSLIAVISVYAAMMSVLNX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

g570.seq..

```

1  atgatccgtt tgaccgcgc gtttgcgcc gccctgatcg gtttatgctg
51  caccacaggc gcgcacgccg acaccttcca aaaaatcgcg tttatcaaca
101 ccgagcgcat ctacctcgaa tccaagcagg cgcgcaacat ccaaaaaacy
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacy
201 cgaaggcttg gatttggaaa ggcagctcgc cggcgcaaaa cttaggagcy
251 caaaaaaggc gcaagccgaa gaaaaatggc gcgggctggt cgaagcgttc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gcgcgaacga
351 agagtgttgc tccctccagc aaaacgccaa ccgcgtcatc gtcaaaatcg

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876

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac  
 451 acccaatagc acgttacgga cagcgtcatt aaagaaatga acgcccgtcg  
 501 a

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

1 MTRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT  
 51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF  
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIIYVN  
 151 TQYDVTDSDVI KEMNAR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG  
 51 CACCGCAGGC GCGCACGCGC ACACCTTCCA AAAAATCGGC TTTATCAACA  
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG  
 151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG  
 201 CGAAGGTCTG GATTTGAAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG  
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC  
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA  
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG  
 401 CCAACACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC  
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG  
 501 A

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT  
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF  
 101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYVN  
 151 TQYDVTDSDVI KEMNAR\*

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTAGAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLDKAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIKIAKQEGYDVILQNVIIYVNTQYDVTDSDVIKEMNARX					
g570	SLQQNANRVIKIAKQEGYDVILQDVIIYVNTQYDVTDSDVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG  
 51 CACCGCAGGC GCGCACGCGC ACACCTTCCA AAAAATCGGC TTTATCAACA  
 101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG  
 151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG  
 201 CGAAGGTCTG GATTTGAAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG  
 251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC  
 301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA  
 351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG  
 401 CCAACACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC  
 451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

501 A

This corresponds to the amino acid sequence &lt;SEQ ID 1706; ORF 570.a&gt;:

a570.pep  
 1 MTRLTRAF~~AA~~ ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT  
 51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF  
 101 RKKQAQFEED YNLRRNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN  
 151 TQYDVTDSVI KEMNAR\*

m570/a570 97.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAF <del>AA</del> AALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
a570	MTRLTRAF <del>AA</del> AALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
a570	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRRNEEFA					
	70	80	90	100	110	120
	130	140	150	160		
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIVNTQYDVTDSVIKEMNARX					
a570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

g571.seq (partial)  
 1 atgcgcttt tccgagtaaa ccgatttgtt gttaccgttt tcggcgccgg  
 51 tataggttct gccgtccac acgtgcctg cgctcgcaaa caggctcagg  
 101 cggacggtgc gtgcgtcttt cgcaccgggc atcggaaga gcagctcggc  
 151 ggagacgttg gctttttgt tgcgcgcta gctgatttt tcgccgtatt  
 201 cgtcatacac ttccgggccc agcgtgcgc ttctgtagcc gcgcacogaa  
 251 ccagggccc cgcgtagaa gtttcaaag aaggggattt ctttggttct  
 301 gccgtagccg ccgcgaatgc cgacttcgcc gccgagcatc agcgtgaagg  
 351 ttttgc...

This corresponds to the amino acid sequence &lt;SEQ ID 1708; ORF 571.ng&gt;:

g571.pep (partial)  
 1 MRVFRVNRV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHRREEQLG  
 51 GDVGFFVA~~AV~~ ADFFAVFVIH FRAERA~~AF~~VA AHRTQAAAVE VFKEGDFFGS  
 101 AVAARNADFA AEHQREGFA...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

m571.seq  
 1 ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCGG CCGGTGCGCG  
 51 AACTGCTGTT GTCGTCGTAG GTTTGCGGT CCCACACGCT GCCTGCGTCG  
 101 GCAAACAGGC TCAGGCGGAC GGTGCGCGG TCTTTCGCGC CGGGCATCGG  
 151 GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CGTAGCTGA  
 201 TTTTTCGCGC GTATTCGTCA TAGACTTTCG GACCGAGCGT GCCGCTTTCG  
 251 TATCCGCGCA CCGAACCCAG GCGCGCGCG TAGAAGTTT CAAAGAAGGG  
 301 GATTTCTTTG GTTCTGCCGT AGCCGCCCCG AATGCCGACT TCGCCGCCGA  
 351 GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG  
 401 GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTCGGCGTT  
 451 CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

This corresponds to the amino acid sequence &lt;SEQ ID 1710; ORF 571&gt;:

m571.pep  
 1 MGIAGAVNVL NPAAGRGTAV VVGVFAVPHA ACVGKQAQAD GARVFRAGHR  
 51 EEQLGGDVGF FVA~~AV~~ADFFA VFVIDFRTER AAFVSAHRTQ AA~~AV~~EVFKEG  
 101 DFFGSAVAAR NADFAAEHQ~~R~~ EGFAQGE~~EP~~G LVVGGGV~~LQ~~ FAARQGD~~FG~~V  
 151 HARQVAARRP \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

**This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:**

m571/a571 98.1% identity in 160 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq. .

**g572.pap..**

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq.

1	ATGTGCGCCA	TCGTGCGGGC	GGTGGGGCTG	CCTTCCGCGC	TGCGAGCGGC
51	GCAAAAAGGC	AAAACCATTT	ATCTGGCAAA	CAAAGAAAGC	CTGGTGGTTT
101	CCGGCGCGTT	GTTTATGAA	ACGCGCCGTG	CAAA CGCGCG	GGCAGCTTGA
151	CCCGTGCAGA	CGGTACGACAA	CGCGTTTTC	CAAGTTTTCG	CGCGCGATTG
201	CGCGGCGCGT	CTGAACGAAC	ACGGCATCGC	TTTCGATTAC	CTGACCGCTT
251	CCGGCGGCCC	GTTTCTGACC	GCGCATTTAA	ACAGCTTCGA	CCGCATTACG
301	CCCGCCCAAG	CGGTCAACA	CCCAATTGG	CGTATGGGAC	GCAAAATCTC
351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGC
401	ATTGCGTGT	CAACTGTCCG	CGGCAAAAC	TGCAAGTCGT	CATCCATCCG
451	CAACTCGTGA	TACACAGCAT	GCTGCGCTAC	CGCGACGCGT	CCGTGCTGGC
501	GCAATCTGGC	AATCCCGATA	TGCGAACGCC	CATCGCTTAT	TTTGTGGGTT
551	TGCCCGCGTG	CATCGATTCC	GGTGTGCGCG	ACCTGGATTT	CGACGCAATTG
601	TCGCGCGTGA	CACTCCAAAG	GCCCGACTTT	GACGCGCTCC	CCTGCGCTGAG
651	GCTGCGCTAT	GAGCCATGTA	AGCGGACGGG	AGCGCGTCCC	TGCGTATTGGA
701	ACGCGCGCAA	CGAAGCCGCC	GTGCGCGCCT	TTTTGGACGG	ACAGATTAAAG
751	TTTACCAGCA	TTGCGAAAAC	CGTGCGCCAC	TGTCCTTGAC	AAGACTTTTC
801	AGACGGCATA	GCGCATATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCGGACAC
851	CGCGCAAGC	GCGAGCATTT	ATCGGCACAC	TGCGCTGA	

m572.pap..

1	<u>MCAIVGAVGL</u>	<u>PSALAAQKQ</u>	<u>KTIYLANKE</u>	<u>LUVSGALFME</u>	<u>TARANGAAVL</u>
51	<u>PQVSEHNHF</u>	<u>QVLPRDYGAR</u>	<u>LNHGHIASII</u>	<u>LTASGGPFLL</u>	<u>ADLTFVTHP</u>
101	<u>PAADKHAIPW</u>	<u>RMGRKISVDS</u>	<u>ATMMNKGLEL</u>	<u>IEAHWLFNCP</u>	<u>PKDLVDIRHP</u>
151	<u>QSVIHSMPRY</u>	<u>RDGSLVALQL</u>	<u>NPDMRTPIAY</u>	<u>CLGLPERIDS</u>	<u>GVGDLDFDAL</u>
201	<u>SALTFFQKPD</u>	<u>DRFFCLRLRL</u>	<u>EAMNAGGAAP</u>	<u>CVLNAANEAA</u>	<u>VAAPFLDGQIK</u>
251	<u>PTDIAKTVAH</u>	<u>CLAQDFSDGI</u>	<u>GDIGGLEAQD</u>	<u>ARTRAQARAF</u>	<u>IGTLR*</u>

m572/g572 92.9% identity in 295 aa overlap

```

              10      20      30      40      50      60
m572 . pep    MCAIVGAVGLPSALAAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVVDSEHNNAV
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572          MCAIVGAAGLPSALAAAQKGKTIYLANKETLVVSGALFMETARANGAAVLVVDSEHNAIF
              10      20      30      40      50      60

              70      80      90      100     110     120
m572 . pep    QVLPRDYAGRLNEHGIASIIILTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572          QVLPRDYTRLNEHGIDSIILTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```



880

	70	80	90	100	110	120
	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGLDFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGLDFGALSALTFOKPDFGRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFS DGI GLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFS SNGMGDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

```

a572.seq
1  ATGTGCGCCA TCCTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCGAA CAAAGAGACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCGTCGACA GCGAACACAA CGCCGTTTTC CAAGTTTTGC CGCGCGATTA
201 CACAGGTCGC CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGGCGGCC GTTCTGACC GCCGATTAA ACACGTTTCA CAGCATTACG
301 CCGACCAAG CGGTCAAACA CCCCATTGG CGTATGGGAC GCAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAACTGTCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCTGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGTGGC
501 GCAACTGGGC AATCCCGATA TCGGAACGCC TATCGCTTAT TGTGTTGGT
551 TGCCCGAGCG CATCGATTG GGTGTCGGCG ACCTGGATT TCGACGATTG
601 TCCGCGCTGA CCTTCCAAA GCCCGACTT GACCGCTTCC CCTGCCTGAA
651 GCTCGCTTAT GAAGCCATGA ACGCAGGCG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCCGCT TTTTGGACG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAT TGTCTTTCAC AAGACTTTTC
801 AGACGGCATA GCGACATAG GGGGGCTCTT GCGCAAGAT GCCCGGACAC
851 GCGACAAGC GCGGGCATT ATCGGCACAC TGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

```

a572.pep
1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAVF QVLPRDYTGR LNEHGIASII LTASGGPFLT ADLNTFDSIT
101 PDQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSMVRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS VVGDLDFDAL
201 SALTFOKPDF DRFPCLKLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIAKTVAH CLSQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572.pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAVF					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m572.pep	QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	QVLPRDYTGRLNEHGIASII LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

881

	130	140	150	160	170	180
m572. pep	ATMMNKGLELIEAHWLFNCPDPKLEVVIHQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDPKLEVVIHQSVIHSMVRYRDGSLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572. pep	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAEAA					
a572	CLGLPERIDSGVGDLDLFDALSALTFOKPDFDRFPCLRLAYEAMNAGGAAPCVLNAAEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572. pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1   atgccctgtt tgtgccgcct taatcgcaat atcggcagtt tccaaatcac
51  gaatctcacc gaccataatg atgtccgggt cctgacgcag gaaagacttc
101 aaagcagcgg caaaagtcag accctgctta tcattgacgt taacctgatt
151 gatgcccgcc aggttaaatct cggcagggtc ttccgcgctt gcaatattta
201 ccgactccgt attcaaaata ttcaaacagg tatagagcga cacogtctta
251 ccggaacccg tcggaccggg taccagcacc atcccgttaag gacggtgaat
301 cgcttccaac aacaattttt tctggaacgg ctcaaaacgg agctggtcga
351 tgttcaaaag cgcggcatcg gaattcaaaa tccgcatcac gaccttttcg
401 ccaaacagcg tcggcaatgt gctgacacgg aaatcgacag gcttgccgcc
451 cttttgaag gtcagctgca tctacccgtc ctgcggatc cgtttttcgg
501 aaatgtccaa acgcgacatt accttaatcc ggaagcaag ctgccccctt
551 accgcaatgg gcggctgaac cacctcggcg agctgcccgt ccacacggaa
601 accgatacgc gcattgtgtt cgtaaaactc gaaatggatg tcggatgccc
651 cgtacagcaa ggcacccgac aaagtattat ggataaacct cggaacaggg
701 ccgtctcttg cctcctcgtc gtcgatatac aggggtgtgc ttctctcttc
751 ctcttgcccc tccccaaagt cctgaagcag cgtatgctga cggaaccca
801 ccaatcgag caaacccgcc aactggctcat cctcgacaat gaccaactca
851 accgcaatcc ctgcggcgca aaccgttttc tgaatttgcg gcatctgggt
901 cggatcgcaa accgcaaaaa atactttgtc gcccccacgg aaaaccggca
951 cacagtggaa ctccaccatc tgetcctcgg tcaacacccc catcagcacc
1001 ctgtggcgcg gataatgacg caaatcaaga atcgaataac tgaacaccct
1051 cgcaatcaat gccgcaagcg acttgggcga aatgacaccg tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1   MPCLRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKQ TLLIIDVNL
51  DARQVNLGRV FRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVRTVN
101 RFQQQFFLER LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPTV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTRIVFVKL EMDVGCPTAQ GIRQSPMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTTRTHPIE QTRQLVILDN DQLNRNPGCR NRFLNLRHLG
301 RIGNRKRYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1   ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG GCCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTAAATCT CGGCAGGGTC TTCGCGCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGTTGAAT
301 CGCTACCAAC aCaw.TTTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTGAAGAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GTGAAGCAAG CTGCCCCCTT

```

```

551  ACCGCAATGG GCGGCTGAAC CACCTGCGG AGCTGCCCGT CCACACGGAA
601  ACCGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651  CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701  CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751  CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801  CCAATCGAG CAAACCCGCC AACTGGTCAT CCTGACAAT GACCAACTCA
851  ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901  CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951  CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

```

m573.pep..
1  MPCLCLRNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51  DARQVNLGRV FRRCNIYRLR IQNIQTGIER HRLTRTRRTG YQHHFVGTVN
101 RYQHXFFLKR LKTELVDVQR RGIGIQNPHH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCLRNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
g573	MPCLCLRNRNIGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573.pep	70	80	90	100	110	120
g573	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	RGIGIQNPHHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPFGNVQTRHYLNPXSK					
	130	140	150	160	170	180
m573.pep	190	200	210	220	230	240
g573	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300
m573.pep	310	320	330	340	350	360
g573	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	RIGNRKKYFVAPTENRHTVELHHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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## a573 . seq

```

1 ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51 GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCGG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAAATTTT TCTGAAACGG CTCAAACCG AGCTGGTCGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCCGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGAGCAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCGT CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCCGAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCTCTTTC
751 CTCCTGCCCC TCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAA ATAATTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

## a573 . pep

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51 DARQVNLGRV FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPBH DLFAKQRRQC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPPAQ GIRQSLMDKP RNRVAFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKRYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573 . pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
m573 . pep	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573 . pep	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVNRYQHFFLKR LKTELVDVQR					
a573	FRRCNIRYLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
m573 . pep	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
m573 . pep	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRVAFCLLV					
a573	LPPYRNGRLNHLAELPVHTETDTGIVFVKLEMDVRCPPAQGIRQSLMDKPRNRVAFCLLV					
	190	200	210	220	230	240
m573 . pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573						
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360

m573.pep	NDTVX
a573	NDTVX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1  atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct tttgcccgtc ttcttcacga
101 tgggctgggt tgcgcgccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc cttcgggatt ttataaaagc ctggacgctt tggtcgaccg
201 caa cagcggg cgcgcggcaa gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaacttta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc ggcgcgcgct cctgtttgaa ttggcgcaaa
401 act accaaag cgcgggtttg gtgatcgtg ccgaacagat tttttgggg
451 ctgcaagacg gtgaaatggc gcgtgaagcc agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaac
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgcgcgcgtc
751 gaagccctatg ccgccatcga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaacgc tctgacagga tatatgcaga cgtttccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg ctaagggcg agaaagaagc
951 cgcgcaaac gcgctcgagc ttgtccgcgc caagcccgac cttaacggcg
1001 tgtaccgcct gtcgggttg aaactcagcg atttgatcc ggcttgaaa
1051 gccgatgcgc acatgatgcg ttcggttacc ggacggcagc tccagcgcag
1101 cgtgatgtac cgttgccgca actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgcctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1  MLEPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSI PSGFYKS LDALVDRNSG RAARELAEV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET AQLLSHDEQT YQFELAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSL LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDLPANK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1  ATGCGCCCGA ATCTACCAAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGGT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCCGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTGAAC CTCACCTCG GCAAACCTTA CCGCCAGCGT
301 GGCAGAAACG ACAAAGCCAT CAACATACAC CGGACAATGC TCGATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCATAGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG TCGCGCGTTT

```

```

651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCGCGCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGGC AGAAAGAAGC
951 CGCGCAAAAC GCCGTCGAGC TTGTCCGCGC CAAGCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AAATCAGCG ATATGAATCC GGCTTGGAAA
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCT
1151 GGCACCTGCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```

1  MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GKPEEGLNRLTG YMQTFPELDL
301 INVVEKSLLL KCEKEAAQT AVELVRRKPD LNGVYRLLGL KLSMDNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFFWHCPACN KWQTFPNKI
401 EV*

```

m573/g573 97.8% identity in 402 aa overlap

m574.pep	10	20	30	40	50	60
	MRPNLPNSLKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
g574	10	20	30	40	50	60
	MLPNLPNSLKADMDNELWIILLPIILLPVFFTMGWFAARVDMKTVLKQAKSIPSGFYKS					
m574.pep	70	80	90	100	110	120
	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
g574	70	80	90	100	110	120
	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
m574.pep	130	140	150	160	170	180
	GEKRARVLFELAQNYQSAGLVDRAEQIFLG LQDGKMAREARQHLLNIYQQDRDWEKAVET					
g574	130	140	150	160	170	180
	GEKRARVLFELAQNYQSAGLVDRAEQIFLG LQDGEMAREARQHLLNIYQQDRDWEKAVET					
m574.pep	190	200	210	220	230	240
	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDVARFNVGKALEANKKCTRANMILGDIE					
g574	190	200	210	220	230	240
	AQLLSHDEQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDIE					
m574.pep	250	260	270	280	290	300
	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
g574	250	260	270	280	290	300
	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
m574.pep	310	320	330	340	350	360
	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLLGLKLSMDNPAWKADADMRSVI					
g574	310	320	330	340	350	360
	INVVEKSLLLKCEKEAAQTAVELVRRKPD LNGVYRLLGLKLSDLDPWKADADMRSVI					
m574.pep	370	380	390	400		
	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFPNKIEVX					
g574	370	380	390	400		
	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTFPNKIEVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1729>:

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC CGTCGGGATT TTATAAAAGT CTGGATGCCT TGGTTGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACCTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTCGATG CCGCGCGTTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGCG AGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCCGCG CAAGCCCGAC CTCAACGGCG
1001 TGTACCGCCT GCTTGGTTTG AAACCTCAGC ATTTGGATCC GGCTTGAAAA
1051 GCCGATGCCG ATATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTCTT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

```
a574.pep
1  MRPNLPNSLE KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINMH QTLSDSPDTH GAKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNVGYRLGL KLSDLDPAWK
351 ADADMRSVI GRQLQSVMY RCRNCHFSQ VFFWHCPACN KWQTFPNKI
401 EV*
```

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDNELWIIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINMHQTLSDSPDTH					
	70	80	90	100	110	120
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGLKLYRQRGENDKAINMHQTLSDSPDTH					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
	190	200	210	220	230	240
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFVARFNVGKALEANKKCTRANMILGDIE					

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	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQKPEEGLNRLTGYMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLGVYRLLGLKLSDMNPAWKADADMMSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPDNLGVYRLLGLKLSDLDPWKADADMMSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFSQVFFWHCPACNKWQTFTPNKIEVX					
a574	GRQLQRSVMYRCRNCHFSQVFFWHCPACNKWQTFTPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

g575.seq (partial)

```

1 ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51 cccgtcaaaca gtccgctttc ggtttcttct tccgcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttacgg gtttcgtcgg tccgcgtgtc gatggcagaa
201 gcggcggttt cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttcgacg ggttacaggt cgggttggtt gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggttcgggtt cgaacggccg gtttttcgcg
351 ttttgcctcg ggccgggcaa cttttgttcc aggtttttca accggttttt
401 cgacagggtt ctctatcggg ttctccacag ttgcctgttt ggacggttca
451 gacggcatgg atgcagtttc ggctttgggt ttccgcgttt gcggtttggg
501 ttgttcgcgt ttgatttttt tgggtgctgc cgttttgatc ctgttcagat
551 tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

g575.pep (partial)

```

1 ..MPCLRRQAAR CTNRRIDRQT VFRFLLRQK FVRQVRQVR RQLHWLFPQQ
51 VRKRCYRFR SACRWQKRRL LGGADSAVS DAAVFAAGTG PGWRSVAEAG
101 VSDTAGLGSG RTAGPSAFAS GAATFASGFS TGFSTGFSIG PSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

m575.seq..

```

1 ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51 GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATGACCGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGCGA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CAGCTGTCT GTGGATTCTA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGT
401 TTGCCGATAA CTCCTCTTCA GATTCCTCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGCG GATTAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCGCA ACAGACCGTC AAACAGTCCG CTTTCGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCCGTCG GCGTGTGAT GGCAGAACCG GCGGCTTCTT GGGGGGCGGA
801 TTCGGCAGCG GTTTCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTTCG
851 GTCGAACGGC CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTTCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGGTT
1001 GTTCCGCTTT GATCCTGTTT AGATTGGAA TGTGA
```



This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

```
m575.pep
1  MVS GEEAFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADNSSS DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNRPNSP LSVSSSAETC STGSETALPV
251 SSVGVSMAEA AASWGADSAA VSDAAVFAAG TSGRTAGFS AFASGAATFA
301 SGFSTGPFSTV ACLDGS DMD AVSALGFAVC GLGCSALILF RFGM*
```

m575/g575 70.2% identity in 114 aa overlap

```

      240      250      260      270      280
m575.pep  SSAETCSTGSETALPVSSGVSMAEAAASWGADSAAVSDAAVFAAGTG-----
g575      LHWLFPPQVRKRCYRFRRSACRWQKRRLGGADSAAVSDAAVFAAGTGPGWRSVAEAGVS
           50      60      70      80      90      100

      290      300      309      310      320
m575.pep  -----SGRTAGFSAFASGAATFASGFGTGFST-----VACLDGS DMD AVSALGFA
g575      DTAGLSSGRTAGFSAFASGAATFASGFGTGFSTGFSIGFSTVACLDGS DMD AVSALGFA
           110     120     130     140     150     160

      330      340
m575.pep  VCGLGCSALI-----LFRFGMX
g575      VCGLGCSALIFLGAAALILFRFGMX
           170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

```
a575.seq
1  ATG G T T T C G G   G C G A G G A A G C   C T T C A G G A A G   C C T G C C A G T C   C G G A G G G T G A
51  G G C A G G T T T T   G C G G A A G C T G   T T T C T T C T G T   G C C G A T A T G G   T T G T T T G A G G
101 G C A G G T T G T C   G G A G A A A T C G   G T A T C G A C G G   T T T C C G G T T T   G T T T C G G C A
151 G T T T G G G C G A   C A G A T T C C G G   T T C G G G C G T G   T C G A T G A C G A   T T T C G A C A G G
201 G T T G T A C G G G   T T G A A G G T C T   C G G G C T C G T A   C A C G C T G T C T   G T G G A T T C G A
251 T G G C G T T C C A   A T C G G C A T C C   G C G C G T T T T T   G G G T T C T T C   A T C C T G C G T A
301 A G T G C G C C G G   A T A A A A T G C C   G T T T T G C G C G   G C T G C C A G G C   T G T C G A A A T C
351 C A A G T C G A T G   C G G T T G G A A G   G C G T A T C G G T   T T C G A C A T C G   A A C G T T T G T T
401 T T G C C G A C A A   C T C T T C T T C A   G A T T C C C C A T   C T A A G G C A A G   T G T G T C G T T T
451 A C A T C G T T T T   T C G G A G C G G G   T T C G G G C G T T   G C C G G A G T T T   C G A C T T C G G C
501 A A A G G T G A T T   T C T A T G C C G T   C G T C T G C C G C   G T C G T C A A G G   T C A G G C T C T T
551 C C T C A G G G A C   G G A T T C T T C G   G T A C G G C G C G   C G C G T T T G G A   T T G G G C A A G G
601 C G C A A A A G C A   G C A G C A G G G C   G A T C A A T G C C   G C G C C T C C G C   C G G C A A G C A G
651 C A A G G T G T A C   G A A C C G C C G A   A C A G T C C G C T   T T C G G T T T C T   T C T T C G G C A G
701 A A A C C T G T T C   G A C A G G T T C G   G A A A C G G C G T   T A C C G G T T T C   G T C G G T C G G C
751 G T G T C G A T G G   C A G A A G C G G C   G G C T T C T T G G   G G G G C G G A T T   C G G C A C G G G T
801 T T C C G A T G C G   G C A G T A T T T G   C A G C G G G T A C   A G G T T C G G G T   C G A A C G G C C G
851 G T T T T C C G C G   T T T T G C T T C G   G G C G C G G C A A   C T T T T G C T T C   A G G T T T T T C A
901 A C C G G T T T C T   C T A C C G T T G C   C T G T T T G G A C   G G T T C G G A C G   G C A T G G A T G C
951 G G T T T C G G C T   T T G G G T T T C G   C C G T T T G C G G   T T T G G G T T G T   T C C G C T T T G A
1001 T C C T G T T C A G   A T T C G G A A T G   T G A
```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

```
a575.pep
1  MVS GEEAFRK PASPEGEAGF AEA VSSVPIW LFEGR LSEKS VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVS GSYTLS VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVC FADNSSS DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
251 VSMAEAAASW GADSAAVSDA AVFAAGTGS RTAGFS AFAS GAATFASGFS
301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *
```

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575. pep	MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
a575	MVSGEAEFRKPASPEGEAGFAEAVSSVPIWLFEGRLSEKSVSTVSGLFSAVWATDSGSGV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m575. pep	SMTISTGLYGLKVGSGSYTLSDVSMFAQSASARFWSSSCVSAPDKMPFCAAARLSKSKSM					
a575	SMTISTGLYGLKVGSGSYTLSDVSMFAQSASARFWSSSCVSAPDKMPFCAAARLSKSKSM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m575. pep	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
a575	RLEGVSVSTSNVCFADNSSSDSPSKASVSFTSFFGAGSGVAGVSTSAKVISMPSAASSR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m575. pep	SGSSSGTSSVRRRLDWARRKSSSRINAAPPPASSKVYEPNRPNSPLSVSSSAETC					
a575	SGSSSGTSSVRRRLDWARRKSSSRINAAPPPASSKVYEPN----SPLSVSSSAETC					
	190	200	210	220	230	
	250	260	270	280	290	300
m575. pep	STGSETALPVSSVGVSMMAEAAASWGADSAAVSDAAVFAAGTSGSRTAGFSAFASGAATFA					
a575	STGSETALPVSSVGVSMMAEAAASWGADSAAVSDAAVFAAGTSGSRTAGFSAFASGAATFA					
	240	250	260	270	280	290
	310	320	330	340		
m575. pep	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
a575	SGFSTGFSTVACLDGSDGMDAVSALGFAVCGLGCSALILFRFGMX					
	300	310	320	330	340	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576. seq.. (partial)

```

1 ..atgggctgacg acatcgagc ctccctgaaa caaatgaagg aacagggcgc
51 ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcttcgagg agcagcaggc taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgcgc
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 caggggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccgcc caccctccct ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggggtgcgg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggta aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576. pep.. (partial)

```

1 ..MGVDIGRSLK QMKEQGAIEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51 FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576. seq.. (partial)

```

1 ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

890

```

51   GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   ..MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AOEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AOEVMKFLQ
              |||
g576           MGVDIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AOEVMKFLQ
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep      EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITK QGEGKQPTKDDIV
              |||
g576           EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITK QGEGKQPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep      TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE
              |||
g576           TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep      QGAGDKIGPN ATLVFDVKLV KIGAPENAPA KQPAQVDIKK VN*
              |||
g576           QGAGDKIGPN ATLVFDVKLV KIGAPENAPA KQPAQVDIKK VN*
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCCGCGC TTCTTCCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG  
 701 GCGACAAAAT CGGCCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

a576. pep

1 MNTIFKISAL TISAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST  
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ  
 101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG  
 151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ  
 201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV  
 251 KIGAPENAPA KQPAQVDIKK VN\*

m576/a576 99.5% identity in 222 aa overlap

m576. pep				10	20	30
				MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV
a576	CGKKEAAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV	DIGRSLKQMK	EQGAEIDLKV
	30	40	50	60	70	80
m576. pep		40	50	60	70	80
		FTEAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK
a576		FTEAMQAVYD	GKEIKMTEEQ	AQEVMMKFLQ	EQQAKAVEKH	KADAKANKEK
	90	100	110	120	130	140
m576. pep		100	110	120	130	140
		KDGVKTTASG	LQYKITKQGE	GKOPTKDDIV	TVEYEGRLID	GTVFDSSKAN
a576		KDGVKTTASG	LQYKITKQGE	GKOPTKDDIV	TVEYEGRLID	GTVFDSSKAN
	150	160	170	180	190	200
m576. pep		160	170	180	190	200
		VIPGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
a576		VILGWTEGVQ	LLKEGGEATF	YIPSNLAYRE	QGAGDKIGPN	ATLVFDVKLV
	210	220	230	240	250	260
m576. pep		220				
		KQPAQVDIKK	VNX			
a576		KQPAQVDIKK	VNX			
		270				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

g576-1. seq

1 ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTCCG CCGCTTTGGC  
 51 ACTTTCCGCC TGCGGC AAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC  
 101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTCAAT CGGCAGCAGC  
 151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA  
 201 ACAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG  
 251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG  
 301 GCCCAGGAAG TGATGATGAA ATTCTGCGAG GAGCAGCAGG CTAAAGCCGT  
 351 AGAAAAACAC AAGGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT  
 401 TCCTGAAGGA AATGCGCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT  
 451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAACAGC CGACAAAAGA  
 501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT  
 551 TCGACAGCAG CAAAGCCAAC GGCGCCCGG CCACCTTCCC TTTGAGCCAA  
 601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA  
 651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG  
 701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC  
 751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA  
 801 CATCAAAAAA GTAAATTAA

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

## g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VI PGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

## n576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCG CCGCTTGGC
51  ACTTTCCGCC TGGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGCGGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GCGGAAGCCT
401 TTCTGAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AATCACCAC ACAGGCGGAA GGCAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCACAGCAGC CAAAGCCAAC GCGGCGCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCGGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGCGGCGCA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CCGTCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

## m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VI PGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASAAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISAL TLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
g576-1.pep	DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH					
m576-1	DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMKFLQ EQQAKAVEKH					
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIV TVEYEGRLID					
m576-1	KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQEGKQPTKDDIV TVEYEGRLID					
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN GGPATFPLSQ VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN					
m576-1	GTVFDSSKAN GGPVTFPLSQ VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN					
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV KIGAPENAPAK QPDQVDIKK VN*					
m576-1	ATLVFDVKLV KIGAPENAPAK QPAQVDIKK VN*					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

## a576-1.seq

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```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  AC'TTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGAGCAGAG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GC'AAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CC'ATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GC'TCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAAGCCGT
351 AG'AAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TT'CTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CT'GCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CG'ACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TC'GACAGCAG CAAAGCCAAC GGGCGCCCGG TCACCTTCCC TTTGAGCCAA
601 GT'GATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AG'CCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GC'GACAAAAT CGGCCCGAAC GCCACTTGG TATTGATGT GAAACTGGTC
751 AA'ATCGGCGC CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CA'TCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

**a576-1.pep**

```

1  MNTIFKISAL TLSAALALSA CGKKEAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENA KDGVRTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

**a576-1/m576-1** 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGRKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGRKEAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	DIGRSLQMKEQGAEIDLKVFTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
m576-1	DIGRSLQMKEQGAEIDLKVFTEAMQAVYDQKEIKMTEEQAQEVMMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLENAAKDGVKTTASGLQYKITKQEGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

### Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577. seq..
1  atggaagga gcggtgtatt tggtaaaatt gtcggcaatc gcataactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatccttg ttcagagtgc gaagctgtcc gtgcgctgtt
151 tttatttacg gagcaaacat gaaacttata tataccgtca tcaaatcat
201 tatcctgctg ctcttcctgc tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcggggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttgcgt cgccatcgtg ttcggaatgt ttgccctggt
351 cggcgctg ctgtccttgc gcggcgaaaa cagccgctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacagcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577. pep
1  MERSGVFGKI VGNRILRMP EHAAYPKP CKSFKLTQSW FRVRSCPCGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTFSYLPG QSVNPLIVV
101 LFGAFVVGIV FGMFALFGR LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577. seq..
1  ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAACTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAACAT GAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCCGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTTGTAGT CGGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGC GCGTTT AC GGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577. pep..
1  MERNGVFGKI VGNRILRMS EHAASYPKP CKSFKLAQSW FRVRSCLGCV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTFSYLPG QKFDLPLIVV
101 LFGAFVVGII FGMFALFGR LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m577/g577 88.1% identity in 160 aa overlap

	10	20	30	40	50	60
m577. pep	MERNGVFGKIVGNRILRMSSEHAASYPKPCKSFKLAQSWFRVRSCLGCVFIYGANMKLI					
g577	MERSGVFGKIVGNRILRMPSEHAAYPKPCKSFKLTQSWFRVRSCPCGVFIYGANMKLI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m577. pep	YTVIKIILLFLLLAVINTDAVTFSYLPGQKFDLPLIVVLFAGAFVVGIIFGMFALFGR					

895

```

|||||
g577  YTVIKIIILLFLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577 .pep  LSLRGENRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
|||||
g577  LSLRGENSRLRAEVKKSARLSGQKLTAPPIQNAESAQKQPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577 .seq
1  ATGGAAGGA ACGGTGTATT TGGTAAATTT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAAATTCG ATTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CGTTTGTCTG CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TCGCGGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577 .pep
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSEKLAQSW FRVRSCPGGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENRL RAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577 .pep  MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSEKLAQSWFRVRSCPGGVFIYGANMKLI
|||||
a577  MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSEKLAQSWFRVRSCPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577 .pep  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIIFGMFALFGRL
|||||
a577  YTVIKIIILLFLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130     140     150     160
m577 .pep  LSLRGENRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
|||||
a577  LSLRGENRLRAEVKKNARLTGKELTAPPAQNAPESAKQPX
      130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578 .seq..
1  atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51  cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatgcg
151 gcggatttcg ctttcgctgt atttcattgt gttgtagcct tcgtgttcgc
201 cgtttttcaa aacacgggatg ccgcgcggtt cgcggaaata aatatcgccg
251 gtaagtccgc gcacaatcaa aatatccaaa ccggcaacga tttcaggcct
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578 .pep
1  MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGD
51  ADFAFVHFG VVAFVFAVFQ NTDAARFABI NIAGKFAHNQ NIQTGNDPRL

```





897

```

51. TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101. CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151. GCGCGGGGTT TGGCGGTGGC GTTGTCTTAA AAAGACCAGC TGTCCAATTT
201. TGCCGCCGGC GCGCTGATTA TCCTGTTCCT CCCGTTCAAA GTCGGCGACT
251. TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301. CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351. CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401. GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451. AAAGAGGCGG TGTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501. CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551. TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601. CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651. CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

g579.ppe..

```

1. MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51. GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101. QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151. KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRWTL
201. QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

m579.seq..

```

1. ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51. TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101. CATTGGGACG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151. GCGCGGGGTT TGGCGGTGGC GTTGTCTTAA AAAGACCAGC TGTCCAATTT
201. TGCCGCCGGC GCACTGATTA TCCTGTTCCT CCCGTTCAAA GTCGGCGACT
251. TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301. CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351. CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401. GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451. AAAGAGGCGG TGTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501. CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551. TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601. CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651. CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

m579.ppe..

```

1. MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51. GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101. QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151. KEAVLKAAAE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRWTL
201. QCDLNEQVVE NLRKVNINIP FPQRDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

	10	20	30	40	50	60
m579.ppe	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
g579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.ppe	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
g579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM					
	70	80	90	100	110	120

898

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	:     :     :     :     :					
g579	GNSIVNRSSLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAAEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	:     :     :     :     :					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

a579.seq

1	ATGAGGGCGG	CGATGACGCG	CGCGCAGGTC	GATGCCACGC	TGATTAGTTT
51	TTTGTGTAAT	GTTGCCAATA	TCGGCTTATT	GATTTTGGTG	ATTATTGCCG
101	CATTGGGCAG	ATTGGGCGTT	TCCACAACAT	CCGTAACCGC	CTTAATCGGC
151	GGCGCGGGTT	TGGCGGTGGC	GTGTCTCTTG	AAAGACCAGC	TGTCCAATTT
201	TGCCGCCGGC	GCGCTGATTA	TCCTGTTCCG	CCCGTTCAAA	GTCGGCGATT
251	TTATCCGCGT	CGGCGGTTTT	GAAGGATATG	TCCGAGAGAT	TAAAAATGGT
301	CAGACTTCTT	TGCGGACGAC	CGACAACGAA	GAAGTCGTGC	TGCCCAACAG
351	CGTGGTGATG	GGCAACAGCA	TCGTCAACCG	TTCCCACTG	CCGCTGTGCC
401	GCGCCCAAGT	GATAGTCGGC	GTGATTACA	ACTGCGATT	GAAAGTGGCG
451	AAAGAGGCGG	TGTTGAAAGC	CGCCGTCGAA	CACCCCTTGA	GCGTCAAAA
501	CGAAGAGCGG	CAGGCCGCCG	CCTACATCAC	CGCCTTGGGC	GACAATGCCA
551	TCGAAATCAC	ATTATGGGCT	TGGCCAAACG	AAGCAGACCG	CTGGACGCTG
601	CAATGCGACT	TGAACGAACA	AGTGGTCGAA	AACCTCCGCA	AAGTCAATAT
651	CAACATCCCG	TTCCCGCAAC	GCGACATACA	CATCATCAAT	TCTTAA

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

a579.pep

1	MRAAMTRAQV	DATLISFLCN	VANIGLLILV	IIAALGRLGV	STTSVTALIG
51	GAGLAVALSL	KDQLSNFAAG	ALIILFRPFK	VGDFIRVGGF	EGYVREIKMV
101	QTSRLRTDNE	EVVLPNSVVM	GNSIVNRSTL	PLCRAQVIVG	VDYNCDLKVA
151	KEAVLKAAVE	HPLSVQNEER	QAAAYITALG	DNAIEITLWA	WANEADRWTL
201	QCDLNEQVVE	NLRKVNINIP	FPQORDIHIIN	S*	

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	:     :     :     :     :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVM					
	:     :     :     :     :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	:     :     :     :     :					
a579	GNSIVNRSTLPLCRAQVIVGVVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	:     :     :     :     :					
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

```

1  A TGGACTTCA AACAAATTGA TTTTTCAC CTGATCAGTG TTTCCGGTTG
51  G GGGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 C GCTGCTTAT TTTCTTGGTC GGGAAATGGG CGGCGAAACG CATTGTCGCC
151 G TAATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 T TTTTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 C CGCATTGGG ACGGTTGGGC GTTTCACAA CATCCGTAAC CGCCTTAATC
301 G GCGGCGCGG GTTGGCGGT GCGTGTGTC TTAAGACC AGCTGTCCAA
351 T TTTGCCGCC GCGCGCTGA TTATCTGTT CCGCCGTTT AAAGTCGGCG
401 A CTTTATCCG TGTGCGCGT TTTGAAGGAT ATGTCGGGA AATCAAAATG
451 G TGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 C AGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCCAGC CTGCCGCTT
551 G CCGCGCCCA AGTGATAGTC GCGTCGATT ACAACTGCGA TTTGAAAGTG
601 G CGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCTT TGAGCGTTCA
651 A AACGAAGAG CGGCGCCG CCGCTACAT CACCGCCTTG GCGACAATG
701 C CATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 C TGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 T ATCAACATC CCGTCCCGC AACCGGACAT ACACATCATC AATTCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

**g579-1.pep**

```

1  M D F K Q F D F L H L I S V S G W G H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A
51  V M R A A M T R A Q V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I
101 G G A G L A V A L S L K D Q L S N F A A G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M
151 V Q T S L R T T D N E E V L P N S V V M G N S I V N R S S L P L C R A Q V I V G V D Y N C D L K V
201 A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W A W A N E A D R W T
251 L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

**m579-1.seq**

```

1  A T G G A C T T C A A A C A A T T T G A T T T T T A C A C T G A T C A G T G T T T C C G G T T G
51  G G A G C A T C T G G C T G A A A A G G C G T G G G C G T T C G G G C T G A A C C T T G C C G C G
101 C G C T G C T T A T T T T T T G G T C G G A A A T G G G C G G C G A A C G C A T T G T C G C T
151 G T G A T G A G G G C G G C G A T G A C G C G C G C A G G T C G A T G C C A C G C T G A T T A G
201 T T T T T G T G T A A T G T T G C C A A T A T C G G C T T A T T G A T T T T G T G A T T A T T G
251 C C G C A T T G G G C A G A T T G G G C G T T C C A C A A C A T C C G T A A C C G C T T A A T C
301 G G C G G C G C G G G T T G G C G G T G C G T T G T C C T G A A A G A C C A G C T G T C C A A
351 T T T T G C C G C G G G C G C A C T G A T T A T C C T G T T C G C C G T T C A A A G T C G G C G
401 A T T T T A T C C G C G T G G C G G T T T G A A G G A T A T G T C G G A G A G A T T A A A A T G
451 G T G C A G A C T T C T T G C G G A C G A C C G A C A C G A A G A G T C G T G C T G C C C A A
501 C A G C G T G G T G A T G G C A A C A G C A T C G T C A A C G T T C C A C A C T G C C G C T G T
551 G C C G C G C C C A A G T G A T A G T C G C G T C G A T T A C A A C T G C G A T T T G A A A G T G
601 G C G A A A G A G G C G T G T T G A A A G C C G C G T C G A C A C C C C T T G A G C G T T C A
651 A A A C G A A G A G C G G C A G G C T G C C G C T A C A T C A C C G C C T T G G C G A C A A T G
701 C C A T C G A A A T C A C A T T A T G G C T T G G G C A A A C G A A G C A G A C C G C T G G A C G
751 C T G C A A T G C G A C T T G A A C G A A A G T G G T C G A A A C C T C C G C A A A G T C A A
801 T A T C A A C A T C C G T T C C G C A A C G C G A C A T A C A C A T C A T C A A T T C T T A A

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

**m579-1.pep**

```

1  M D F K Q F D F L H L I S V S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A
51  V M R A A M T R A Q V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I
101 G G A G L A V A L S L K D Q L S N F A A G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M
151 V Q T S L R T T D N E E V L P N S V V M G N S I V N R S T L P L C R A Q V I V G V D Y N C D L K V
201 A K E A V L K A A V E H P L S V Q N E E R Q A A Y I T A L G D N A I E I T L W A W A N E A D R W T
251 L Q C D L N E Q V V E N L R K V N I N I P F P Q R D I H I I N S *

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	M D F K Q F D F L H L I S V S G W E H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q					
g579-1	M D F K Q F D F L H L I S V S G W G H L A E K A W A F G L N L A A A L L I F L V G K W A A K R I V A V M R A A M T R A Q					
	10	20	30	40	50	60
m579-1.pep	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
g579-1	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
	70	80	90	100	110	120
m579-1.pep	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
g579-1	V D A T L I S F L C N V A N I G L L I L V I I A A L G R L G V S T T S V T A L I G G A G L A V A L S L K D Q L S N F A A					
	130	140	150	160	170	180
m579-1.pep	G A L I I L F R P F K V G D F I R V G G F E G Y V R E I K M V Q T S L R T T D N E E V L P N S V M G N S I V N R S T					

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNDLKVAKAEVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTGTGTC GGAAATGGG CGGCGAAACG CATTGTCCGC
151 GTGATGAGGG CGGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTGTGTGT AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATTGGG CAGATTGGGC GTTTCACAA CATCCGTAAC CGCCTTAATC
301 GCGGCGCGGG GTTGGCGGTT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCC GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCGAGA GATTAAATG
451 GTGCAGACTT CTTTGGCGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTTCACA CTGCCGTGT
551 GCGCGGCCCA AGTGATAGT GCGTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCCGTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CGGCCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTCCCGC AACCGGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQDFDLH LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAARKIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVVLPSNVV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAY EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQDIHII NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQDFDLHLISASGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAARKIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQDIHIINSX

```

901

m579-1      |||||  
 AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQRDIHIINSX  
                  250        260        270        280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq  
 1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc  
 51 cgcgctcgag ccatttcga tggcaaggca gacttcgccg atcatgtcgc  
 101 caacggtcgg accgacaatg ccgcccgcga tgatgcggcc ggtttcggca  
 151 tcgaaaaatca gcttggtaaa gcggtgtcgc caaccgttgg caatcgcacg  
 201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg  
 251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg  
 301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..  
 1 MDSPKVGC GW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA  
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV  
 101 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..  
 1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGTTTTCGC CGATGTCTGC  
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC  
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCGGCA  
 151 TCAAAAATCA GCTTGGTAAA GCCGTTGTCG CAACCGTTGG CAATCGCACG  
 201 GCCGGAAGCC GCCCAGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG  
 251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGAAGTG  
 301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..  
 1 MDSPKVGC GW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA  
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV  
 101 \*

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGC GW MVLPSAASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA SKISLVKPLS					
g580	MDSPKVGC GW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA SKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEVX					
g580	QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq  
 1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGTTTTCGC CGATGTCTGC  
 51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCCG  
 101 CACCGTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTCAGCA  
 151 TCAAAAATCA GCTTGGTGAA ACCATTGTCG CAACCGTTGG CAATCGCACG  
 201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGAGG  
 251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG  
 301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep  
 1 MDSPKVGC GW MVLPSAASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA  
 51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

902

101 \*

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMSAASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSVSPHATSGEVX					
a580	QPLAIARPEAAHGKLALVILRPEALADNSVSPHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggtaaacc ggtatagaac aaaatacgtt
51 ctgtcgctgt ggttttacc gcacgatgat gggcggaat accgatgttg
101 cggtagagcg tgatcggggt cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagttagaga atgctttgtt ggcttcagcc atacggtgta
201 cttcttcacg tttttcaac gcacgcccac ggccttcgga cgcataatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttcggggc
301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ INGPLTTTFAG
101 RVANPTHQCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACCTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CCGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTCACG GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCTCG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATGCGCA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGPLTTTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLTTFAGRANPAHCQSQTAX					
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLTTFAGRANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

## a581.seq

```

1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTCGGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

## a581.pep

```

1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTQADRG LTSHFISLSK
51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTQADRG	LTSHFISLSKLETEVRECFV				
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX		
a581	GFSHTVYFFTFFQRTATAFG	RINQFACQTQVHGFLLTFAG	RINPAHCQSQTAX		
	70	80	90	100	110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

## g582.seq..

```

1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgttttg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttctcgc cgacagtgcg ggcgaaaccg ccgatatcta tacgccttgc
301 agcctgatgt acgacttgga caaaaacgat ttgcgcgggc tggtcggcgt
351 acgcgaacac aatccgatgt accttatgcc gtttgggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttcggacagc agaaacgtgc ggaacccaaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgc ttaaaacccg cgcggatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttccgca ataccgatta caaacctgaa atttccctga cccagcctgt
651 gaagggcgat ttgcccgtcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgct ccgaatcgcg ttctggaac
751 aggatattat ccattggcagg catggaatgg ggcaaattga cggtgattcc
801 gcgcgtgtgg gtgcgtgctg tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatggcgc acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgttaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttcogatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcgggtatc gggttgatgt tcaacgactg
1101 ggacgggcac tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

## g582.pep ..

```

1 MRYILLTGLL PTASAPGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPPFW NNSPNYAPSS PTRGTTVQEK
151 FGQKRAATK LQVSPKSKIA ENLFKTRADL WFGYTQSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDIDYDM GYGDKVLQYR
301 LNDRQNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKVVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1 ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51 AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CCGTCATTGT TGTGAAAAAA GCGGGGGATG
251 CGCTTCTCTG CGACAGTGGG GCGGAAACCG CCGACATCTA TAGCCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAAACGAT TTGCGCGGGC TGTGCGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCG
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAAATTGCC AAGATTGTGT TTAATAACCG CCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT CGGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CGAATCGCG TTGTTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAAATGA CCGTGATTCC
801 GCGCGTGTGG GTGCGTGGCT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CCACTATATG GGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGCGATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1 MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51 EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQOKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVPVWV VRAFDQSGDK NDNPDADYIM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTOYG AIEAAYTFPI KGLKGVVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLGI *
```

m582 / g582 98.6% identity in 370 aa overlap

	10	20	30	40	50	60
m582.pep	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYIMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYIMGYGDVKLQYR					
	250	260	270	280	290	300
m582.pep	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYIMGYGDVKLQYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVPVWVRAFDQSGDKNDNPDADYIMGYGDVKLQYR					
	310	320	330	340	350	360

905

```

m582.pep  LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
g582      LNDQRNVSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
          310      320      330      340      350      360

          370
m582.pep  GLMFNDLDGIX
          ||||| |||
g582      GLMFNDWDGIX
          370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.s eq
1   ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
1 01 CGTGTTACGA CAGGATTTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
1 51 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
2 01 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
2 51 CGCTTCTGCG CGACAGTGGC GCGGAAACCG CCGACATCTA TACGCCTTTG
3 01 AGCCTGATGT ACGACTTGGG CAAAAACGAT TTGCGCGGGC TGTGCGCGGT
3 51 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCGC
4 01 CCAACTATGC CCCGGGTTCG CCGACGCGCG GTACGACTGT ACAGGAAAAA
4 51 TTCGGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTCAAAAG
5 01 CAAAATTGCC GAAGATTGTG TTAACACCCG CCGGATCTG TGGTTCGGCT
5 51 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
6 01 CCGTTCCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
6 51 GAAGGCGGAT TTGCCGTTCC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
7 01 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
7 51 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
8 01 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CGGCGATAAA AACGACAATC
8 51 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
9 01 CTGAACGACA GGCAGAATGT GTATCCGTA TTGCGCTACA ATCCCAAAAC
9 51 GGGCTACGGC GCGATTGAAG CCGCTACAC GTTTCGATT AAGGGCAAAC
10 01 TCAAAGCGCT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
10 51 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
11 01 GGACGCGATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1   MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
1 01 SLMYDLKND LRGLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
1 51 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQSDW QIYNQGRKSA
2 01 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
2 51 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDKVLQYR
3 01 LNDQRNVSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
3 51 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

          10      20      30      40      50      60
m582.pep  MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          ||||| ||||| ||||| ||||| ||||| |||||
a582      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
          10      20      30      40      50      60

          70      80      90      100     110     120
m582.pep  LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRGLLGVREH
          ||||| ||||| ||||| ||||| ||||| |||||
a582      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPSLMYDLKNDLRGLLGVREH
          70      80      90      100     110     120

          130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
|||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQOKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

              190      200      210      220      230      240
m582.pep      WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRLGAGFVHQSN
|||||
a582          WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRLGAGFVHQSN
              190      200      210      220      230      240

              250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
|||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVKLQYR
              250      260      270      280      290      300

              310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKGNGIGI
|||||
a582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGKLGKGVVRGFHGYGESLIDYNHKGNGIGI
              310      320      330      340      350      360

              370
m582.pep      GLMFNDLDGIX
|||||
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1  atgataattg accaaagcca aatatttacc catcttgcc tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tgcactgcat aatcgatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gcccagcgtt tttcttcaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aaatcataac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaaacgca ctcaacgcat cgctcatcgc cgcgcccggg ttgtcggcgg
351 ttacgcgggt tactgcgacc aaccgcagcg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcc
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1  MIIDQSOIFT HLAFCAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIHRH RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1  ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTTCGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCAA
201 AAACGCGGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AAATCATAAC TCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCGGT TTGTGCGCGG
351 TTACGCGGGT TACTGCGACC AACCAGCGG CAATAATCGA CAGCGCGCCC
401 AACGCGATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACGAGGCG GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

907

551 CCCAATTCA TCATATTGAC CTCGTAATAA AAGACCGTCC CGAAAAATCG  
601 GAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ  
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI  
101 GERTQRIHR RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG  
151 QQRPSLRDLP VGYGQCQNG AQYCGNGEGY RFETQFHID LRKKDRPEKS  
201 EK\*

m583 / g583 98.5% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
g583	MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m583.pep	AQRFSKNGDK QISDTHPQP CFEQTARNHN CDGNQPNQRI GERTQRIHR RARFVGGYAG					
g583	AQRFSKNGDK QISDTHPQP CFEQTARNHN CDGNQPNQRI GERTQRIHR RARFVGGYAG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m583.pep	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRDLP VGYGQCQNG AQYCGNGEGY					
g583	YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG QQRPSLRDLP VGYGQCQNG AQYCGNGEGY					
	130	140	150	160	170	180
	190	200				
m583.pep	RFETQFHID LRKKDRPEKSEKX					
g583	RFETQFHID LRKKDRPEKSEKX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT  
51 TTGCGGGATT GGAGCCGTAA CTGCCGCAA TCGACTGCAT AATCGGATGT  
101 ATAATGCCGC CGCCGCGCG GGTATTGGAA GGGGTAACGG GAGCCAGCAG  
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGT TTTCTTCCAA  
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCAGCCC TGTTTTGAGC  
251 AAACCGCGCG AATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT  
301 GGCGAACGCA CTCACGCAT CGCTCATCGC CGCACC CGGT TTGTCGCGG  
351 TTACGCCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC  
401 AACGGCATGG CCTTGCCGAT AATGGCGGCA ATCACACCGA TAAACATGGC  
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA  
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA  
551 CCCAATTCA TCATATTGAC CTCGTAATAA AAGACCGTCC CGAAAAATCG  
601 GAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ  
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI  
101 GERTQRIHR RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG  
151 QQRPSLRDLP VGYGQCQNG AQYCGNGEGY RFETQFHID LRKKDRPEKS  
201 EK\*

m583/a583 99.0% identity in 202 aa overlap

	10	20	30	40	50	60
m583.pep	MIVDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					

a583	MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRGNGSQQQFGKSETVTD	10	20	30	40	50	60
		70	80	90	100	110	120
m583.pep	AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG						
a583	AQRFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG						
		70	80	90	100	110	120
		130	140	150	160	170	180
m583.pep	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY						
a583	YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY						
		130	140	150	160	170	180
		190	200				
m583.pep	RFETQFHHLDLRKKDRPEKSEKX						
a583	RFETQFHHLDLRKKDRPEKSEKX						
		190	200				

q584.seq. .

1	atgctgcgct	ctattttggc	ggcttcctcg	ctggcggtat	cttttcgggc
51	ggcggtcgag	gcattgaatt	acaattattgt	cgaattttcc	gaatcggcgg
101	gtatcagggt	ggctcaggat	acgaattgtccg	cgcttttcca	ggtagcgggc
151	gaaggcaggg	acaaaaatgc	cgtcaatgcc	gagttgttta	aaaaattcaa
201	caatttcacc	agaaaaatcga	aaaatggtag	ctttaaaacc	gaattggtat
251	cgcgcagtcg	gatgccgcgc	tatcaatatca	ccaacggcag	acgcattcaa
301	acaggctggg	aggagcgtgc	ggaatttaag	gcggagggca	gggattttga
351	tgcgttaaac	cggtttattgt	ctgatgttca	gcagcgatgct	tcgcttgaag
401	ataccgattt	cagcgtgtcg	cgcgaacgcg	gaaacagaggt	catcgatcag
451	gtcagcaagg	atgcgctttt	gcgtttcaag	gcgcgctccg	aaaaattggc
501	ggcgcttcg	ggtgcgttcg	gttataaaat	cgtcaaatgt	aattttggcg
551	aaatcgccag	ccatattgcg	ggcgatgggg	ctgttcgggc	aaaaatgctg
601	cgcgcgatcg	cgatggcggc	aagcgtcaat	atgaagggta	cggattcagc
651	cgcaccgggt	gtggaggaaa	tcagcatcag	catcaatggg	acggttcagt
701	ctctaa				

q584.pep Length:..

```

1  MLRSILAAFL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKKFNNT RSKSNGSFKT ELVSRSAFPR YQYTNGRIRI
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RRRRNEVIDQ
151 VSKDAVLRFK ARAEKLAGVL GASGYQIVKL NFGQIGSHA DGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEISISING TVQP*

```

m584.seq. .

1	ATGTTGCGTC	TTGTTTGGC	GGCTTCGCTG	TCGGCGGTAT	CTTTCCGGC
51	AGCGGCTGAA	GCAATGAATT	ACAATATTGT	CGAATTTTCC	GAATCGGCGG
101	GTGTCGAGGT	GGCTCAGGAT	ACGATGTCCG	CAGTTTCCA	AGTGA CGGCG
151	GAGGACGGG	ACAAAAATGC	CGTCAATGCT	GAGTTTGTA	AAAAATCAA
201	CAAGTTCATC	AGAAAAATCGA	AAAATGGTAG	CTTTAAAAAC	GAATTGGTAT
251	CGCGCAGTGG	GATGCCGCGC	TATCAATATA	CCAACGGCAG	ACGCATTCAA
301	ACAGGCTGGG	AGAGCGGTGC	GGAATTTAAG	GTGGAAGSTA	GAGATTGTGA
351	TGAGTTAAAC	CGTTTATTATG	CCGATATTCA	AGCAGATGCC	CGGTTGGmAT
401	ATACGGATT	CCATGTGTGTG	CGCGAAGGCC	GCAACGGAGT	CATCATCAGT
451	GTACGCAAGG	ATGCCGTTT	GGGTTTCAAG	CGCGCTGGCG	AAAATTTGGC
501	GGGCGTTTGT	GGTGCGTCCG	GTTATAAAAT	GCTCAAAATG	AAATTGGGAC
551	ACATCGGCAG	CCATATCGCG	GGAGGGGGAG	CTGCTCAGGC	AAAAATGCTT
601	CGTGCCATGC	CGATGGCGGC	AAGCGTCAAT	ATGAGGGGTG	CGGATTCCGC
651	CGCGCCTGGT	GTGGAGGAAA	TCAGCATCAG	CGTCAATGGG	ACGGTTCAGT
701	TCCTGA				

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1 MLRLVLAASL SAVSFPAABE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNKFI RSKNGSPKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAIEFK VEGRDDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

      10      20      30      40      50      60
m584.pep MLRLVLAASLSAVSFPAABEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
      ||| :|||
g584      MLRSILAASLLAVSFPAABEALNYNIVEFSSESAGIEVAQDTMSARFQVAEGRDKNVNA
      10      20      30      40      50      60

      70      80      90     100     110     120
m584.pep EFVKKFNKFIKSKNGSPKTELVSRSAMPRYQYTNRRRIQTGWEERAIEFKVEGRDDELN
      ||| :|||
g584      EFVKKFNFTKSKNGSPKTELVSRSAMPRYQYTNRRRIQTGWEERAIEFKVEGRDDELN
      70      80      90     100     110     120

      130     140     150     160     170     180
m584.pep RFIADIQADAALXYTDFHVSERRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL
      ||| :|||
g584      RFIADVQTDASLEDTFVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL
      130     140     150     160     170     180

      190     200     210     220     230
m584.pep NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
      ||| :|||
g584      NFGQIGSHIAGDGAVERAKMLRAMPMAASVNMKGTDAPGVEEISISVNGTVQFX
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

```

a584.seq
1 ATGTTGCGTT CTATTTTGGC GGCTTCCCTG CTG.....
51 .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAATGTC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTCAAC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGGGTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1802; ORF 584.a&gt;:

```

a584.pep
1 MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51 EGRDKNVNA EFVKKFNFT RSKNGSPKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAIEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

      10      20      30      40      50      60
m584.pep MLRLVLAASLSAVSFPAABEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
      ||| :|||
a584      MLRSILAASLL-----IVEFSSESAGVEAVQDTMSARFQVTAEGRDKNVNA
      10      20      30      40

```

910

	70	80	90	100	110	120
m584 . pep	EFVKKFNKFIKRSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNNTKRSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584 . pep	RFIADIQADAALXYTDFHVSRRERNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRERNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584 . pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585 . seq . .

```

1  atgaaactgt  tccaacgcat  ttctgccaca  ttttgccg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattatgt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gcccgtctc  atccgctgtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaac  gctatatcga  caattacacc
301  atagaacgcg  cccggtctgt  tgccgccaac  aacccccatt  ccaacctgtg
351  ccgcatcgaa  tacgaccgtt  tcggcgaa  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccctggcg  ttgcccgcgt  ttggcacgaa  ttcateatcc  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aacccatcag  aatcttaggc  aacggcatgg  acaggggtgc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585 . pep . .

```

1  MKLFQRIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQDEKKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGBEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLFLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCCQVR  DRDELADVA  MQPDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585 . seq . .

```

1  ATGAAACTGT  TCCAACGCAT  TTTGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCGG  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATCCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAGACA  GCCCGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCGGCTTTT  CGCCGCCGGA  CACCGGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCTGCG  CCAGCCCCCT  GTTGATCCCC
451  GGCCTGCGCG  TCGCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGAATGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AATCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AACCGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCG  ACAAATGGT  GGAATAACTC  GAAAAACTCG
701  TTGCCAAAGA  ACGCCACCTG  CTCCATCAG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTGCGA  CTGATTCAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACTG  TTAACCTGT  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGCTGCGGA  CGGAAAAATC  CCCGAAAACA  CAACATCCT  TGCCAACGAA

```

```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGA CGAAATGCAG
1201 CTCCCGCACA TCTTACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGBT TCCAAAACAG AAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLQRIQIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRRAG DAGAREILTE WKDSPVSSGV YVIQDEKQD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELHLA IQFDKMVEKL EKLVAKEHRL LHHVSHMRS
251 PLARMQAIIV LIQAQPKQOE QYLKRLEGEL TRMDTLAGEL LTLRLETNS
301 MALEKESLKL LPFLGNLVED NQSIQAQNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFQNV IRNAVNYSPS GSTILINIGQ DHKHWIIDVT DNGPGVDEM
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCCKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

	10	20	30	40	50	60
m585.pep	MKLQRIQIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFRRAG					
g585	MKLQRIQIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRRRTIETTLMGSIISAFKTRG					
	10	20	30	40	50	60
m585.pep	DAGAREILTEWKDSPVSSGVYVIQDEKQDILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
g585	DNGAREILTEWKNSPVSSAVYVIQDEKQDILNRYIDNYTIERARLFAANNPHNSNLVRIE					
	70	80	90	100	110	120
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPILLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
g585	YDRFGEEYLF FIKGWDNHQAQRLPSPLFIPLGLPLAPIWHEFIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDRDDELHLAIQFDKMVEKLEKLVAKEHRL					
g585	NIAKPIRILGNGMDRVAERELEDRVCQQVRDDELADVAMQFDTMVEKLEX					
	190	200	210	220	230	240
m585.pep	LHHVSHMRSPLARMQAIIVGLIQAQPKQOEQYLKRLEGELTRMDTLAGELLTLRLETNS					
g585	LHHVSHMRSPLARMQAIIVGLIQAQPKQOEQYLKRLEGELTRMDTLAGELLTLRLETNS					
	250	260	270	280	290	300
m585.pep						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAACTGT TCCAACGCAT CTTGCCACA TTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATTT CCGCATTCGG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCGGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCCGAT TTGGCACGAA CTCATCATAT TGTCTTCAT
501 CATCATCGTC GGAATGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AACCCATCAG AATCTTAGGC AACGGCATGG ACAGGTGGC AACCGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTGCAC GACCGCGACG ACGAATTGTC

```



```

651 CCATCTTGCC ATCCAATTCG ACAAATGGT GGAAAACTC GAAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTGCGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAAGT TTAACCCTGT CCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```

1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQDEKDD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHMERS
251 PLARMQAIVG LIQAQPKQKE QYLKRLEGEL TRMDTLAGEL LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNSPE GSTILINIGQ DHKHIIIDVT DNGPGVDMEQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG					
a585	MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQDEKDDILNRYIDSYTIERARLFAAGHPHNSNLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQDEKDDILHRYIDSYTIERARLFAAGHPHNSNLVHIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLF FTKDWDKLQARRLPSLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNGMDRVANGELETRISQQVDDRDELSHLAIQFDKMVEKLEKLVAKERHL					
a585	NIAKPIRILGNGMDRVANGELETRISQQVDDRDELSHLAIQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m585.pep	LHHVSHMERSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELLTLRLETSN					
a585	LHHVSHMERSPLARMQAIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGELLTLRLETSN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m585.pep	MALEKESLKLPLFLGNLVEDNQSIQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV					
a585	MALEKESLKLPLFLGNLVEDNQSIQKNGQTVTSLADGKIPENTTILANESYLYRAFDNV					

913

	310	320	330	340	350	360
m585.pép	370	380	390	400	410	420
	IRNAVNYSPGEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPGEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
m585.pép	430	440	450	460	469	
	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1809>:

g586.seq..

```

1  atggcagccc atctcgaaga acaacaagag ttagacaact ttaaatattt
51  ttggaaaacc acgggcaaat ggctgtttgc cctgctgatt ttggcggcac
101 tcggctactt gggatacacg gtttaccaaa accgtgcggc ttcccaaat
151 caggaagcgg cggcgggtgt ggcaaacatc gtggaaaagg cgcaaaacaa
201 agcccccgaag agcgaaatca atgcggaact gtccaaactc caacaaagct
251 acccccattc catttccgcc gcccaagcca cgctgatggc ggcggcaacc
301 gaatttgacg cgagcggtta cgatgttgcc gaaggtcatt tgaatgggt
351 gttgtccaac caaaaagaca gcctgattca ggcgttgagg ggcgagcgtc
401 tggcggttgt gttgttgcaa caaaaaaat acgatgccgc gcttgccgca
451 ctccgacacg cggttgaggg ggacttcgcc cccctgctga tggaaactaa
501 aggcgatggt tatgccgcac aggaaaaaag ccaggaagcc ttaaaaaact
551 acggacaggg tttgaaaaaa atgcctcaag attctgtcgg tcgcgaattg
601 cttcaaatga aactcgattc gctgaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1810; ORF 586.ng>:

g586.pep..

```

1  MAAHLEEQQE LDNFKYFWKT TGKWLFPALLI LAALGYLGYT VYQNRRAASQN
51  QEAAAVALANI VEKAQNKAPQ SEINAEISKL QOSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKWLVLN QKDSLIQALA AQLGVLVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 LQMKLDSLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1811>:

m586.seq

```

1  ATGGCAGCCC ATCTCGAAGA ACAACAAGAG TTAGACAAC TTAATATTT
51  TTGGAAGAAC ACGGGCAAAAT GGCTGTTTGC CTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAA ACCGTAAAGT TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTAGAAAAGG CGCAAAGCAA
201 AGCCCGCGCA AGCGAAATCA ATGCCGAAT GACCAAACTC CAACAAAGCT
251 ACCCGCATTC CATTCCGCC GCCCAAGCCA CACTGATGGC GGCGGCAACC
301 GAATTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAATGGGT
351 GTTGTCCAAC CAAAAGACA GCCTGATTCA AGCGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACATGCCCG GCTTGCCGC
451 CTCGATACGC CGGTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGAAAAAG CCAGGAAGCC TTAATAAAT
551 ACGGACAGGC TTTAGAAAA ATGCCTCAAG ATTCTGTCG TCGCAATTG
601 GTTCAAATGA AACTGATTG GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1812; ORF 586>:

m586.pep

```

1  MAAHLEEQQE LDNFKYFWKT TGKWLFPALLI LAALGYLGYT VYQNRKVSQN
51  QEAAAVALANI VEKAQSKAPQ SEINAEITKL QOSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKWLVLN QKDSLIQALA AQLGVLVLLQ QKKYDAALAA
151 LDTFVEADFA PLLMETKGDV YAAQKSQEA LKNYQALEK MPQDSVGREL
201 VQMKLDSLK*

```

m586 / g586 97.1% identity in 209 aa overlap

	10	20	30	40	50	60
m586.pep	MAAHLEEQQE LDNFKYFWKT TGKWLFPALLI LAALGYLGYT VYQNRKVSQN QEAAAVALANI					

914

```

g586      MAAHLEEQQELDNFKYFWKTTGKWLFAALLILAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAE LTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWL VLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      VEKAQNKAPOSEINAE LSKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWL VLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

           190     200     210
m586.pep  LKNYGQALEKMPQDSVGR ELVQMKLDSLKX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g586      LKNYGQALEKMPQDSVGR ELQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1  ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAAC TTAATATTT
51  TTGGAACACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTGCGGC TTCCCAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAAGCT
251 ACCCCCATTC CATTTCCGCC GCCCAAGCCA CGTGATGGC GGCAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTC AAC CAAAAGACA GCCTGATCCA GCGGTTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAGG CCAGGAAGCC TTAATAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1  MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASQN
51  QEAAAVLANI VEKAQNKAPO SEINAE LAKL QSYPHSISA AQATLMAAAAT
101 EFDAQRYDVA EGHKLKWL VLSN QKDSLIQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGKSQEA LKNYGQALEK MPQDSVGR EL
201 VQMKLDSLK*

```

m586/a586 97.6% identity in 209 aa overlap

```

           10      20      30      40      50      60
m586.pep  MAAHLEEQQELDNFKYFWKTTGKWLFAVLI LAALGYLGYTVYQNRAASQNQEAAAVLANI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      MAAHLEEQQELDNFKYFWKTTGKWLFAVLI LAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAE LTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWL VLSN
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      VEKAQNKAPOSEINAE LAKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWL VLSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a586      QKDSLIQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGKSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586. pep      LKNYGQALEKMPQDSVGRELVMKLDLKLKX
                |||||
a586           LKNYGQALEKMPQDSVGRELVMKLDLKLKX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587. seq..
1   atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51  ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatcccg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggcagcggca gctatctgtg gcacgaagaa cgcaactcgc acggcaacgg
351 caaaacccgc acaaacgga tgtccgacat atccgcgggc atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587. pep..
1   MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSNSR
51  AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587. seq..
1   ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51  TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGGCG TACGGACTGA CCGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAACTCG ACGGCAACAG
351 CAAAACCGGC AACAAACGGA TGTCGACGCT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CGCCCGCCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTTGCTGC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587. pep..
1   MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10

20

30

40

50

60

916

```

m587. pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENSRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587. pep      TGATSFIPTEIQENGSNITMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           TGATSFIPTEIQENGSNITMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

                130     140     150     160     170     180
m587. pep      NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
g587           NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKRGKLCFPYNLRINYEY
                130     140     150     160     170     180

                190     200     210     220     230     240
m587. pep      LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587. seq
1  ATGAAGCGCA TCTTTTGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAAGTGG CCGCACCAGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCACGCT CGGTTTGCGC TACGGACTGA CCGGGAATAC CGACATTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTCGCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCGTCGTC CTCTCATTGA
551 CCGCTGCCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587. pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNRR
51 AEELAAPVYIQ TGATSFIPIP TEIQENGSNIT DMLVGTGLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

                10      20      30      40      50      60
m587. pep      MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
a587           MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSITYLNSENNRAELAAPVYIQ
                10      20      30      40      50      60

                70      80      90      100     110     120
m587. pep      TGATSFIPTEIQENGSNITMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
                |||||:|||||:|||||:|||||:|||||:|||||:|||||
a587           TGATSFIPTEIQENGSNITMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
                70      80      90      100     110     120

```

	130	140	150	160	170	180
m587. pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587. pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLGRQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587. pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1   atgcttaaac atctcgatt cctactgcc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagagac gggcttcctt caggcaaagg catatggcgt
151 tggcgggatg ggcgcgggta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataccg ttgccgccgg ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1   MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1   ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCTGA CTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAGAC GGTAAACCG CCGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCT TTTAAAAACG GCAAATTCGA
201 CGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAG GCTTGGCACA CGGCAGATT ACCGTCTCGC AAAACGGCGA
351 AACCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1   MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTIWR
51  QDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10            20            30            40            50            60



```

301 atcggatatgg tagggatgat gctaaaaggg ctgaattgga cacggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaagc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgcgatttta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggctgta tgggtatcgg ttttgtgtcg
601 ctgggtaagt ttttgaaca ccgcaccaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttatc
751 cgcaccaacc acggcgaacg catcgtgcc gacggcatta tcgaaagcgg
801 cagcggttgg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggg gggcggcaaa gtgttggcgg gcgcgctgat gaccgaaggg
901 agcgtggtgt accgcgcgcg gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagtaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaactgt cgtgggcac
1051 gcgcttctga cttttatcgt tgcttggctg attaagggcg attggacggt
1101 cgcactgatg cacgccgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gaccctgcc gcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttaa agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtattgg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttgc gcgcgttat tacgttccc acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgccg cccaccgcgt
1401 cgcccgcgc atcgtctccg ccgcacaagc gcgcggttg gagattcccg
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagt
1501 gaaggcgtgg gtttggtaaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgg atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaag tacggtcgaa tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaact caaagccgcc ggcaaaaccg tggcgatggt
1851 cggcgacggc atcaacgacg cggccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcggtgcg gacgttgccg aacacaccgc ctccgcacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatatggg cattccgctc gccgcgctcg gctttttaaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcgggt tcggtattgg gcaatgcctt
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIAKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGMVGMMLKG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEKKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVALM HAVAVLVIAV PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAABVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGA DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTTGAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCCGCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTCT

```



```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACTGGG TAAATTTTGG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGGCGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTG GCGGGGCGCG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AAGCCAGCTC GCGGACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TCGCGCGTA GCCGATAAAG
1001 CCGCTGCGGT ATTCGTGCCT GCCGTGCTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTAAACA CGGTATTGGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCAGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCGG
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCCGCGCGG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCGCGC CAAGCGCGCG GTTGGACAT TCCCGCCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGCGGTT TGGGATATTG CAAGCATTGT TCGGGTCTCA GTCGATAACA
1601 AACCATCGG CGCATTCGCA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGGCG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGATTTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTG
2051 CTCTCGCCGC GCTTGGCTTT TTAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADI AKI IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LFTINV PFL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151 DHLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVEFEVGMV IGFVSLGKFL
201 EHRTKSSLN SLGLLLKLTQ TQNVNQRNGE WKQLPIDQVQ IGDILIRANH
251 ERIAADGIE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTESGVVYR
301 ATQLGSQTQL GDMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTE
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEA AHVDAVVDK TGTLTGSPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKQ LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADI AKI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

921

g589 MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIKI  
10 20 30 40 50 60

m589.ppep IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVFPFLIGMAGMMIG-----RHDWMI  
70 80 90 100 1 110  
|||||:|||||:|||||:|||||:|||||:|||||

g589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLTINIPFLIGMVGMMLKGLNWTNRHDWMI  
70 80 90 100 110 120

m589.ppep PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA  
120 130 140 150 160 170  
||:|||||:|||||:|||||:|||||:|||||:|||||

g589 PPVWQFVLASIVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA  
130 140 150 160 170 180

m589.ppep AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP  
180 190 200 210 220 230  
|:|||||:|||||:|||||:|||||:|||||:|||||

g589 AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP  
190 200 210 220 230 240

m589.ppep IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG  
240 250 260 270 280 290  
|||||:|||||:|||||:|||||:|||||:|||||

g589 IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLAGALMTEG  
250 260 270 280 290 300

m589.ppep SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPVVGIALLTFFIVTWL  
300 310 320 330 340 350  
|||||:|||||:|||||:|||||:|||||:|||||

g589 SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVGIALLTFFIVAWL  
310 320 330 340 350 360

922

	360	370	380	390	400	410
m589 . pep	IKGDWTVVALMHAVAVLVIAACPCALGLATFAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVVALMHAVAVLVIAACPCALGLATFAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589 . pep	VVLDKTGTLTEGSPQVAAYVCPD SGFDE DALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPD SGFDE DALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589 . pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSGKAEFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589 . pep	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSALKADTAEAIIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589 . pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589 . pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVSVLGNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589 . pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

```

a589 . seq
1  ATGCAACAAA AAGTCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCATG
51  TGCTTCGCGC ATTGAAAAAG TGTGAACAA AAAAGATTTT GTCGATTCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCTC AGGTAGTGT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GAGGTTGTGG CTTTGTCTGG CCATCAATAT CCCGTTCCCTT
301 ATCGGTATGG TAGGGATGAT GCTAAAAGGG CTGAATTGGA CACGGCATGA
351 TTGGATGTTG TCGCCCTTGT TGCACTTTGC ATTGGCGAGT GTGGTGCAGC
401 TTTGGCTGGC GGTGCCATTT TACAAAAGCG CGTGGGCGAG CATTAAAGGC
451 GGGCTGGCGA ATATGGACGT ACTCGTTACC ATCGGCACGG TCTCGATTTA
501 CCTGTATTCC GTCTATATGC TGTTTTTCAG CCCGCACGCG GCGTACGGTA
551 TGGCGCATGT GTATTTTGAA GTAGGCATAA TGGTGATTGG TTTTGTGTCA
601 CTGGGTAAAT TTTTGGAACA CCGCACCAA AAATCCAGCC TGAACAGCTT
651 GGGCTTGCTG CTCAAATCA CGCCAACCCA AGTCAACGTG CAACGCGATG
701 GCGAATGGCG GCAGCTACCC ATCGACCAAG TGCAATCGG CGACCTAATC
751 CGCGCCAATC ACGGCGAACG CATTGCCGCC GACGGCATCA TAGAAAGCGG
801 CAGCGGCTGG GCGGACGAAA GCCATCTTAC CGGCGAATCC AATCCGGAAG
851 AGAAAAAGGC AGGCGGCAAA GTATTGGCGG GCGCGCTGAT GACTGAAGGC
901 AGCGTGGTGT ACCGCGCCGC GCAGCTCGGC AGCCAAACCC TGCTCGGCGA
951 CATGATGAAC GCGCTCTCCG AAGCGCAAGG CAGTAAAGCA CCGATTGCGC
1001 GTGTGGCGGA CAAGGCGGCG GCGGTATTCC TGCCTGCCGT TGTGGGCATC
1051 GCACTTTTGA CTTTATCGC TACTTGGCTG ATTAAGGGCG ATTGGACGCT
1101 CGCATTGATG CACGCCGTCG CCGTTTGGT GATTGCCTGC CCGTGTGCAC

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTGCG CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAACGCGG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCAGGC GCGCGGTTG GAGATTCCCA
1451 CCGCACAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTGGTAATA AGCAGGCAAA GCCGAATTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAA CGGCAAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCGAAGC CATAGCCGT CTGAAAAAAC ACAATATCGA
1701 TGTCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 KCCGCCGAAG TGCAGAACT CAAAGCCGCC GGCAAAACCG TGGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCCGCGCT CGCCGCGGCC AACGTCAGCT
1901 TCGCCATGAA AGGCGGTGCA GACGTGCGG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTTTAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGTAATAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

```

a589.pep
  1  MQQKVRFOIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
 51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101  IGMVGMMLKG LNWTRHDWML SPLLOFALAS VVQLWLAVPF YKSAWASIKG
151  GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201  LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251  RANHGERIAA DGIIESGSGW ADESHLTGES NPEEKAGGK VLAGALMTEG
301  SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351  ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401  KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKQPQAAVY CVPDSGFDED
451  ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501  KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551  KADTAEAGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601  AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGA DVAEHTASAT
651  LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701  AGAAMAASSV SVLSNALRLK RVKID*

```

m589/a589 94.9% identity in 725 aa overlap

```

          10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      MQQKVRFOIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
          10      20      30      40      50      60

          70      80      90     100      110
m589.pep  IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLAINIPFLIGMVGMMMLKGLNWTRHDWML
          70      80      90     100      110      120

          120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAI PFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      SPLLOFALASVVQLWLAVPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
          130     140     150     160     170     180

          180     190     200     210     220     230
m589.pep  AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWRQLP
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a589      AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
          190     200     210     220     230     240

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924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
a589	250	260	270	280	290	300
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPVAVGIALLTFTVITWL					
a589	310	320	330	340	350	360
	SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPVAVGIALLTFTATWL					
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
a589	370	380	390	400	410	420
	IKGDWTLALMHAVAVLVIA PCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVAAVYCVPSGDFEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
a589	430	440	450	460	470	480
	VVLDKTGTLTGEGKPQVAAVYCVPSGDFEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTIVGAGITA EGVGLVKAGKA EFAELALPKFLDGVWDIASIVAVSVDNKP					
a589	490	500	510	520	530	540
	EIPTAQNAQTIVGAGITA EVKAGLVKAGKA EFAELTLPKFSDGVWEIASVAVSVNGKP					
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTA EAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
a589	550	560	570	580	590	600
	IGAFALADALKADTA EAIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVMVGDGIN DAPALAAANVSFAMKGGADVAEHTASATIMQHSVNQLA					
a589	610	620	630	640	650	660
	AAEVQKLKAAGKTVMVGDGIN DAPALAAANVSFAMKGGADVAEHTASATIMQHSVNQLA					
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
a589	670	680	690	700	710	720
	DALSVSRATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSSVLSNALRLK					
m589.pep	720					
	RVKIDX					
a589	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcgga gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctgggttac ctctacggaa acgacggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtggttga acagccggtt acgctggtta accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgctgtaa acggaaaaag ttttggaaac cttttttggg aaacaagttc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtggtc cgcgtttcga ttatgaagaa ctgtcgggca tcaggctgca

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925

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501 ctgggaagggc ctgacggggg aaacggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggtca aaatcaagct ggcagacaaa
601 ggcgatgccc cggttgaaaa agcgcatctt gattcggaat cttcagacgg
651 catcaatccc cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gtcaacctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctgggt ttttcaacca
851 agaccgggga atcgggcgcg tttatcgaca gcgaagggcg gttccgtttc
901 gatacgttgg tgtacggcga tgaaaaatac ggcccgttgg acatccatat
951 cgctgcgcaa cacctcgatg cttctgcctt aacogtattg aaacgcaagt
1001 ttgacacaaa ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgcgg cagtcaaagg cgatgcttcc ggattattta cccatgaccc
1101 ggtactaaaat atcaaaattt tccgcttcac cctgcctcag ggaataattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggaa tgatgtttaa gaaaaccgag gcaaacatca gaatgagtat
1251 tccctcaaaa atgttggaag atttggcggg aagtcaggct ggaatatatt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatggtggac agtacggtcc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggtcattt
1451 cccttaaaaa caacgcctg aagttaaacg ggaaaacgct gcaaaatgaa
1501 ccgatccctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVAEES LTQQQKILQK TGFLTVESHQ
51 YDRGWFSTSE TTVIRLKPFL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTOAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNSYDA PLFKIKLADK
201 GDAAFKAHAF DSETSDGINP LALGSSNLT L EKFSLEWKEG VDVNVKLNEL
251 VNLVTDLQIG APINPNISIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTBEEQIRND
351 LIAAVKGDAS GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMMKEDLN
401 QLGLMLKKEE ANIRMSIPQK MLEDLAVSQA GNIFSVNAED BAEARASIAE
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNAL KLNGKTLQNE
501 PDPDFDEGDM VSGQPH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 .. TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAAATACC TGCCGGATAA CCTGAAAACA GTGTGTGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCCGGCAGC AGCGGTACAT TGAAACCGAG TTCAAATACG CGCCTGAAAC
201 GGAAAAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAA GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AGCTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGTTT CAAAGCTAC CCGAACGGCT
401 ATGATGCCCC CTGTGTTTAA ATCAAGCTGG CAGACAAAGG CGATGCCCGC
451 TTTGAAAAAG TGCATTTTGA TTCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAAGTGT CAATCTTGT
601 ACCGATTTGC AGATTGGCGC GTTTATCAAT CCCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCGCTGGAC ATCCATATCG CTGCGGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTTACC AACAATCCCG TATTGGACAT
951 TAAAACCTTC CGATTACGCG TGCCATCGGG AAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 TTGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCCAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTTCA AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGGCGACC AGATTGATAC TGCCATTCT CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGTT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

## m590.pep. (partial)

```

1  WFTSMETTVI RLKPELLNNA RKYLPDNLKT VLEQPVTLVN HITHGPFAGG
51  FGTQAYIETE PKYAPETEKV LERFFGKQVP ASLANTVYFN GSGKMEVSVF
101 AFDYEELSGI XLHWEXLTGE TVYQKGFKSY RNYGDAPLFK IKLADKGDAA
151 FEKVHFDSET SDGINPLALG SSNLTLEKFS LEWKEGVVDYN VKLNELVNLV
201 TDLQIGAFIN PNGSIAPSKI EVGKLAFSTK TGESGAFINS EGQFRFDTLV
251 YGDEKYGPLD IHIAAEHLDA SALTVLKRKF AQISAKKMT EQIRNDLIAA
301 VKGEASGLFT NNPVLDIKTF RFTLPSGKID VGGKIMPKDM KKEDLNQLGL
351 MLKKT EADIR MSIPQKMLED LAVSQAGNIF SVNAEDEAG RASLDDINET
401 LRLMVDSTVQ SMAREKYLT NGDQIDTAIS LKNNQLKING KTLQNEPEPD
451 FDEGGMVSEP QQ*

```

m590 / g590 93.1% identity in 462 aa overlap

```

                                10      20      30
m590.pep                      WFTSMETTVIRLKPELLNNA RKYLPDNLKT
g590                          VKAESLTQQQKILQKTGFLT VESHQYDRGWFTSTETT
                                30      40      50      60      70      80
m590.pep                      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
g590                          VLEQPVTLVNHITHGPFAGGFGTQAH IETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
                                90     100     110     120     130     140
m590.pep                      GSGKMEVSVPAFDYEELSGIXLHWEXLTGETTVYQKGFKSYRNYGDAPLFKIKLADKGDAA
g590                          GSGKMEVSVPAFDYEELSGIRLHWEGLTGETTVYQKGFKSYRNSYDAPLFKIKLADKGDAA
                                150     160     170     180     190     200
m590.pep                      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVVDYNVKLNELVNLVTDLQIGAFIN
g590                          FEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVVDYNVKLNELVNLVTDLQIGAFIN
                                210     220     230     240     250     260
m590.pep                      PNGSIAPSKIEVGKLAFSTKTGESGAFINSEGGFRFDTLVYGDEKYGPLDIHIAAEHLDA
g590                          PNGSIAPSKIEVGKLAFSTKTGESGAFIDSEGRFRFDTLVYGDEKYGPLDIHIAAEHLDA
                                270     280     290     300     310     320
m590.pep                      SALTVLKRKFAQISAKKMT EEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
g590                          SALTVLKRKFAQISAKKMT EEQIRNDLIAAVKGDASGLFTHDPVLN I KIFRFTLPQ GKID
                                330     340     350     360     370     380
m590.pep                      VGGKIMPKDMKKEDLNQLGLMLKKT EADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAG
g590                          VGGKIMPKDMKKEDLNQLGLMLKKT EANIRMSIPQKMLEDLAVSQAGNIFSVNAEDEARA
                                390     400     410     420     430     440
m590.pep                      RASLDDINETLRLMVDSTVQSMAREKYLTNGDQIDTAISLKNQLKINGKTLQNEPEPD
g590                          RASIADINETLRLMVDSTVQSMAREKYLTLDGNQIDTVISLKNALKLNGKTLQNEPD PD
                                450     460     470     480     490     500
m590.pep                      FDEGGMVS-EPQQX
g590                          FDEGDMVSGQPHX
                                510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCAGCCTT TATTATTGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGAA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGTGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCTT
301 TTTGCCGGCG GATTCCGGAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTTGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTGGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GCGGATGCCG CGTTTGAAAA AGTGCAATTC GATTGCGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTAC GCTGCCATCG GAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGAAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGCGCA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAES LTQQQKILQE AGFLTVESHO
51  YERGWFTSTE TTVIRLKP EL LHNAQKYL PD NLKTVLEQ PV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTlNGDQID TAISLKNQL KLNGKTLQNE
501 PEPDFDEGGM VSEPQQ*
```

m590/a590 97.8% identity in 462 aa overlap

```

                                     10      20      30
m590.pep                               WFTSMETTVIRLKPPELLNNARKYLPDNLKT
a590      VKAESLTQQQKILQEAGFLTVESHOYERGWFTSTETTVIRLKPPELLHNAQKYL PDNLKT
           30      40      50      60      70      80

           40      50      60      70      80      90
m590.pep  VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
a590      VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN
           90     100     110     120     130     140

           100     110     120     130     140     150
m590.pep  GSGKMEVSVPAFDYEE LSGIXLHWEXLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDA
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928

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|||||
a590      GSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKGFSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVVDYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVVDYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGOFRFDTLVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGOFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTNPNVLDIKTFRFTLPSPGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTLNGDQIDTAISLKNQLKLNKGTQLONEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTLNGDQIDTAISLKNQLKLNKGTQLONEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPQQX
          |||||
a590      FDEGGMVSEPQQX
          510

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTTCGGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGGG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGCTCTGA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCGG GATTCCGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCGG CGTTTGAAAA AGTGCAATTC GATTGCGAAA CTTGACACGG
651 CATCAATCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGTG
751 GTCATCTTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAAACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGGAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

```

1251 TC CCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT  
 1301 TC AGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC  
 1351 AT CAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC  
 1401 AA GGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATT  
 1451 CT CTGAAAAA CAATCAGTTG AAATTGAACG GTAAAACGTT GCAAAACGAA  
 1501 CC GGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA  
 1551 A

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

1 MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQOKILOE TGFLTVESHO  
 51 YE RGFWSME TTVIRLKEP LNNARKYLPD NLKTVLEQPV TLVNHITHGP  
 101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME  
 151 VS VPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFRKLADK  
 201 GDAAFEKVHF DSETSDGINP LALGSSNLTLEKFSLEWKEG VDYNVKLNEL  
 251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF  
 301 DT LVYGDEKY GPLDIHIAAE HLDASALTVL KRFQAISAK KMTEEQIRND  
 351 LI AAVKGEAS GLFTNNPVL D IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN  
 401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD  
 451 IN ETLRMLVD STVQSMAREK YLTNGDQID TAILKNNQL KLNGKTLQNE  
 501 PE PDFDEGGM VSEPQQ\*

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAAALLGVALGTPYYLGVKAEESLTQOKILOETGFLTVESHOYERGFWSME					
g590	MKKPLISVAAVLLGVALGTPYYLGVKAEESLTQOKILOKTGFLTVESHOYDRGFWSME					
	10	20	30	40	50	60
	70	80	90	100	110	120
m590-1.pep	TTVIRLKEPELLNNARKYLPDNLKTVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE					
g590	TTVIRLKEPELLHNAQKYLDPNLKIVLEQPVTLVNHITHGPFAGGFGTQAHIEYEFKYAPE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m590-1.pep	TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
g590	TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
g590	FKSYRNSYDAPLFKIKLADKGDAAFEKAHFDSETSDGINPLALGSSNLTLEKFSLEWKEG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m590-1.pep	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF					
g590	VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGRFRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRFQAISAKKMTEEQIRNDLIAAVKGEAS					
g590	DTLVYGDEKYGPLDIHIAAEHLASALTVLKRFQAISAKKMTEEQIRNDLIAAVKGDAS					
	310	320	330	340	350	360
	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK					
g590	GLFTNHPVLNLIKIFRFTLPQSKIDVGGKIMFKGMKKEDLNQLGLMLKKTEANIRMSIPQK					
	370	380	390	400	410	420
	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA GNIFSVNAEDEAEGRASLDDINETLRMLVDSTVQSMAREKYLTLNGDQID					
g590	MLEDLAVSQA GNIFSVNAEDEAEARASIAADINETLRMLVDSTVQSMAREKYLTLNGDQID					
	430	440	450	460	470	480
	490	500	510			
m590-1.pep	TAISLKNQLKLNGKTLQNEPEPDFDEGGMVS-EQQX					

930

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|:||||| |||||:||||| ||:|:
g590 TVISLKNNAKLNGKTLQNEPDPDFDEGDMVSGQPHX
      490      500      510

a590/m590-1 98.3% identity in 516 aa overlap.

      10      20      30      40      50      60
a590.pep MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQEAGFLTVESHQYERGWFTSTE
m590-1 MKKPLISVAAALLGVALGTPYYLGVKAESLTQQQKILQETGFLTVESHQYERGWFTSME
      10      20      30      40      50      60

      70      80      90      100     110     120
a590.pep TTVIRLKPPELLHNAQKYLDPNLTQVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
m590-1 TTVIRLKPPELLNARKYLPDNLKTQVLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPE
      70      80      90      100     110     120

      130     140     150     160     170     180
a590.pep TEKVLERFFGKQVPVSLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
m590-1 TEKVLERFFGKQVPASLANTVYFNGSGKMEVSVPAFDYEELSGIRLHWEGLTGETVYQKG
      130     140     150     160     170     180

      190     200     210     220     230     240
a590.pep FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
m590-1 FKSyrNGYDAPLFKIKLADKGDAAFEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEG
      190     200     210     220     230     240

      250     260     270     280     290     300
a590.pep VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFIDSEGQFRF
m590-1 VDYNVKLNELVNLVTDLQIGAFINPNGSIAPSKIEVGKLAFTSTKTGESGAFINSEGQFRF
      250     260     270     280     290     300

      310     320     330     340     350     360
a590.pep GTLVYGDKEYGPLDIHIAAEHLASALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEAS
m590-1 DTLVYGDKEYGPLDIHIAAEHLASALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEAS
      310     320     330     340     350     360

      370     380     390     400     410     420
a590.pep GLFTNPNVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
m590-1 GLFTNPNVLDIKTFRFTLPSGKIDVGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQK
      370     380     390     400     410     420

      430     440     450     460     470     480
a590.pep MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRMLVDSTVQSMAREKYLTNGDQID
m590-1 MLEDLAVSQAGNIFSVNAEDEAEGRASLDDINETLRMLVDSTVQSMAREKYLTNGDQID
      430     440     450     460     470     480

      490     500     510
a590.pep TAI SLKNNQLKNGKTLQNEPEPDPDFDEGGMVSEPOOX
m590-1 TAI SLKNNQLKNGKTLQNEPEPDPDFDEGGMVSEPOOX
      490     500     510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1841>:

```

g591.seq
1  TTGCAAACCC TTCTAGCTTT TATCTTCGCC ATCCTGATT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG GTTGTGCGGC GTCAAGGTTG
101 TGCGTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGCT ACGTCAAAAT
201 GGTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGTCCG
301 CTGACCAACC TCGCActggc ggTTTTGCTG TACGGACTGa gctTttcctt
351 cggcgtaaCC GAACTGCGGC Cctatgtcgg cacagtgcgaA cccgacaccg

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931

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401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtgc ccgtcgggcT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGc ctcaTGCAG
751 GAATGggcaa acctgACccg cCAAAGCCCg ggcAAAAAA Tcacctgac
801 ctacgAaCGC GCcgacaaa cccaTaccgc CGACATCCGC CccgATactg
851 TCGAAacagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtccgcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCG TTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGTGT
1251 CCAAACATC GGTGTGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591. pep..

```

1 LQTLIAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRK
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGOHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRSPVVRA FGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLALMM LMMAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591. seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGCGCGGT ACGTCAAAAT
201 GTTCGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGAATGA GCTTTTCCTT
351 CGGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 TGGCACACCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAACATC GGTGTGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CCGTCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591. pep..



933

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCGG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGCACACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGACG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAA AACC GTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GTCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT GGCATGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGCTTGC CCTCATGATG CTGATGATGG
1301 CGGTCGCCTT CTCAACGAC GTTACCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

a591.pep

```

1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRKG
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGL M PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR A FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNL L PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMVAFFND VTRLLG*

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m591/a591 99.6% identity in 446 aa overlap

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          10      20      30      40      50      60
m591.pep  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRGDTEWCLAPIP
          |||
a591      LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRGDTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGPLTNLALAVLL YGLSFSFGVT
          |||
a591      LGGYVKMVD TREGEVSEADL PYAFDKQHPA KRIAIVAAGPLTNLALAVLL YGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTV EPDTIARAGF QSGDKIQSVNGTPVADWGS AQTEIVLNLEAGKVAVGVQTA
          |||
a591      ELRPYVGTV EPDTIARAGF QSGDKIQSVNGTPVADWGS AQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          |||
a591      SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGRDLTA
          190     200     210     220     230     240

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	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcgt tcaaattcga
51  cgcggcagca ggcggcttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcy
151 ccgaacgcgc ccgcgcgcgc cgaagtgaac caccctgttt cgcaaggat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 cgcgcttcac catcttgatt taccaacagc cttatggcga tttgagcgg
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatggt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcggtgg tctatttcgg
501 cgcgggttgc aatgtgcctt tggctcggga tatggcggtt atggcgatgg
551 gcatcatggc gtggatcaac ctgcgcgcca tctgctgctc ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgtttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGA
51  PNAAAAAEVK HPVSQGMQM LGVFVDTIIV CSCTAPIILI YQQPYGDLG
101 AALTQAAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTTTC TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCTG TATTCCAACG AGGCGGTAT GGGTTCGCG
151 CCGAACGCCG CCGCGCGCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTGATAC CATCATCGTT TGTTCCTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 CGGCGCGTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTTCATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATG
451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCGG
501 CGCGGTGTC AATGTGCTT TGGTCTGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTGCGCA TCCTGCTGCT CTCGCCCTG

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601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCGGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..  
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPYGDLG  
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSAPNAAAAAEVK					
g592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMGIKRLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQPYGDLGSAALTQAAIVSQVGQWGAGFL					
g592	HPVSQGMQIMLGVFVDTIIVCSCTAFIILIYQPYGDLGSAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
g592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVW*					
g592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVW*					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq  
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA  
 51 CGCGGCAGCA GCGGGCTTAC TCGGGCGTCT GATTTCGCAA ACGATGATGA  
 101 TGGGCATCAA ACGCGGCTTG TATTCCAACG AGCGGGTAT GGGTCCCGC  
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT  
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA  
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGCGA TTTGAGCGGT  
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC  
 351 GGGCTTCCTC GCCGTCATCC TGTATTGTT TGCCTTTTCC ACCGTTATCG  
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG  
 451 CTGATTACCG CCGTTTTCGG TATGCTGGTT TTGGCGTGGG TCTATTTCCG  
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG  
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG  
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA  
 651 CCGGAGTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT  
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep  
 1 MIPDVFGQIF SGAFKFDAAA GLLGGLISQ TMMGIKRL YSNEAGMGS  
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQPYGDLG  
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW  
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL  
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW\*

m592/a592 100.0% identity in 237 aa overlap



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	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQMLGVFVDTHIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMQMLGVFVDTHIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLLSPLAFMLLRDYTAKLKMKGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

g593.seq..

```

1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcac
151 gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg ttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctgccttgtg cggcacttgc
351 cgaagtccgg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcaactggcg gcgctttggt tgtccgcctt
451 tccctgctgt tgctggatga atcgttttcc agtttggaca cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcat tcgcccgaa aggcctgcac ggcggcgag
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgccga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgccgt ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtec gcctgccga
801 ctgcgtccgg ctttcgccc tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcggtc
901 cgcattccgg tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

g593.pep..

```

1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISIMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAEER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSLR LSAVHPEHGE LTLNLTVGQH TDGISGNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

m593.seq

```

1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GGCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCCG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

```

```

2 01 TATGCCGCCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
2 51 TGTTCCTCCA TATGAGTGGC CTGGAATATG CGGCATTCCG TTTGAAAATG
3 01 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACCTGC
3 51 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACCTTCCG
4 01 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
4 51 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTCGCG
5 01 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GGCAGCATCC
5 51 CTGCCGTTT GTTAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
6 01 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
6 51 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTGCGCCGA CTGATGGGTT
7 01 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
7 51 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
8 01 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
8 51 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
9 01 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
  1 MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
 51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESF SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LOYGTPELTV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDMECRVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
m593.pep	NGENITRMPPKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
m593.pep	NGENITRMPPKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMOKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSSLDTHLRGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSSLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSSLDTHLRGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSSLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILOYGTPELTVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILOYGTPELTVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIAVMHEGKILQCGTPETLIQTPAGVQVARLMGLPNTDDD					
	190	200	210	220	230	240

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECRVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :					
g593	RHIPQNAVCLDNHGTCECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGISGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	::  :  :  :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGCGGCA AAACGGTTGC
51  CGACGATATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGCGTCCGG CTGCGGCAAA TCCACCTGCG TGAATATGAT TGCGGGCATC
151 GTCCGGCCCG ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCA TATGAGTGCA CTGGAATG CGGCATTGCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAACACG AGGCGCACCG CAAGCCTGAN AAACTTCCG
401 GAGGCGAAAA GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTCC AGTTTGACA CGCATTGCG
501 CGACCGGCTG CGCCGCATGA CTGCCGAACG TATCCGCAAG GCGGCATCC
551 CTGCCGTTT GTTAACGCAT TCGCCGAAG AGGCCTGCAC GCGGCAGAC
601 GAAATCGCCG TCATGCACGA GGGGAAAATC CTCAATGCG GTACGCCCGA
651 AACCTTGGTT CAAACGCCTG CCGGCGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC GCACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCCGCACGCC GGTGAAATAT CGGGAACGA TACGGTACGC
901 ATCCATATCG AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAES LAMAALAEVG LENEHRKPEX KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLV QTPAGVQVAH LMGLENTDDD RHIPQHAVRF
251 DQDGMCECRVL SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGEIWL					
	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :					
a593	MLELNLCKRFGGKTVADDICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEERLAMAALAEVG					
	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMOKMPKAEESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
	:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :					
a593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTADEIAVMHKGRILQYGTPTLVKTPSCVQVARLMGLENTDDN					

[illegible]

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

g594.seq..

1	atgggtgcag	ataccgatgg	cgacaaggat	gttcggctta	atcgaacggg
51	tctcgttttt	agcatactcc	ggctgctgtt	ccgcatacga	attgggatcg
101	gtaagtctgc	cgttcaggcc	tttcaggtct	ttaagctgct	gatctgtacg
151	gttgagcacc	caaatcggtt	tgccttgcca	ctcggcggtc	agcagctgac
201	ccgctctgat	tttactgaca	tccacctcga	cgcagcacc	ggaggccttg
251	gctttttccg	aagggaaaaa	actggccaca	aacggcggtg	ccacacccaa
301	tgctgccact	ccgcccgcgc	cgcaggtcgc	aagtgtcagg	aaacggcggc
351	ggccgattgt	gatttcttga	ttatccatta	ttcagtcgtc	ctaataattt
401	gggaatgccc	agccattaaa	cattgcaatt	ttaccagtt	tgcagtgata
451	ctcaaagcat	tatttaaaat	aaggtaa		

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

g594.pap

1 MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT  
51 VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ  
101 CCHSARAAGR KCQETAAAVV DFLIIHYSVV LIFWECRAIK HCNFTQFAVI  
151 LKALFKIR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

m594.seq

1	ATGGGTGCAG	ATACCGATGG	CGACAAGGAT	GTTCCGGCTTA	ATCGAACGGG
51	TCCTCGTTTT	AGCATACTCC	GGCTGCCTGT	CCGCATCGGA	ATTGGGATCG
101	GTAAGTTCGC	CGTTACGGCC	TTTCAGGTC	TTAAGCTGCT	GATCTGTACG
151	GTTAGCACC	CAATCGGTT	TGCCTTGCCA	CTCGGCGGTC	AGCAGCTGAC
201	CCGCTTCGAT	TTTACTGACA	TCCACCTCGA	CCGCAGCACC	GGCGGCGTTG
251	GCTTTTTCCG	AAGGGAAAAA	ACTGGCCACA	AACGGCGTTG	CCACACCCAA
301	TGCTGCCACT	CCGCCCGCGC	CGCAGTCCGC	GAGTGTGAGG	AAACGGCGGC
351	GGCCGCTGTT	GATTTCTTGA	TTATCCATTA	TTCAGTCGTC	CTAATATTTT
401	GGGAATACCG	AGCCATTAAA	CGTTGCAATT	TTACCCAGTT	TGCAGTGATA
451	CTCAAAGCAT	CTATTTAAAT	AAGGTTAA		

**This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:**

m594.pep

1 MGADTDGDKD VRNRTGLVF SILRLFRIG IGIGKFAVQA FQVFKLLICT  
51 VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ  
101 CCHSARAAGR ECQETAAAVV DFLIHYSV LIFWEYRAIK RCNFTQFAVI  
151 LKALFKIR\*

**Computer analysis of this amino acid sequence gave the following results:**

### Homology with a predicted ORF from *N. gonorrhoeae*

**m594 / g594 98.1% identity in 158 aa overlap**

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRNLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRNLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```

a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTCGC GAGTGTGAGG AAACGGCGGC
351 GGCCGTTGTT GATTTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAG CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```

a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRNLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRNLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```

g595.seq..
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggggtt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgt ccg
101 gtgagacca atccgccaac gaaggcgggt cggtcggtat cgccgtc aac

```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcgatgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgcg gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgatcgc gatgcgtgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttccac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcgggcag taaaatcagc ggcgaaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg ccaaaaacaa agccttggtg gaaaaaaccg
1001 ataccaactt caaacaggtc aacgaaattc tggcgaaata ccgcacaaaa
```

q595.pap

1	<u>MRKFNLTALS</u>	<u>VMLALGLTAC</u>	QPPEAEKAAP	AASGETQSAN	EGGSVGIAVN
51	DNACEPMNLT	VPSGQVFFNI	KNNSGRKLEW	EILKGMVMD	ERENIAPGLS
101	DKMNRNLPG	EYEMTCGLLT	NPRGKLVAD	SGFKDTANEA	DLEKLPQPLA
151	DYKAYVQGEV	KELAAKTKTF	TEAVKGADIE	KAKSLFAATR	VHYERIEPIA
201	ELFSELDPVI	DACEDDFKDG	AKDAGFTGFH	RIEHALWVEK	DVSGVKETAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGASEL	IEEAAGSKIS	GEEDRYSHTD
301	LSDFQANADG	SKKIVDLFRP	LIEAKNKALL	EKTDTNFKQV	NEILAKYRTK
351	DGGFTYDKLS	EADRKALQAP	INALAEPLAO	LRGILGLK*	

m595.seq

1	ATGAGAAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACGCGGTGC	CAGCGCGCGG	AGGCGGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGGCGGTT	CGGTCAGTAT	CGCCGCTCAAC
151	GACAATGCCT	CGGAACCGAT	GGAACTGACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCATATTT	AAAAACAACA	CGCGCCGCAA	GTCGAATGG	GAATCCTGTA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATGCCCCC	CGGACTTTCC
301	GATAAAATGA	CCGTCAACCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGTT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CACACAGCG	GATTTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCCTACGTTCA	AGGCGAGGTT	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACTTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AATCGATCGA	ACCGATTGCC
601	GAGCTTTTCA	CGCAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	CGCAAGATGA	CCCGATTATC	CGGCTTTCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	CGGTGAAGGA	AATTGCAAGC
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	CGCGCGCGCG	GTCCGAACTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAAACTCAG	GGCGGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGCAT	TCCAAGCCAA	TGTGACGCGA	TCTAAAAAAG	TCGTGATATT
951	GTTCCTGTCG	CTGATCGAGG	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGAATAAA
1051	GACGTTTTCG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAGCGGTT
1101	ACAGGCTCTT	ATTACGCGCG	TGCGCAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAAA			

m595.pap

1	<u>MRKFNLTALS</u>	<u>VMLALGLTAC</u>	QPPEAEKAAP	AASGEAQ TAN	EGGSVSI AVN
51	DNACEPMELT	VPSGQVV FNI	KNNSGRKLEW	EILKGV MVVD	ERENIAQPLS
101	DKMTYVLLPG	EYEMTCGLLT	NPRGKLVTDD	SGFKDTANE A	DLEKLSQPLA
151	DYKAYVGQEV	KELVAKTKTF	TAEAVKGADIE	GAKSLFADTR	VHYERIEPIA
201	ELFSELD PVI	DAREDDFKDG	AKDAGFTGFH	RIEYALWVEK	DVSGVKETIAA
251	KLMTDVEALQ	KEIDALAFPP	GKVVGGASEL	IEEVAGSKIS	GEEDRYSHTD
301	LSDFAQNV DG	SKKIVDLFRP	LIEAKNKALL	EKTDTNFKOV	NEILAKYRTK
351	DGGFTYDKLG	EADDRKALQS	INALAEDLAQ	LRIGLGLK*	

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSI	IAVN	DNACEP	MELT		
		:	:	:		:
g595	MRKFNLTALSVMLALGLTACQPPEAEKAAPASGETQSANEGGSVG	I	AVN	DNACEP	MNL	T
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m5 95. pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g5 95	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m5 95. pep	130 140 150 160 170 180
	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE
g5 95	NPRGKLVVADSGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTTFTEAVKAGDIE
	130 140 150 160 170 180
m5 95. pep	190 200 210 220 230 240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
g5 95	KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m5 95. pep	250 260 270 280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD
g5 95	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD
	250 260 270 280 290 300
m5 95. pep	310 320 330 340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG
g5 95	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS
	310 320 330 340 350 360
m5 95. pep	370 380 389
	EADRKALQASINALAEDLAQLRGILGLKX
g5 95	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

a595. seq

1	ATGAGAAAAT	TCAATTTGAC	CGCATTGTCC	GTGATGCTTG	CCTTAGGTTT
51	GACCGCGTGC	CAGCCGCCCG	AGGCCGAGAA	AGCTGCGCCG	GCAGCGTCCG
101	GTGAGGCGCA	AACCGCCAAC	GAGGCGGTT	CGGTCAATAT	CGCCGTCAAC
151	GACAATGCCT	GCGAACCAGT	GGAAGTACC	GTGCCGAGCG	GACAGGTTGT
201	GTTCAATATT	AAAAACAACA	GCGGCCGCAA	GCTCGAATGG	GAAATCCTGA
251	AAGGCGTGAT	GGTGGTGGAC	GAGCGCGAAA	ACATCGCCCC	CGGACTTTCC
301	GATAAATGA	CCGTCAACCT	GTTGCCGGGC	GAATACGAAA	TGACTTGCGG
351	TCTTTTGACC	AATCCGCGCG	GCAAGCTGGT	GGTAACCGAC	AGCGGCTTTA
401	AAGACACCGC	CAACGAAGCG	GATTTGGAAA	AACTGTCCCA	ACCGCTCGCC
451	GACTATAAAG	CCTATGTTCA	AGGCGAAGTC	AAAGAGCTGG	TGGCGAAAAC
501	CAAAACCTTT	ACCGAAGCCG	TCAAAGCAGG	CGACATTGAA	AAGGCGAAAT
551	CCCTGTTTGC	CGACACCCGC	GTCCATTACG	AACGCATCGA	ACCGATTGCC
601	GAGCTTTTCA	GCGAACTCGA	CCCCGTCATC	GATGCGCGTG	AAGACGACTT
651	CAAAGACGGC	GCGAAAGATG	CCGGATTAC	CGGCTTCCAC	CGTATCGAAT
701	ACGCCCTTTG	GGTGGAAAAA	GACGTGTCCG	GCGTGAAGGA	AATTGCAGCG
751	AAACTGATGA	CCGATGTCGA	AGCCCTGCAA	AAAGAAATCG	ACGCATTGGC
801	GTTTCCTCCG	GGCAAGGTGG	TCGGCGGCGC	GTCCGAACTG	ATTGAAGAAG
851	TGGCGGGCAG	TAAAATCAGC	GGCGAAGAAG	ACCGGTACAG	CCACACCGAT
901	TTGAGCGACT	TCCAAGCCAA	TGTGGACGGA	TCGAAAAAAA	TCGTGATTT
951	GTTCCGTCGG	TTGATCGAGA	CCAAAAACAA	AGCCTTGTTG	GAAAAAACCG
1001	ATACCAACTT	CAAACAGGTC	AACGAAATTC	TGGCGAAATA	CCGGACTAAA
1051	GACGGTTTTG	AAACCTACGA	CAAGCTGGGC	GAAGCCGACC	GCAAAGCGTT
1101	ACAGGCCTCT	ATTAACGCGC	TTGCCGAAGA	CCTTGCCCAA	CTTCGCGGCA
1151	TACTCGGCTT	GAAATAA			

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

a595. pep

1	MRKFNLALS	VMLALGLTAC	QPPEAEKAAP	AASGEAQTN	EGGSVSIQVN
51	DNACEPMELT	VPSGQVVFNI	KNNSGRKLEW	EILKGMVVVD	ERENIAPGLS



```

101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPIV DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTALSVMALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
a595	MRKFNLTALSVMALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
a595	VPSGQVVFNIKNNSGRKLEWEILKGVVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
a595	NPRGKLVVTD SGFKDTANEA DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLFADTRVHYERIEPIAELFSELDPIV DAREDDFKDGAKDAGFTGFHRIEYALWVEK					
a595	KAKSLFADTRVHYERIEPIAELFSELDPIV DAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG					
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDG FETYDKLG					
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1 ..atgctgctct tggacgagcc gaccaaccac ttggatgcgg aatcgggtgga
51 atgctggag caattcctcg tgcgttccc cggcacagt gtcgcggttaa
101 cgcacgaccg ctacttctc gacaacgccg ccgaatggat tttggaactc
151 gaccgaggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

```

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451   ttccggcgata aagtgtctgat tgacgggttg agcttcaaag tgccggcgagg
501   cgcgattgtc ggcatcatcg gcccgaaacg cgcgggtaaa tcgacgctgt
551   tcaaaatgat tgcggggcaaa gagcagcccg attcgggcca agtgaaaatc
601   gggcaaacccg tgaaaatgag cttgattgac caaagcccg aagggtttgca
651   aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701   aggtcggaca gtttgaaatc cccgcccgc aatatttggg acgcttcaac
751   tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801   acgcgccgt ctgcacttg caaaaacctt gttggcggc ggcaatgtgt
851   tgctgtgga cgaaccgtcc aacgatctcg acgtgaaaac cctgcgcgcg
901   ttggaagacg cattgttga atttgccgc agcgtgatgg tgatttcgca
951   cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1 001   gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1 051   gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1 101   atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1   ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51  DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRNNAKG
101 ROAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNYSKS
151 FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201 GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVGQFEI PARQYLGRFN
251 FKGSQSKIA RQLSGGERGR LHLAKTILGG GNVLLLDPEPS NDLDVETLRA
301 LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351 DKRRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1   ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCG
51  GCCGCAGAAA ACCATCATTG AAGATATTTT CCTTCTTTT TTCCCGCGCG
101 CGAAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTTGATCCGG
251 AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTGGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351 GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGAA GCGATTATTG
401 CGGCAGGTTT GTCCACGGGC GCGGTTGCGG AACACGAATT GGAAATCCGC
451 GCGACGCGC TGCGCTGCTC GGAATGGGAT GCCAAAATCG ATAATTTGTC
501 CCGCGGTGAA AAACGCCGCG TTGCCTTTGT CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGG TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGCGA CAGTCGTTGC
651 GGTAACGCAC GACCGCTACT TCCTCGACAA CGCGCCGAA TGGATTTTGG
701 AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751 CTGGAGCAGA AAGAAAAACG CTTGGAAGAC GAGGCAAAAT CCGAAGCCGC
801 GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901 AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951 CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1 001 AATCGTTTCG CGATAAAGTG CTGATTGACG ATTGAGCTT CAAAGTGCCCT
1 051 GCGGGCGCGA TTGTGCGCAT CATCGGCCG AACGGCGCGG GTAAATCTAC
1 101 GCTGTTCAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GCGGAGGTGA
1 151 AAATCGGACA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1 201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAG GCCCGGACAT
1 251 TTTGCAGGTT GGTGAGTTTG AAATCCCGC CGCCAATAT TTGGGGCGTT
1 301 TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1 351 GCGGAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTGTA GCGGCGGCAA
1 401 TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGC
1 451 GCGCGTTGGA AGACGCATTG TTGGAATTG CCGGCAGCGT GATGGTGATT
1 501 TCGCACGACC GTTGGTTTCT CGACCGCATC GCCACGCATA TCTTGGCGTG
1 551 TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGCAACTAT CAGGAATACG
1 601 AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1 651 ATCAAAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPPOK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPD LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAHEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLDAES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILEDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEARVK AMKQLEWVR QNAKGROAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGRHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m596 g596 98.4% identity in 373 aa overlap

```

m596.pep      160      170      180      190      200      210
LPWDKIDNLSGGEKRRVALCKLLLSKPDMLLLDPEPTNHLDAESVEWLEQFLVRFPFPTV
g596          MLLLDPEPTNHLDAESVEWLEQFLVRFPFPTV
                    10      20      30

m596.pep      220      230      240      250      260      270
VAVTHDRYFLDNAAEWILEDRGHGIPWKGNYSWLEQKEKRLNEAKSEARVKAMKQE
g596          VAVTHDRYFLDNAAEWILEDRGHGIPWKGNYSWLEQKEKRLNEAKSEARVKAMKQE
                    40      50      60      70      80      90

m596.pep      280      290      300      310      320      330
LEWVRQNAKGROAKSKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
g596          LEWVRQNAKGROAKPKARLARFEEMSNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKS
                    100     110     120     130     140     150

m596.pep      340      350      360      370      380      390
FGDKVLIDDLSEFKVPAGAIIVGIIPNGAGKSTLFKMISGKEQPDGGEVKIGQTVKMSLID
g596          FGDKVLIDGLSFKVPAGAIIVGIIPNGAGKSTLFKMIAGKEQPDGGEVKIGQTVKMSLID
                    160     170     180     190     200     210

m596.pep      400      410      420      430      440      450
QSREGLQNDKTVFDNIAEGRDILQVVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
g596          QSREGLQNDKTVFDNIAEGRDILQVVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
                    220     230     240     250     260     270

```

947

	460	470	480	490	500	510
m596.p	LHLAKTLLSGGNVLLLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	:					
g596	LHLAKTLLGGGNVLLLDVETLRALEDALLEFAGSVMVISHDRWFLDRIATHIL					
	280	290	300	310	320	330

	520	530	540	550	559
m596.p	ACEGDSKWVFFDGNVQEYADKKRRLGEEGAKPKRIKYPVTRX				
	:				
g596	ACEGDSKWVFFDGNVQEYADKKRRLGKEGAKPKRIKYPVTRX				
	340	350	360	370	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1875>:

```

a596.seq
1  ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51  GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTT TCCCCGGCG
101 CGAAATCGG TTTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151 CGGATTATGG CGGCGTGGA TAAAGAATT GAGGGCGAAG CCGTGCCGAT
201 GGGCGGTATT AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGTATCCGG
251 AAAAAACCGT GCGTGAGGAA GTGGAAGCG GTTTGGGCGA AGTGGCTGCC
301 GCGCAGAAAC GTTTGGAGGA AGTGTATGCC GAGTACGCCA ATCCCGATGC
351 GGATTTTGAC GCGTTGGCGG AAGAGCAGGG GCGTTTGGA GCGATTATTG
401 CGGCGGGTTC GTCCACGGGC GCGGTGCGG AACACGAATT GGAAATCGCT
451 GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAATCG ATAATTTGTC
501 CGGCGGTGAA AAACGCGCGC TCGCTTTGTG CAAACTCTTG TTGAGCAAGC
551 CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGA TGCGGAATCG
601 GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TTCCCGGTA CAGTCGTTGC
651 CGTAACACAC GACCGTACT TCCTCGACAA CGCCGCGGAA TGGATTTTGG
701 AACTCGACCG CGGGCACGGT ATTCCGTGGA AAGGAAATTA CTCGTCTTGG
751 TTGGAGCAGA AAGAAAAACG TTTGAAAAC GAGGCGAAT CCGAAGCCGC
801 GCGCGTGAAA GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851 AAGGCCGTCA AGCCAAGTCC AAAGCGCGTT TGGCGGTTT TGAAGAAATG
901 AGCAACTATG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTCATTCC
951 CGTCGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTG AATGTTTCCA
1001 AATCGTTCGG CGACAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCCT
1051 GCGGGCGCGA TTGTGCGCAT CATCGGTCCG AACGGCGCGG GTAAATCGAC
1101 ACTGTTTAAA ATGATTGCGG GCAAAGAGCA GCCCGATTCC GGTGAAGTGA
1151 AAATCGGGCA AACCGTGAAA ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201 TTGCAAAACG ACAAACCGT GTTCGACAAC ATTGCCGAAG GTCGCGATAT
1251 TTTACAGGTC GGGCAGTTTG AAATCCCCGC CCGCAATAT TTGGGACGCT
1301 TCAATTTCAA AGGCAGCGAC CAAAGCAAAA TCACGGGGCA GCTTTCGGC
1351 GCGCAACGCG GACGTTTGCA CTTGGCAAAA ACCTGTGTGG GCGGTGGCAA
1401 TGTGTTGCTG CTGGACGAAC CGTCCAACGA CCTCGACGTG GAAACCTGCG
1451 GCGCGTTGGA AGACGCATTG CTGGAATTG CCGGCAGCGT GATGGTGATT
1501 TCGCACGACC GCTGGTTCCT CGACCGTATT GCTACGCATA TCTTGGCTTG
1551 CGAAGGCGAC TCCAAATGGG TGTTCTTTGA CGGCAACTAT CAGGAATACG
1601 AAGCCGACAA GAAACGCCGA CTCGGCGAAG AAGGCACGAA ACCGAAACGC
1651 ATCAAATACA AACCAGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1876; ORF 596.a>:

```

a596.p
1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG INGAGKSTVL
51  RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101  AQKRLEEVYA EYANPDADFD ALAEQGRLE AIIAAGSSTG GGAHELEIA
151  ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLD EPTNHLDAES
201  VEWLEQFLVR FPGTVVAVTH DRYFLDNAEE WILELDRGHG IPWKGNYSW
251  LEQKEKRLN EAKSEAAVRK AMQELEWVR QNAKGRQAKS KARLARFEEM
301  SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEKVP
351  AGAIVGIIGP NGAGKSTLFK MIAGKEQPDG GEVKIGQTVK MSLIDQSREG
401  LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKITGQLSG
451  GERGRHLAK TLLGGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501  SHDRWFLDRI ATHILACEGD SKWVFFDGNV QEYADKKRR LGEEGTEKPKR
551  IKYKPVTR*

```

m596/a596 99.3% identity in 558 aa overlap

948

	10	20	30	40	50	60
m596.pep	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTI IKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m596.pep	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m596.pep	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m596.pep	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m596.pep	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQLEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQLEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m596.pep	SNYEYQKRNETQEIFIPVAERLGNIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
	370	380	390	400	410	420
m596.pep	NGAGKSTLFFKMSISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFFKMSISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m596.pep	GQFEIPARQYLGRFNFKGSQSKIAGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSQSKITGQLSGGERGRHLAKTLLSGGNVLLDEPSNDLDV					
	430	440	450	460	470	480
	490	500	510	520	530	540
m596.pep	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFDGNYQEYADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFDGNYQEYADKKRR					
	490	500	510	520	530	540
	550	559				
m596.pep	LGEEGAKPKRIKYPVTRX					
a596	LGEEGAKPKRIKYPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACCGCAA CAGCGCGAGG CTGGGACAA ATTCCAAAAA

```

```

151 C TCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 G CAGATTTCG CGTTTCGTAT CGGGGAACCTA TAAAAACAGC CGGCCGAATG
251 C GGTGGCCCT GTTCTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 T TGCCTTATA CGCGTTATGT AAACGCCCTCC AATCGGGGAG TTGTCAAGGA
351 T TTTGAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 A TGAAGTTGC CCGTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 A AAAAAACAGG GTGTAACCGA TCGGCGGAA CAGACGGAAA GCCGCAGACA
501 G AATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 A CAGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaaaaagcc
601 g aacaccgCA TtcaggAtgc ggAagcaaaa agaAAATTGG CTGAagCaa
651 a CtGgcggca gccgAAAAAG CCAGAAAAGA AGCGGCGCAG CAGAAGGCTG
701 A AGCGCGCAGC TGCGGAAATG TCCAACTGA CCGCCGAAGA CAGGAACATC
751 C AAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 G CAGGGACGT TTGAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 G CAGAGAACCG GAGCGGcgGc GATGTTTGA AAGCGGTGTT CTATTCCACT
901 C CGCCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCCGA
951 c gaGTTGGAC GGCTACGGCA AAGTGGTCGT GATCGATCAC GGCGAGAACT
1001 A CATCAGCAT CTATGCCCGT TTGAGCGAAA TTTCCGCCGG CAAGGGTTAT
1051 A CCGTCGCGG CAGGAAGCAA AATCGGCACg AGCGGGTCGC TGCCGGACGG
1101 G GAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 C TTCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQERIROA RGNLASVNRK OREAWDKFOK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNALFLK NAEPGQKNRF
101 LRYTRVYNAS NREVVKDLEK QOKALAVQEQ KINNELARLK KIQANVSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ OKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVP T GLFGQNRSGG DVWKGVFYST
301 A PATVESIAP GTVSYADELD GYGKVVVIDH GENYISYIAG LSEISAGKGY
351 T VAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAAGC CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAAAACAGC CGAGGCTTGG GACAAGTTCC AAAAACTCAA TACCGAGCTG
151 AACCCTTTGA AAACGGAAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTC
251 TGA AAAACGC CGAACCGGGT CAGAAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGG AAAAACAGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCCGTT
401 TGAAGAAAAT TCAGGCAAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCCGC AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAACTGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 ACAAGCTCTT GAGCAATTG GAGAAGAAAA AGGCCGAACA CCGCATTGAG
601 GATGCCGGAAG CAAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGCTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAGC GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCCGGCAG AACCGGAGCG
851 GCGGCATAT TTGAAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTG CGCCGGGAAC GGTAACTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAGTGT GTCGTGGTCG ATCACGGCGA GAACTACATC AGCATCTATG
1001 CCGGTTTGA GCGAAATTTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGGAG AGGGGCTTTA
1101 CCTGCAAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.pep

```

1 MLLHVSNSLK QLQEEIRIQE RIRQARGNLA SVNRKOREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREVV KDLEKQOKAL AVQEQKINNE LARLKKIQAN VQSLKKQGV
151 TDAEQTESR RONAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKRLAE ARLAAAEKAR KEAAQOKAEA RRAEMSNLTA EDRNIQAPSV
251 MGIGSADGFS RMQGRLLKPV DGVPTGLFGQ NRSGGDIWKV VFYSTAPATV
301 ESIAPGTVSY ADELGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEGLYLQI RYQGQVLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QOKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYIYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYIYAGLSEISVKGGMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGQVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCCTCAAG	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAA	CGTATCCGCC	AAGAGCGTAT	CCGTGAGGCG	CGCGGCAACC
101	TTGCTTCCGT	CAACCGCAAA	CAGCGCGAGG	CTTGGGACAA	GTTCCAAAAA
151	CTCAATACCG	AGCTGAACCG	TTTGAACACG	GAAGTCGCCG	CTACGAAAGC
201	GCAGATTTC	CGTTTCGTAT	CGGGGAAC	TAAAAACAGC	CAGCCGAATG
251	CGGTTGCCCT	GTTCTTGAAA	AACGCCGAAC	CGGGTCAGAA	AAACCGCTTT
301	TTGCGTTATA	CGCGTTATGT	AAACGCCCTC	AATCGGGAAG	TTGTCAAGGA
351	TTTGGAAAAA	CAGCAGAAAG	CTTGGCGGT	ACAAGAGCAG	AAAATCAACA
401	ATGAGCTTGC	CGGTTTGAAG	AAAATTCAGG	CAAACGTGCA	ATCCCTGCTG
451	AAAAAACAGG	GTGTAACCGA	TGCGGCGGAA	CAGACGGAAA	GCCGCAGACA
501	GAATGCCAAA	ATCGCCAAAG	ATGCCCGAAA	ACTGCTGGAA	CAGAAAGGGA
551	ACGAGCAGCA	GCTGAACAAG	CTCTTGAGCA	ATTGAGAGAA	GAAAAAGGCC
601	GAACACCGCA	TTCAAGGATG	GGAAGCAAAA	AGAAAATTGG	CTGAAGCCAG
651	ACTGGCGGCA	GCCGAAAAAG	CCAGAAAAGA	AGCGGCCGAG	CAGAAGGCTC
701	AAGCACGACG	TGCGGAAATG	TCCAACCTGA	CCGCCGAGAA	CAGGAACATC
751	CAAGCGCCTT	CGGTTATGGG	TATCGGCAGT	GCCGACGGTT	TCAGCCGCAT
801	GCAAGGACGT	TTGAAAAAAC	CGGTTGACGG	TGTGCCGACC	GGACTTTTCG
851	GCGAGAACCG	GAGCGGCGGC	GATGTTTGGG	AAGGCGGTGT	CTATTCCACT
901	GCACCGGCAA	CGGTTGAAAG	CATTGCGCCG	GGAACGGTAA	GCTATGCGGA

951

```

951 CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GGCGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

```

a597.pep
1  MLLHVSNSLK QLQEEIRQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51  LNTLNLRLKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGG VLPSSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

```

          10      20      30      40      50      60
a597.pep  MLLHVSNSLKQLQEEIRQEIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNLRLKT
m597      MLLHVSNSLKQLQEEIRQEIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNLRLKT
          10      20      30      40      50

          70      80      90     100     110     120
a597.pep  EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
m597      EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK
          60      70      80      90     100     110

          130     140     150     160     170     180
a597.pep  QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
m597      QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE
          120     130     140     150     160     170

          190     200     210     220     230     240
a597.pep  QKGNEQQLNKLLSNLEKKKAHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
m597      QKGNEQQLNKLLSNLEKKKAHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM
          180     190     200     210     220     230

          250     260     270     280     290     300
a597.pep  SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST
m597      SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST
          240     250     260     270     280     290

          310     320     330     340     350     360
a597.pep  APATVESIAPGTVSYADELDGYGKVVVDHGENYISYAGLSEISVGKGYMVAAGSKIGS
m597      APATVESIAPGTVSYADELDGYGKVVVDHGENYISYAGLSEISVGKGYMVAAGSKIGS
          300     310     320     330     340     350

          370     380     390
a597.pep  SGSLPDGEEGLYLQIRYQGGVLPSSWIRX
m597      SGSLPDGEEGLYLQIRYQGGVLPSSWIRX
          360     370     380

```



The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151 AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201 GCTGAAAATG GGTTCGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251 GCACGCCGAA ACCCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTCGCGG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401 TCGCGCGCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451 ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501 TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGCGCGC aaagcgtca
551 tgaGCCGCGC CGCACgcggtg attatggaaa gttgGGTGCg cgttcccgat
601 gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101 SGKTVNAADI DLPVRALSMG KLHHAMMGIA SVAIAAAVLG TLVNLAAGGG
151 TRKEVRFGHP SGTLRVGAAA ECQDQGWTA KAVMSRSARV IMESWVRVPD
201 DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTCGCTG TACGCGCCCT
351 GAGCATGGGC AAATGCAACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCGCCGTA CCCGGTACGC TGGTCAACCT TGCCGAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCGG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTCATGAG CCGTAGCGCA CGCGTGATGA TGGAAGGTTG GGTGAGGGT
601 CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTRKEVRFG HPSGTLRVGA AAECQDQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

	10	20	30	40	50	60
m601.pep	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
g601	MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m601.pep	KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG					

953

```

g601      |||||
          TIRAYGALKMGLISDVSEAAARATPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          |||||
g601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          130     140     150     160     170

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |:|||||:|:|||||:|
g601      AAKAVMSRSARVIMESWVRVPDDCFX
          180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1  ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
51 CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
1 01 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
1 51 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
2 01 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
2 51 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCTCC
3 01 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTGCTGG TACGCGCCCT
3 51 GAGCATGGGC AAATTCGACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
4 01 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
4 51 GCGGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
5 01 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
5 51 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGAAGGTTG GGTGAGGGTG
6 01 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51 NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
1 01 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
1 51 GGTRKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
2 01 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

          10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
a601      MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10      20      30      40      50      60

          70      80      90      100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
          |||||
a601      KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
          70      80      90      100     110     120

          130     140     150     160     170     180
m601.pep  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          |||||
a601      KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECDGQWT
          130     140     150     160     170     180

          190     200
m601.pep  ATKAVMSRSARVMMEGWVRVPEDCFX
          |||||
a601      ATKAVMSRSARVMMEGWVRVPEDCFX
          190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTTCTGCT
51  CGGCAGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCCTGCAAA TgcgagattA TATCACTGTC TTTtgccgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGQ INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQIAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLAA
101 CLQMRDYITC FWRLLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHGQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGV S AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPLLSRQVNRHGQTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
g602	MLLHQCDKARHMRPFLGGQINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHVIIVEMCAWYGVSA-GEYTVN---LQMRDYITRF*QLHX					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRQMPSEKTLAAQLQMRDYITCFWRLLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTCAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHGQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGV S TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602. Pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
a602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNGLDAFCSLQGNRKAQVFDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602. Pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAEYTVNLQMRDYITRFQQLHX					
a602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITRFQQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603. seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGCCCC CGCACCAAAA AAACAACCAC AACTACAAG GAGAAACATC
151 ATGTCGACCC AACTATTCTT TGTCCTGAAC TCGCTCAGTT CATCGCTCAA
201 AGGCGCGGTT ATCGACCGCA AAAGCGGCAG CGTCGTCTTA AGTGCCTCG
251 GGGAAACGCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGCGCGC AACTGCCACG CCGCGCGCGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGGCGC GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCCGCGCAG
551 AACACTTTCC CGGCCTGCCC AACGTGCGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCGCG GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTACGCCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GCGGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GTTTCCCGG GTATTTCCga actTCCCAAC GACTGCCGCA
1001 CCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCCGCTT CGCAAATAC ATCGCTTGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTCAC CGGCGGTATC GGCGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCCT ATCTTGATT CTGGGCTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGCTACGGCA ATTCGGGCAT
1251 TATCAGCCCG ACCGATCTT CTCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCG CATCTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603. pep

```

1  MDSRLRGND RYKIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTRRNI
51  MSDQILILVN CVSSSLKGAV IDRKSGSVVL SCLGERLTPP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDSFHF
201 QTMPERAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISSELPN DCRTLEIAAD EGREGARLAL
351 EVMTCLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYGNISGIISP TDSSPAVLVV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603. seq

```

1  CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCCGTC TGAAACACCT TCGCCTGAT GTCTGC.CTT
101 TTTGAGACGA CCCACACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGCGGCC GTTATCGACC GAAAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

m603.ppt

```

1      LSSRRRGRNN DRKCGIRFAQ RGRLKHLAPD VCXFSDDPTL KQOPQOTRRN
51     IMSDQLILVL NCGSSSLKGA VIDRXSGSVV LSCLGERLTT PEAVITFNKD
101    GNKRQVPLSG RNCHAGAVGM LLNELEKHGL HDRIKAIGHR IAHGGEKYSE
151    SVLIDQAVMD ELNACIPLAP LHNPAITSGI LAAQEHFPGL PNVGVMDTSF
201    HQTMPERAYT YAVPRELRKK YAFRRYGFHG TSMRYVAPEA ARILGKPLED
251    IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS
301    YLTSHAGMDV AQVDEMLNKK SGLLGISELS NDCRTLLEIAA DEGHEGARLA
351    LEVMTYRLAK YIASMAVGC GVDALVFTGG IGENSNRIRA KTVSYLDFLG
401    LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELAGIL
451    *

```

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/g603

	10	20	30	40	50	60
m603.pep	LSSRRRG	RNRDKCGIR	FAQRGLKHL	APDVCFSD	DPDLKKQP	QOTTRNIMSDQLILVL
	:	:	:	:	:	:
g603	MDSRLRG	-NDARKYGIR	FAQRGLKHT	PPNAHPFSD	GPAPKKQP	QOTTRNIMSDQLILVL
	10	20	30	40	50	
	70	80	90	100	110	120
m603.pep	NCGSSSLK	GAVIDRXSG	SVVLSCLGER	LTTPEAVIT	FNKDG	NKRQVPLSGRNCHAGAVGM
	:	:	:	:	:	:
g603	NCVSSSLK	GAVIDRXSG	SVVLSCLGER	LTTPEAVIT	FNKDG	NKRQVPLSGRNCHAGAVGM
	60	70	80	90	100	110
	130	140	150	160	170	180
m603.pep	LLNELEKH	GLHDRIKA	IGHRIAHG	GKEYSESV	LIDQAVMDEL	NACIPLAPLHNPANISGI
	:	:	:	:	:	:
g603	LLNELEKH	GLHDRIKA	IGHRIAHG	GKEYSESV	LIDQAVMDEL	NACIPLAPLHNPANISGI
	120	130	140	150	160	170
	190	200	210	220	230	240
m603.pep	LAAQEHF	PGLPNVG	VMDTSFHQ	TPERAYT	YAVPREL	RKKYAFRRYGFHGTSMRYVAPEA
	:	:	:	:	:	:

```

g603      LAAQEHFPPLNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180          190          200          210          220          230

          250          260          270          280          290          300
m603.pep  ARILGKPLEDIRMIIAHLGNASITAIKNGKSVDSMGTFTPIEGLVMGTRCGDIDPGVYS
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g603      ARILGKPLEDIRMIIAHLGNASITAVKNGKSVDTGMGTFTPIEGLVMGTRCGDIDPGVYS
          240          250          260          270          280          290

          310          320          330          340          350          360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISSELSNDCRTLEIAADEGHEGARLALAEVMTYRLAK
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISSELPNDCRTLEIAADEGREGARLALAEVMTCLAK
          300          310          320          330          340          350

          370          380          390          400          410          420
m603.pep  YIASMAVAGCGVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIIS
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIIS
          360          370          380          390          400          410

          430          440          450
m603.pep  PTDSSPAVLVVPTNEELMIACDTAELAGILX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g603      PTDSSPAVLVVPTNEELMIACDTAELAGILX
          420          430          440          450

```

```

a603.seq
1 CTGTCTCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51 CTTTGCCCAA AGAGGCCGTC TGAAACACAC TCCGCCCAAC GCCCATCCTT
101 TTTCAGACGA CCCACACC. AAAAAACAAC CACAAACTAC AAGGAGAAAT
151 ATCATGTCCG ACCAATCTCAT TCTTGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCGG TCATTACGTT CAGCAAAGAC
301 GGCAACAACG GCCAAGTTCC CCTGAGCGGC CGGAACTGCC ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGAAAA ACACGAAC TG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG CGGCGAAAA ATACAGCGAG
451 TCTGTTTTGA TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGGCGCG CTGCACAACC CCGCAAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATT CCCCGGTCTG CCCAATGTCG GCGTGTATGGA TACTTCGTTT
601 CACCAACACCA TGCCGAGCG TGCCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTCC GCGCTACGCG TTTCACGCGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAACC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GCGCATCCA TTACGCCCAT
801 CAAAAACGCG AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TGCGCCGATA TCGACCCTGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTT CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCG GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGTTT CGATGGCTGT
1101 GGGCTGCGCG GCGCTTGACG CACTCGTGTT CACCGCGGCT ATCGGCCGAA
1151 ACTCGCGTAA TATCCGTGCC AAAACCGTTT CCTATCTTGA TTTCTTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGCG TGTTTTGGTT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TGCACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

```
a603.pep
  1  LSSRRRRGRNN DRKCGIRFAQ  RGRLLKHTPPN  AHPFSDDDPTX  KKQPQTTRRN
51  IMSDQLILVL  NCGSSSLKGA  VIDRKSGSVV  LSCGLGERLTT  PEAVITFSKD
101 GNKRQVPLSG  RNCHAGAVGM  LLNELEKHEL  HDRIQAVGHR  IAHGGEKYDE
151 SVLIDQAVMD  ELNACIPLAP  LHNPNANISGI  LAAQEHFPGI  PNVGVMDSF
```

958

201 HQTMPERAYT YAVPRELRKK YAFRRYGFGH TSMRYVAPEA ACILGKPLED  
 251 IRMIIAHLGN GASITAIKNG KSVDTSMGFT PIEGLVMGTR CGDIDPGVYS  
 301 YLTSHAGLDV AQVDEMLNKK SGLLGISELS NDCRTLEIAA DEGHEGARLA  
 351 LEVMTYRLAK YIASMAVGCG GVDALVFTGG IGENS RNIRA KTVSYLDFLG  
 401 LHIDTKANME KRYGNSGIIS PTDSSPAVLV VPTNEELMIA CDTAELVGIL  
 451 \*

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNDRKCGIRFAQRGRKLHAPDVCKFSDDPTLKKQPQTTRRNIMSDQLILVL					
a603	LSSRRRGRNDRKCGIRFAQRGRKLHAPDVCKFSDDPTLKKQPQTTRRNIMSDQLILVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m603.pep	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFNKDGNGKRVPLSGRNC HAGAVGM					
a603	NCGSSSLKGAVIDRXSGSVVLSCLGERLTTPEAVITFSKDGNGKRVPLSGRNC HAGAVGM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m603.pep	LLNELEKHLHDRIKAIGHRIA HGGEKYESVLIDQAVMDELNACIPLAPLHN PANISGI					
a603	LLNELEKHLHDRIKAIGHRIA HGGEKYESVLIDQAVMDELNACIPLAPLHN PANISGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m603.pep	LAAQEHFPGLPNVGVM DTSFHQTMPERAYTYAVPRELRKKYAFRRYGFGH TSMRYVAPEA					
a603	LAAQEHFPGLPNVGVM DTSFHQTMPERAYTYAVPRELRKKYAFRRYGFGH TSMRYVAPEA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m603.pep	ARILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTR CGDIDPGVYS					
a603	ACILGKPLEDIRMIIAHLGN GASITAIKNGKSVDTSMGFTPIEGLVMGTR CGDIDPGVYS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m603.pep	YLTSHAGMDVAQVDEMLNKK SGLLGISELSNDCRTLEIAA DEGHEGARLA LEVMTYRLAK					
a603	YLTSHAGLDVAQVDEMLNKK SGLLGISELSNDCRTLEIAA DEGHEGARLA LEVMTYRLAK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m603.pep	YIASMAVGCGGVDALVFTGG IGENS RNIRAKTVSYLDFLGLHIDTKANME KRYGNSGIIS					
a603	YIASMAVGCGGVDALVFTGG IGENS RNIRAKTVSYLDFLGLHIDTKANME KRYGNSGIIS					
	370	380	390	400	410	420
	430	440	450			
m603.pep	PTDSSPAVLVVPTNEELMIACDTAELAGILX					
a603	PTDSSPAVLVVPTNEELMIACDTAELVGILX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

1 ATGCCCGAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GAGCACGGCG GCGGCGATGG CGACCGAGGC GATGCCCATC  
 101 ATAGCGTGGT GCAGTTTGCC CATGCTCAGG GCGCGTACCG GCAAATCGAT  
 151 GTCGGCGGCG TTTACGGTTT TGCCGCTGGA GGCGGTGTAA TCGGCGGCGG  
 201 GCGCGACGAA GGCGGGTTTC GCGGTGCGCG CGCGGGCGGC GGCTTCGGAT

959

251 ACCTCGCTGA TCAAACCCAT TTTCAGCGCG CCATATGCGC GGATGGTTTC  
 301 AAATTTTCC AGCGCGGCGG CATCGTTGTT GATGTCGTCC TGCAACTCTT  
 351 TGCCCGTGTA GCCCAAGTCG GCGGCGTTCA GGAAAACGGT CGGAATGCCC  
 401 GCGTTGATGA GCGTGCTTT CAGACGACCT ATATTGGCA CATCAATTTC  
 451 GTCGACCAA TTGCCGTTG GGAACATACT GCCTTcgCG TCGGCTGGAT  
 501 CTA

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604.pep

1 MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVQFA HAQGAYRQID  
 51 VGGVYGFAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF  
 101 KFPORGIVV DVVLQLFARV AQVGVQENG RNARVDERGF QTTYIRHINF  
 151 VDQIAGWEHT AFAVGWI\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GGTACGCGG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA  
 101 CCATCATCG CGTGTGCG TTTGCCCATG CTCAGGGCGC GTACCAGCAA  
 151 ATCGATGTCG GCGGCGTTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG  
 201 CGGCGGGCGG GACGAAGGCG ACTTTCGGCG TGTGCGCGG AGCGGCAGCT  
 251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT  
 301 TTTCTCGAAT TTTCCAAAG CCGCGGCATC GTTGTGATG TCGTCTTGCA  
 351 ACTCTTTGCC TGTGTAGCCC AAGTCGGCGG CATTCAAGAA AACGGTCGGA  
 401 ATGCCCCGCT TGATGAGCGT GGCTTTCAA CCGCCTATAT TCGGCACATC  
 451 AATTTTCATG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCGTCGG  
 501 CTGGATC

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604.pep

1 MPEAHFFTRS AACGKVDQRT GYGGGGRNGN RGGTHHRVQ FAHAQGAYQQ  
 51 IDVGGVHGFA TGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFORTVSAD  
 101 FLEFFQSRGI VDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI  
 151 NFIDQIAGWE HTAFAVGWI

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

	10	20	30	40	50	60
m604.pep	MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
g604	MPEAHFFTRSAACGKVDQRTTEHGG--DGDGDAHHSVVQFAHAQGAYRQIDVGGVYGF					
	10	20	30	40	50	
	70	80	90	100	110	120
m604.pep	TGGGVIGGRDEGDFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLFA					
g604	AGGGVIGGRDEGDFRRARAGGFGYVADQTHFQRAICADGFKFFQRGGIVVDVVLQLFA					
	60	70	80	90	100	110
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI					
g604	RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX					
	120	130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

1 ATGCCCCAAG CGCACTTCTT TACGCGTTCC GCCGCTGCG GCAAGGTTGA  
 51 CCAGCGTACC GGGCACGGCG GCGGCGGTCG CAATGGCAAC AGAGGCGGTA  
 101 CCCATCATCG CGTGTGCAA TTTGCCCATG CTCAGGGCGC GTACCAGCAA  
 151 ATCGATGTCG GCGGCATTCA CGGTTTGGC ACTGGAGGCG GTGTAATCGG



960

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201 CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGGCAGCT
251 TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301 TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351 ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTGAGGAA AACGGTCGGA
401 ATGCCCAGCGT TGATGAGCGT GGCTTTCAAA CGGCCTATAT TCGGCACATC
451 AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501 CTGGATCAAG AAATTTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551 TCGAGCTCAA AATCGCCTGT TTCCAAAACT GCGCCGTTTT GCATCGGTAC
601 ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651 AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFORTVSAD
101 FLEFFQSCGI VVDVVLQLEA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NPIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNCVLHRY
201 MGNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

	10	20	30	40	50	60
m604.pep	MPEAHFFTRS AACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA					
a604	MPEAHFFTRS AACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA					
	10	20	30	40	50	60
m604.pep	TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFORTVSADFLEFFQSRGIVVDVVLQLEA					
a604	TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFORTVSADFLEFFQSCGIVVDVVLQLEA					
	70	80	90	100	110	120
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINPIDQIAGWEHTAFAVGWI					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINPIDQIAGWEHTAFAVGWIKKFDLYFGCRE					
	130	140	150	160	169	
m604.pep	CVAQVGGIQENGRNARVDERGFQTAYIRHINPIDQIAGWEHTAFAVGWI					
a604	RVAQVGGIQENGRNARVDERGFQTAYIRHINPIDQIAGWEHTAFAVGWIKKFDLYFGCRE					
	130	140	150	160	170	180
a604	RYAVELKIACFQNCVLHRYMGNGFADVFLPDFDCADAVX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251 TCATctacCc cgGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351 CTCCGCTCC GGCTAcccgT CCGAACAAGG CATCAAAGGC TTGTTTGACG
401 ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAC
451 AAACGCCTTG CCGCCGTCCT TAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551 TTTCCAAC TA CGCgcCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGGCAGGA
651 GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAATATGTT
801 TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GCGGACACGC
851 TGACCAACCC CAAACTCAAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901 AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCCAGGATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATC CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCGtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CCTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

```

g605.pep
1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDEFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIIIEGFF
251 GQEIHNHTTYN LARMNMFHVN VNYNKFHIEL GDTLTNPKLK DSKPFDVVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAFIL HALNYLSGRG
351 RAAIVSFPFI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTCAIVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LPADKADVPK
451 IAQNAAQQT V KDNNGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

```

m605.seq
1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTCACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCAGC CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCGCA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACCAG CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCGGCAA
501 TTTTGAAAAA CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAACCTA CGCTGCCAAC GCAGGCAAAT CCGCGGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CGGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCGCA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GGCAGACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCCAGGATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCGG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

```

m605.pep
1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLA AVLKGV AELDFGNFEN HHIDLFGBAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLQAKKQF DEHIEEGFF
251 GQEIHTTYN LARMNMFHN VNYNQFHIEL GDTLTNPCLK DSKPFDAIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI RQYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng)

from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVIRGAVDGVDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFENHHIDLFGBAY					
g605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLA AVLKGV AELDFGNFEDHRIDLFGBAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEIHTTYN LARMNMFHN VNYNQFHIELGDTLTNPCLKDSKPFDAIVS					
g605	DEHIEEGFFGQEIHTTYN LARMNMFHN VNYNQFHIELGDTLTNPCLKDSKPFDAIVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAL HALNYLSGRGRAAIVSFPGI					
g605	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAL HALNYLSGRGRAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLEEHIAEIVKLFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLEEHIAEIVKLFADKADVP HIAQNAAQQT VKONGYNLAVSSYVEAEDTRE					

```

                                430          440          450          460          470          480
                                490          500          510
m605.pep      IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX
               :|||:|||||:|||||:|||||:|||||:|||||:
g605          VIDIRQLNAEISETVAKIERLRREIDEVIAEITX
               490          500          510

```

**a605.s eq**

This corresponds to the amino acid sequence <SEQ ID 1912; ORF 605.a>:

a605.pcp

**m605/a605 98.1% identity in 514 aa overlap**

```

      10      20      30      40      50      60
m605.pep  MMTEMQQR AQLHRQIWKIADEVRGAVD GDFKQYVLGTLFYRFISENFTDYMQAGDSSID
          |||:||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a605       MMTEIQQR AQLHRQIWKIADEVRGAVD GDFKQYVLGTLFYRFISENFTDYMQAGDSSID
      10      20      30      40      50      60
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m605.pep  YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS
      70      80      90     100     110     120

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a605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS	70	80	90	100	110	120
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEALDFGNFENHHIDLFGDAY	130	140	150	160	170	180
a605	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGVAEALDFGSFEDHHIDLFGDAY	130	140	150	160	170	180
m605.pep	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF	190	200	210	220	230	240
a605	EYLISNYAANAGKSGGEFFTPQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF	190	200	210	220	230	240
m605.pep	DEHIIIEGFFGQEIINHHTYNLARMNMFHLNVNYNQHFIELGDTLTNPCLKDKSKPFDIVS	250	260	270	280	290	300
a605	DEHIIIEGFFGQEIINHHTYNLARMNMFHLNVNYNKFHIELGDTLTNPCLKDKSKPFDVVS	250	260	270	280	290	300
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFATILHALNYLSGRGRAAIVSFPGI	310	320	330	340	350	360
a605	NPPYSINWIGSGDPTLINDDRFAPAGVLAPKSKADFATILHALNYLSGRGRAAIVSFPGI	310	320	330	340	350	360
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF	370	380	390	400	410	420
a605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDAGGF	370	380	390	400	410	420
m605.pep	FKKETNNNVLEEIHIAEIVKLFADKADVPHIAQNAAQQTVKDNGYNLAVSSYVEAEDTRE	430	440	450	460	470	480
a605	FKKETNNNVLTEEHIAEIVKLFADKADVPHIAQNAAQQTVKDNGYNLAVSSYVEPEDTRE	430	440	450	460	470	480
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX	490	500	510			
a605	IIDIKQLNAEISSETVAKIERLRREIDEVIAEIEAX	490	500	510			

g606.seq

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNATFATGAS RNSSLIAVST GLLDHMTREDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSLL STHPSLDNRI ARLKSL*

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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq

```

1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAATGGCA CACGTCGGCA ACGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCCT GGTCAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCGGAA AATGATTTC GCCCTGCAA
551 GGCTCAAAGG CAACCCGGTC GATTGCGCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTGCTGGA
651 CAACCGTATC GCCCGCCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep

```

1 MSKFIAKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51 EPNATFATGAS RNSSLIAVST GLLDHMTREDE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSLL STHPSLDNRI ARLKSL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

m606.pep	10	20	30	40	50	60
	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNATFATGAS					
g606	MSKFIAKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNATFATGAS					
	10	20	30	40	50	60
m606.pep	70	80	90	100	110	120
	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	130	140	150	160	170	180
	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	190	200	210	220		
	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1   ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGCGCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTGTGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTGCGCA ACGGCGATAT GGTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGACGC
501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTC GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCC AAGAAATGAA CGCAATGGGC
601 ATCGCCGAG ATACGCGCA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCCTCA AATCGCTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1   MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKSL*

```

m606/a606 100.0% identity in 226 aa overlap

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAARQWNLTPEVAIYHSPEPNAFATGAS					
a606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAARQWNLTPEVAIYHSPEPNAFATGAS					
	10	20	30	40	50	60
m606.pep	RNSSLIAVSTGLLDHMTREVEAFLAHEMAHVGNGDMVTTLTIQGVVNTFVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREVEAFLAHEMAHVGNGDMVTTLTIQGVVNTFVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREVEAFLAHEMAHVGNGDMVTTLTIQGVVNTFVFLSRIIAN					
a606	RNSSLIAVSTGLLDHMTREVEAFLAHEMAHVGNGDMVTTLTIQGVVNTFVFLSRIIAN					
	70	80	90	100	110	120
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
a606	LIARNNDGSQSOGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
m606.pep	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
a606	ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1   ATGCTGCTCG accTegaCCG CTTTTCCTtt tccGTCTTCC TGAAAGAAAT
51  CCGCCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTGCG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGATGATT TGTGTGGGC
351 GCGGATTACG CCGTTCGCGA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAAatggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGCGGCA
451 ATGGTACACC GCGCACTGCA CGCTACGCT TCCAGCCTGA ACCGCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGTGCGGCA

```

```

601 GGTTCGGCG TGGCGACAAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAAATTCTT CCGCCCGTTC GGAATGACAG
701 CGAAATTCGg caaACCGGat tGGgcGGTGT TCAAACAGAT TtGGAAAATC
751 gGcgcgCCCA TCGGGCTGTC TTATTTTTTG GAAGccaGcg cGTTTTCGTT
801 TATCGTGTGTT TTGATTGCGC CtttcggCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTGCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCAG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CAGGAGTGTC GCTGGTGTGCG GGCTGGGTGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGCA
1051 AGCATGTACA ACGATGaTCC GGCAGTTTAA AGCATCGCCT CCACCGTCTT
1101 GCTGTTTCGCC GGCCTGTtcc aACCGGCAGA CTTCAACCAA TGTATCGCGT
1151 CCTATGCCCT GCGCGGCTAC AAAGTACCA AGGTGCCGAT GTTCATCCAC
1201 GCGCGCGCCT TCTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC AGCCGTCGCC TTGGTGTGGT GCTTGGAAAA ATACAGTATG
1351 GAGTTGGTCA AATCACACAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1 MLLDLDRFSF SVFLKEIRLL TALALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT GEAGETGRQG
101 IWFGILIGIF GMILMWAAT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRLAHAYA SSLNRPRILM LVSPFAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGVATMAVF WFSALALWIY IAKEKFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSIFV LIAPFGEDYV AAQQVGISLS GILYMPIQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWVLAVITVL SLVLFERSPLA
351 SMYNDPAVL SIASTVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFMFIH
401 AAAFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAVA LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1 ATGCTGCTCG ACCTCAACCG CTTTTCTTTT CCGTCTTCC TGAAAGAAGT
51 CCGCCTGCTG ACCACTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTGCGCG
101 AGGTGGGCAT CGGTTTTGTC GATACTGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CCGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGTAATAACC GACGAAGTGG GCGAAACGGG GCGCGAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTC GGCATGGTCT TGATGTGGGC
351 GCGGATTACG CGGTTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACGATGGC GCAGTATATG TTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCGCTGCA CGCCTACACT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAATGACCG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTGTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTCGGCAT CAGTTTGTGCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GGCGCGAATT
951 TTCGCGGGCG CGTTATATTT CCGGCGTGTC ACTGGTGTTA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCGG CCACCGTCTT
1101 ACTGTTTCGCC GGCTTGTTC AACCAGCAGA CTTCAACCAA TGTATCGCCT
1151 CCTACGCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCCGCGCCT TTTGGGGCTG CGGCCTGCTG CCGGGCTATC TGCTCGCCTA
1251 CCGTTTCAAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCATCGCC TTGGTGTGGT GCTTGGAAAT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1 MLLDLNRFSF FVFLKEVRLT TTLALPMLLA QVAQVGIGFV DTMAGGAGK
51 EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG

```



**Homology with a predicted ORF from *N.gonorrhoeae***

from *N. gonorrhoeae*:

m607/g607

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTLALPMLLAQVAQVGI	GFVD	TMAGGAGKED	LA	AAV	ALGS
	:	:	:	:	:	:
g607	MLLDLDRFSFSVFLKEIRLLTALALPMLLAQVAQVGI	GFVD	TMAGGAGKED	LA	AAV	ALGS
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNP	MI	AQLYGAGKTDEV	GETGRQGIWFG	LFLGVFGM	VL
	:	:	:	:	:	:
g607	SAFATVYITFMGIMAALNP	MI	AQLYGAGKTGE	AGETGRQGIWFG	LILGIFGM	IL
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQ	YMLFTSL	AMPAA	MVHRALHAYT	SSLNRP	RLIMLV
	:	:	:	:	:	:
g607	PFRNWLTLSDYVEGTMAQ	YMLFTSL	AMPAA	MVHRALHAY	ASSLNRP	RLIMLV
	130	140	150	160	170	180
m607.pep	190	200	210	220	230	240
	VPLNYIFVYGKFGMPALG	GAGCG	LATMAVFWFS	SALALWII	YIAKENFF	RPFG
	:	:	:	:	:	:
g607	VPLNYIFVYGKFGMPALG	GAGCG	VATMAVFWFS	SALALWII	YIAKEK	FFRP
	190	200	210	220	230	240
m607.pep	250	260	270	280	290	300
	WAVFKQIWKIGAPIGLS	YFLEAS	AFSFI	VFLIAPFG	EDYVAAQ	QVGISL
	:	:	:	:	:	:
g607	WAVFKQIWKIGAPIGLS	YFLEAS	AFSFI	VFLIAPFG	EDYVAAQ	QVGISL
	250	260	270	280	290	300
m607.pep	310	320	330	340	350	360
	GSAGTVRIGFSLGRREF	SRARYI	SGVSLV	LGWMLAVIT	TVLSVL	FRSP
	:	:	:	:	:	:
g607	GSAGTVRIGFSLGRREF	SRARYI	SGVSLV	SGWVLAVIT	TVLSVL	FRSP
	310	320	330	340	350	360
m607.pep	370	380	390	400	410	420
	SIAATVLLFAGLFQPA	DFTQCI	ASYALRGYK	VT	KVPMFI	HAAAFW
	:	:	:	:	:	:
g607	SIASVLLFAGLFQPA	DFTQCI	ASYALRGYK	VT	KVPMFI	HAAAFW
	370	380	390	400	410	420
m607.pep	430	440	450	460		
	MGIYGFWTALIASLTIA	AAIALV	WCLELCS	REMV	VRSHK	AVX
	:	:	:	:	:	:
g607	MGIYGFWTALIASLTIA	AAIALV	WCLEKYS	MELV	KS	HKAVX
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TCGGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGGTAAAACC GACGAAGTGG GCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGCGCAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCTACGCC TCCAGCCTGA ACCGCCGCGC
501 CCGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTCTT CCGCCCATTC GGACTGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGAAAAATC
751 GGCGCACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCTGT
801 TATCGTGTTC TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTTGTG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTGCGGCG GGACGGTGCG CATCGGCTTT TCGCTGGGCG GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGTGTC ACTGGTGTC GGATGGATGC
1001 TCGCGTGAT TACCGTGCT TCCTTGATAT TATTCCGTTT GCCGCTGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTCCGC GGCTTGTTCC AACCGGCAGA CTTACCCAA TGTATCGCCT
1151 CCTACGCCTT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGCTG CGGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSE SVFLKEVRLT TALALPMLLA QVAQVGIGFV DTVMAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRAHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNNPVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFMFIH
401 AAFFWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSPFVFLKEVRLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSPFVFLKEVRLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFLFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFLFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYASSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAVHRAHAYASSLNRPRILMLVSFAAFVLN					
	190	200	210	220	230	240

970

```

m607.pep      VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a607          VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
              190      200      210      220      230      240

              250      260      270      280      290      300
m607.pep      WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV
a607          WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPOSV
              250      260      270      280      290      300

              310      320      330      340      350      360
m607.pep      GSAGTVRIGFSLGRREFSRARYISGVSLVGLWMLAVITVLSLVLFRSPLVSMYNNDPAVL
a607          GSAGTVRIGFSLGRREFSRARYISGVSLVSGWMLAVITVLSLVLFRSPLVSMYNNDPAVL
              310      320      330      340      350      360

              370      380      390      400      410      420
m607.pep      SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIHAAAFWGCGLLPGYLLAYRFN
a607          SIAATVLLFAGLFQPADFTQCIASALRGYKVTKVPFIHAAAFWGCGLLPGYLLAYRFD
              370      380      390      400      410      420

              430      440      450      460
m607.pep      MGIYGEFTALIASLTIAAIALVWCLELCSREMVRSRKAVX
a607          MGIYGEFTALIASLTIAAIALVWCLELCSREMVRSRKAVX
              430      440      450      460

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGAT
201 ACGGAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCATcaaa cAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1   MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPEGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1   ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGCAG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAACG GCTTTGCAGA CACCGAAATT ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAATC CGAGTCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

```

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEPPAGD IGLEGLIIG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng) from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
g608	MSALLPIINRLILQSPDSRSELT SFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPPAGDIGLEGLIIGIAVLSLLGSLRSRASDELARIFGTQADIGS					
g608	TFRNSAIRKILQGGEPPAGDIRLEGLIIGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADC LDEISRLRDGVERLNERLDR					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADC LDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq

1 ATGTCCGCCC TCCTCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA  
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA  
101 TTGCCGGGTT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG  
151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT  
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG  
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG  
301 CGTTCGCGCG CATCGGACGA ATTGGCACGG ATTTTCGCA CGCAGGCAGA  
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAA CAAATCGGCA  
401 GGAACATCGC CGAACAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA  
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT  
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG  
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep

1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS  
51 AGNGFADTEI TFRNSAVQKI LQGGEPPAGD IGLEGLIIG IAVLSLLGSL  
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA  
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID\*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep    MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608        MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
              10      20      30      40      50      60

              70      80      90     100     110     120
m608.pep    TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608        TFRNSAVQKILQGGEPPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
              70      80      90     100     110     120

              130     140     150     160     170     180
m608.pep    RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608        RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
              130     140     150     160     170     180

              189
m608.pep    LERDIWIDX
a608        LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAAATTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTCTG TGGCCGTATG
351 CCCCCTCTTT CATTTACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GLFGNVFFIG
51 AFEQAVELAA RLRFHIIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TCGGTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTCTG TGGCCGTATG
351 CCCCCTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDDETLDAFV GNQRSSDIAH HIFHEFRVFEV GFFGNVFFIG
51 AFEQAVELAA RLRHIIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFAETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

              10      20      30      40      50      60
m609.pep    MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFEVGFNGNVFFIGAFEQAVELAA
a609        MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFEVGLFGNVFFIGAFEQAVELAA
              10      20      30      40      50      60

              70      80      90     100     110     120
m609.pep    RLRHIIIDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
a609        RLRHIIIDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF

```

```
a609.seq
1 ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACCTTTGA
51 TGC GTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTTTCTGA GGCTTTTTTCG GTACAGTATT TTTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGGTTGTG CGCGCCATAT TGGGAATTT CTTTGGAAAC
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCATACTG TGGCCGTATG
351 CACCGTCTTT CATTTCGCCG GTGAGGCTGA CATCATAACT CAGTAA
```

```
a609.pep
1  MVVDRLEILA LDDETLDFAV GNQRSSDIAH HIFHEFRV FV GFFGNVFFIG
51  AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAILGNFFGT
101 RAKRGYGNHD LHTVAVCTVF HFAREADIII Q*
```

```

                                10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFGVFFGNVFFIGAFEQAVELAA
           |||||:|||||
a609       MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFGVFFGNVFFIGAFEQAVELAA
           10      20      30      40      50      60

                                70      80      90      100     110     120
m609.pep  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
           |||||:|||||
a609       RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
           70      80      90      100     110     120

                                130
m609.pep  DFARETDIIIX
           |||:|||||
a609       HFAREADIIIX
           130

```

```

g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCCCTTAC  CGCAATGTTT  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  ATGATTTTTC  ACGC CGCTG  ATGCGCGAGC
101 ATATGCTGAC  CGCCGATGAT  TTGATTATC   CGGTGTTCTG  ATTGGAGGGG
151 GCGGCGCGCG  AGGAGGATGT  GCCTTCTATG  CGCGGCTGTA  AGCGTCAGAG
201 TTTGGACAGG  CTGCTGTTTA  CGCGCGAAGA  GCGCGTGAAG  CTCGGTATTC
251 CGGATGTGGC  ACTCTTTCCC  TGCTTACGG  CAAACAAAAC  CGCGCGTCGG
301 CAGGAGCGCT  ACAATCCCA  AGGACTCGTG  CGGTCAACTG  tccgagccTT
351 GCGCGAGAGG  TttcCgaa  tggggattat  gacggatgtc  cgctcgatC
401 cttatacgtt  gcaacGGT  GAGCAGCTGA  CGGACgaaa  gggtaCGTC
451 ATGAatgAtg  aaaCCGTAG  AGTCTTGGTG  AAACAGGCTT  TATGTCATGC
501 AGAGGCGGGC  ACGCAGGTG  TTGCTCCTTC  CGATATGATG  GACGGGCGTA
551 TCGGCGCCAT  CCGCGAGCT  TTGAGGATG  CGGCACATAT  CCATACGGCG
601 ATTATGGCAT  ATTCGCGCAA  ATGCTCTTCT  GCATTCTACG  GCGCTTTCCG
651 TGATCGCGTA  GGCAGTTCGG  GCAATTGGG  AAAGGCAGAT  AAAAAGACCT
701 ATCAGATGGA  TCCTGCAAT  ACCGATGAGG  CGCTGCATGA  AGTGCGGCTC
751 GATATTCAGG  AAGGTGCGA  TATGCTGATG  GTGAAGCCCG  GTTTCGCGTA

```

801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG  
 851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC  
 901 GGC TGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA  
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA  
 1001 AGA TGCTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

**g610.pep**  
 1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG  
 51 AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA  
 101 QEA YNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHVG DGLTDENGIV  
 151 MND ETVELV KQALCHAEAG QVVPASDMM DGRIGAIRES LEDAGHIHTR  
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYYQMDPAN TDEALHEVAL  
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAVAN  
 301 GWLDGGKVVL ESLLAFFKRA GADGILTYAI EAAKMLKR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

**m610.seq**  
 1 ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTC CGGCTTCGCG  
 51 TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCCTG ATGCGCGAAC  
 101 ACACGCTGAC CGCCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG  
 151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG  
 201 TTTGGACAGG CTGCTGTTTA CGCGGGAAGA GCGGTAAAG CTCGGTATTG  
 251 CGATGTTGGC ACTGTTCCCC GTGGTACGG CAAACAAAAC CGAGCGTGCG  
 301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT  
 351 GCGCGAGAGG TTTCCGGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC  
 401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG  
 451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC  
 501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTC CGATATGATG GACGGGCGTA  
 551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG  
 601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG  
 651 TGATGCGGTA GGCAGTTCGG GCAATTGGG CAAGGCAGAT AAAAGACCT  
 701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG  
 751 GACATTACAG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTGCCGTA  
 801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG  
 851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC  
 901 GCGTGGCTGG ACGGCGGCAA AGTGGTTTG GAAAGCCTGC TGGCATTCAA  
 951 ACGTGGCGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA  
 1001 AGATGTTGAA GCGTTGA

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

**m610.pep**  
 1 MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG  
 51 SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA  
 101 QEAYNPEGLV PSTVRALRER FPGLGIMTDV ALDPYTVHVG DGLTDENGIV  
 151 MND ETVELV KQALCHAEAG QVVPASDMM DGRIGAIRES LEDAGHIHTR  
 201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYYQMDPAN TDEALHEVAL  
 251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLQAAIAN  
 301 GWLDGGKVVL ESLLAFFKRA GADGILTYAI EAAKMLKR\*

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPGLGIMTDVALDPYTVHVGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVVPASDMM					
g610	FPGLGIMTDVALDPYTVHVGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVPASDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYYQMDPAN					

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```
g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLKGADKKTYQMDPAN
           190      200      210      220      230      240
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
           250      260      270      280      290      300
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330      339
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```
a610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCCTG ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GCGGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTACAG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCGCGG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGCGGCAA AGTGGTTTGG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```
a610.pep
1  MIGGLMQFPY RNVSASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGO DGLTDENGIV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLKGAD KKTQYMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSGE YAMLOAAVAN
301 GWLDGGKVVV ELLAFKRAG ADGILTYAI EAAKMLKR*
```

m610/a610 99.4% identity in 338 aa overlap

```
           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNVPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
a610      MIGGLMQFPYRNVSASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60
           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120
           130     140     150     160     170     180
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```

m610.pep    FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
a610        FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
              130      140      150      160      170      180

              190      200      210      220      230      240
m610.pep    DGRIGAIRESALEDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLKGADKKTYQMDPAN
a610        DGRIGAIRESALEDAGHIHTRIMAYSAKYASAFYGFPRDAVGSSGNLKGADKKTYQMDPAN
              190      200      210      220      230      240

              250      260      270      280      290      300
m610.pep    TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAIAIAN
a610        TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAIAIAN
              250      260      270      280      290      300

              310      320      330      339
m610.pep    GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
a610        GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
              310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTCCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCTGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tctcctTGGG CGGGCTGggt tgtttgcccg ccataaTtTc cagtacctga
251 TcgcgGTCTa tggtttccCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggaacCTGA TACTgctcgt
351 ccaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTCGG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gCTCATgcCG TAGCGCGTTA
501 CCATTTCCGG TGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIADVGF FHQGFARHNF
101 LVAVFIEDFV GNLLLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAFHV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1  ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTCCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCTGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTGA TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTCGG AACGGGTtac GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GCTCATGCCG TAGCGCGTTA
501 CCATTTCCGG CGCCATTGG GTTGC GCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1  MPSENGMKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHNF
101 LVAVFIEDFV GNLLLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAFHV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
g611          MPSENGMGKRQLAGCRLFGKLSLVFRLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
g611          LAQVVAVILGRAGLFARHNFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
g611          ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
              130     140     150     160     170     180

m611.pep      X
              |
g611          X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGCTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTTGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCGA TGGTTTCCCA TTCCATCAGG GCTTGCACA TCGTTTCCAT
301 CTTGTCGCGG TTTTCATCGA GGATTGTGTA GGCAACCTGA TACTGCTCGT
351 CCAAATCCG GCGGATTTC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTGC GTCATGCCG TAGCGCGTTA
501 CCATTTGCGC CGCATTGTT GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFL
101 LVAVFIEDFV GNILLVQNP ADFRIDVLLG FLGNVLRGTY AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

              10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              |||||
a611          MPSENRMGKRQLAGCRLFGKLSLVFRLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
              10      20      30      40      50      60

              70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
a611          LAQVVAVIFGRAGLFARHDFQYLIADVGFPHQGFARHFLVAVFIEDFVGNLILLVQNP
              70      80      90      100     110     120

              130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
a611          ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
              130     140     150     160     170     180

m611.pep      X

```

a611

|  
X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

```
g612.seq
1  ATGGGcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51  AGCCTttgac ttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CCGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

```
g612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFGR DDAVRHSGVI NAAVAGLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRFFY GHSN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

```
m612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTTAC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

```
m612.pep
1  MGFGGNIAKK LAGVDEIAFN FDGIVDFGR DDAVRHSGVI NTAVACLHIV
51  GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLNKSK SPDIFRFFY GHSN*
```

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFGRDDAVRHSGVINAAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVPPIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	KCAENVLFKVPPIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFY					
g612	KCAENVLFKVPPIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

```
a612.seq
1  ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51  AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTAAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTTT.AC GGCATTCAA ATTAA
```

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101 NPYXKLNKSK SPDIFRFFFX GHSN*

m612/a 612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep      MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
a612           MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFDKAVE
              10      20      30      40      50      60

              70      80      90      100     110     120
m612.pep      KCAENVLFKVPAIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRFFFX
a612           KCAENVLFEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRFFFX
              70      80      90      100     110     120

m612.pep      GHSNX
a612           GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 tgtttGcgGA CTCGGGTTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTgtttGat GCCGTGTCCG ATGTCGGTGG CACGgtgcc
201 gatgcCTGCC TGCCTGCCGA AAATCCGTGC CAATTCgtCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301 CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CCGTATCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATTGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT
601 ATTTTACAGG CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFFAESKPS SVMRPAFSP
151 AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201 ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
1  ATGTCGCGTT CGAGCCGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTTGCGGA CTCGGATTTCG CGGGAAAATC CGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGCTGCC
201 GATGTCTGCC TGCCTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCCGA AGGTAATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGCGGCAA GTTCCGAGCG
501 GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTGCCGCTT

```

601 ATTTTACAGG CTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```
m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMEFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFFAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMEFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRICTA					
	:					
g613	MSVARLPMPACVVKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSPAPGSPPWRICTA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPKAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1  ATGTGCGCGTT CGAGCCGGTC GAGGCGTTCG TTGAGGCGTT CCACGCCGTC
51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCGTTGCCGA
101 TGTTCGCGGA CTCGGGTTTCG CGGGAATATC TGCCGATTTC TTCGGCGATG
151 TTCCTGCCGA TTTGTTTATG GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201 GATGTCCTGC TCGGTGCCGA AAATCCGTGC CAATTCGTCC GATGCGCGGG
251 AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301 CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCGCCTT GGAGGATTTT
351 CTGTACCGCG CTGTTGCCGA AGGTGATTTC GGTGTCTGCA AAGCCGTTTC
401 CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAACCCG
451 GCAATGTTCA GGGTCAGTGT TTTGCCTGCG AAGCGGCGAA GTTCCGAGCG
501 GCTGTCCGGG CTTTCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551 ACATATTTTC TGATCGGGGC GGAGAATGCC TGTGTTGCT GTTACGCTT
601 ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSGS RENLPICAM
51  FLPICLMPCP MSAARLPSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101 PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KPFFAESKPS SVMRPASFNP
151 AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLTL
201 ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSGSRENLPICAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
a613	MSAARLPSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFNPAMFRVSVLPKAASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

## g614.seq

```

1   AtggcTgcgt tcAacgcttt ggacggcaaa aaagaagaca acgggcaaat
51  cgaaTATTCT CAGTTCATCC GACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGTT ACCTGATTAA AGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCCTTGGATG ACAACCTGAT
201 TCAAACCTTT TTGAACAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGACTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGGTTCTA CTTTATGCGT ATGCAGGCGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCCT TCGGCAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCAC CGAACCGCta
501 tcaAAGcctc ggcggccgtg ttcCGCGCGG CATCctgCtg gcgGgcagcc
551 CGGGAaccgg taaAACACTC TTGGCGAAAG CCATTGCAGG CGAGGCCGGC
601 GTGCCGTTCT TCAGCATTTT CCGTTCGGAT TTTGTGAAA TGTTCGTGCG
651 TGTCCGTTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCA AAGAAAAACG
701 CCCCATGCAT TATCTTTATC GACGAGATTG ACGCGGTAGG CCGCCAACGC
751 GGCGCAGgTT TGGCGGCGG CAATGATGAG CGCGAGCAA CATTAAACCA
801 ATTATTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GCGCGCTTCG ACCGCCAAGT CGTCGTCCCC CTGCCGACA TCCGGGGGCG
951 CGAACAGatn ttGAACGTCC ATTCTaaaAAA AGTGCcttTG gacgaATCTg
1001 tggatTTTATT GTCCCTCGCG CGCGGCACGC ccggtttTtc cggcgcgat
1051 tTggcgaaac tgytcaacga agccccctg tttgccggcc gccgcaacaa
1101 agtgaaagtc gatcaaagcg attTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

## g614.pep

```

1   MAAFNALDGK KEDNGQIEYS QFIRQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFFTNA PLDDNLIQTL LNKNVVRVKVT PEEKPSALTA LFYSLLPVLL
101 LIGAWFYFMR MQAGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAGEAG
201 VPFFSISGSD FVEMFVGUGA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGNDE REQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQX LNVHSKKVPL DESVDLLSLA RGTGPFSGAD
351 LAKLVNEAPL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

## m614.seq

```

1   ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
51  CGAATACTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101 TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151 ACCGACAAAA GCACCTTCTT CACCAACGCG CCTTGGACG ACAACCTAAT
201 TAAACACTG CTGACAAAAA ACGTCCGCGT AAAAGTAACG CCGGAAGAAA
251 AACCGAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCCTGCTG
301 CTGATTGGCG CATGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGTAAAAG CCGCGCCCGC CTGCTGGACA
401 AAGATGCCAA CAAAGTGACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TACAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCG
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTCCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGAAA TGTTCGTGCG
651 TGTCCGTTGCG AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGCGAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGCGGCGG CAATGATGAG CGCGAGCAA CATTAAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACGCCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GCGCGTTTCG ACCGCCAAGT GGTGTGCCCC CTGCCGACA TCCGAGGGCG
951 CGAACAGATT TTGAACGTCC ATTCTAAAAA AGTGCCTTTG GACGAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

```

m614.pep
  1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
 51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101  LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151  KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201  VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251  GAGLGGGND EQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301  GRFDRQVVV LPDIRGREQI LNVHSHKKVPL DESVDLLSLA RGTPGFSGAD
351  LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m614/g614 98.0% identity in 391 aa overlap

m614.pep	10	20	30	40	50	60
	MAAFNALDGKKEEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
g614	10	20	30	40	50	60
	MAAFNALDGKKEEDNGQIEYSQFIRQVNNGEVSGVNIIEGSVVSGYLIKGERTDKSTFFTNA					
m614.pep	70	80	90	100	110	120
	PLDDNLIKTLDDKNVRVKVTPPEEKPSALAAALFYSLLPVLLIGAWFYFMRMQTGGGKGG					
g614	70	80	90	100	110	120
	PLDDNLIQTLLNKNVRVKVTPPEEKPSALTALFYSLLPVLLIGAWFYFMRMQAGGGKGG					
m614.pep	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLLKAPNRYQSLGGRVPRGILL					
g614	130	140	150	160	170	180
	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLLKAPNRYQSLGGRVPRGILL					
m614.pep	190	200	210	220	230	240
	AGSPGTGKTLAKAIAEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
g614	190	200	210	220	230	240
	AGSPGTGKTLAKAIAEAGVPFFSISGSDFVEMFVGASRVDRMFQAKKNAPCIIFI					
m614.pep	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
g614	250	260	270	280	290	300
	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTIVIVIAATNRPDVLDPALQRP					
m614.pep	310	320	330	340	350	360
	GRFDRQVVVPLPDIREQILNVHSHKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
g614	310	320	330	340	350	360
	GRFDRQVVVPLPDIREQXLNVHSHKKVPLDESVDLLSLARGTPGFSGADLAKLVNEAPL					
m614.pep	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	370	380	390			
	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1965>:

```

a614.seq
  1  ATGGCTGCGT TCAACGCTTT AGACGGTAAA AAAGAAGACA ACGGGCAAAT
 51  CGAATATTCT CAGTTCATCC AACAGGTCAA CAACGGCGAA GTATCCGGCG
101  TCAACATCGA AGGATCCGTC GTCAGCGGCT ACCTGATTAA GGGCGAGCGC
151  ACCGACAAA GCACCTTCTT CACCAACGCG CCTTTGGACG ACAACCTGAT
201  TAAACACTG CTCGACAAA ACGTCCGTGT AAAAGTAACG CCGGAAGAAA
251  AACCAGCGC GCTGGCTGCC CTGTTTACA GCCTGCTGCC CGTCTGCTG

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301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCCTGA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTGAAA TGTTCGTCGG
651 TGTCGGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCTGTCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAA CATTAAACCA
801 ATGTTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCCGTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAA AGTGCCCTTG GACAAATCTG
1001 TGGATTATT GTCCCTCGCG CGCGCAGCG CGGGTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGAA CGCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQVNNGE VSGVNIIEGVS VSGYLIKGER
51  TDKSTFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIAEAG
201 VFFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND EQLTNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKVP LDKSVDDL SLARGT PGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

m614/a614 99.7% identity in 391 aa overlap

          10      20      30      40      50      60
m614.pep  MAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGVS VSGYLIKGERTDKSTFFTNA
          |||
a614       MAAFNALDGKKEDNGQIEYSQFIQVNNGEVSGVNIIEGVS VSGYLIKGERTDKSTFFTNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m614.pep  PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG
          |||
a614       PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGKGG
          70      80      90      100     110     120

          130     140     150     160     170     180
m614.pep  AFSFGKSRARLLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
          |||
a614       AFSFGKSRARLLDKDANKVT FADVAGCDEA KEEVQEIVDY LKAPNRYQSL GGRVPRGILL
          130     140     150     160     170     180

          190     200     210     220     230     240
m614.pep  AGSPGTGKTL LAKAIAEAG VFFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          |||
a614       AGSPGTGKTL LAKAIAEAG VFFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI
          190     200     210     220     230     240

          250     260     270     280     290     300
m614.pep  DEIDAVGRQRGAGLGGGNDEREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          |||
a614       DEIDAVGRQRGAGLGGGNDEREQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
          250     260     270     280     290     300

          310     320     330     340     350     360
m614.pep  GRFDRQVVVPLPDIRGREQI LNVHSHKVP LDKSVDDL SLARGT PGFSGAD LANLVNEAAL
          |||
a614       GRFDRQVVVPLPDIRGREQI LNVHSHKVP LDKSVDDL SLARGT PGFSGAD LANLVNEAAL

```

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	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

g615.seq

1	ATGTGGA	AAAC	GGCGGCGGCG	CGGTGtcggc	AGCTTtgaag	agcagcGaAT
51	agatgCGCC	GGCAAACAC	AATGCGGAAa	gcaggCtgaa	gcGGTTgcgC	
101	GGCagcTTca	tGCCGCCTCC	TcGTCCaGCC	ACGtttGgca	gattttggac	
151	agcgcgAGga	ATTTGCcgCc	gcgtgcggCA	agtatgtcgc	gcCAttgtgc	
201	cacttcttcg	gcggacggTG	cttcgtcgaT	gctgCATTcG	TACagcagga	
251	aatcgagggt	ttcttcgatg	acggGgatgg	AttccgTTTG	GataAgCTgc	
301	ttgagttcgt	tcatgactGt	TCgGATAcgg	aaatcgggaa	aatgccgtct	
351	gAaagggtct	CAGACGGCat	tggATTATTT	GCTGTGCAGG	Aagcgcggtg	
401	cctcttccca	tttgcCGGAA	AtgATGTCGg	gtacggcctg	cAGGGATtg	
451	gCGACGGcat	cgtcgatttg	ccgGcggtgc	ttCcgcgctc	ggtttGTTca	
501	agacgtagcc	gaCGACGagg	ttcggtcGC	CGGGGtggcC	GATGCCGAGG	
551	CGCAGGCGGt	aatagctcgC	CGTGCCGAGT	TTTGcctgAA	TGTCTTTCAA	
601	GCCGTTGTGT	CgcCGttgc	cgcCGCCGAG	TTTGAATTTg	ATCCGTCCGC	
651	AAGGGATGTC	GAGTTCGTcG	TGGACGACGA	GGATTCTTC	GGGTTTGATT	
701	TTGTAGAAct	GTGCAAGCGC	GGCAACCGCC	TGTCCGGAAC	GGTTCATGAA	
751	CGTGGCCGGT	TTGAGCAGCC	AAACATCGCC	GTCGGGCAGG	GCGGCGCGGG	
801	CAACTTCGCC	GAAGAATTTT	TTTTCTTCTT	TAAACGAAGC	CTTCCATTTC	
851	CAGCCAGTT	CGTCGAGGAA	CCAAAAGCCC	GCATTGTGGC	GGGTCTGTTC	
901	GTATTCTTTG	CCCGGGTTGC	CCAAGCCGAC	AACCATTTTG	ATTGTGtctg	
951	acatgataTT	TtccgtgTTT	CTgTCGaag	cggTctgaAG	GCTTCAGacg	
1001	gcatggTtaT	TCTTCTTgat	TTtgaACgcg	tgtgcggCGC	GCTTCTTTGG	
1051	GGTCGATCAA	CAGCGGGCGG	TACACTTCGA	TGCGGTGCC	GTCGCGCAGC	
1101	GGCGTGTCTG	CTTTGA				

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

g615.pep

1	MWKRRRRGVG	SFEEQRIDAA	GKPQCGKQAE	AVARQLHAAS	SSSHVWQILD
51	RRRNLPPrAA	SMsRHcATSS	ADGASSMLHS	YSRKsRVSSM	TGMDSVWISC
101	LSSFMtVRIR	KSGKcRLKGL	QTALDYLlCR	KRVASSHLPE	MMSGtACRDL
151	ATASSICRRc	FRARFVQDVA	DDEVAVAGVA	DAEAQAVIVc	RAEFCLNVfE
201	AVVSAAVAaE	FEFDPSARDV	EFVVDDEFF	GFDFVELCKR	GNRLSGTVhE
251	RGRFEQPNIA	VGQGGAGNFA	EEFFFFFKRS	LPFPQFVEE	PKARIVAGLf
301	VFFARVAQAD	NHFDCVRHDI	FRVSVEcGLK	ASDGMVILLD	FERVCGALLW
351	GRSTAGGTLR	CGRRAAAACR	L*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

m615.seq Length: 1116

1	ATGCGGAAAA	GGCGGTGGCG	CGGTTTCGGC	AGCTTTGAAA	AGCAGTGAGT
51	AAATGCTGCC	TGCAAACAC	AATGCCGAGA	GCAGGATAAA	GCGGTTGCGT
101	GGCAGATTCA	TGCTTGTTCC	TCTTCAAGCC	ATGTCTGGCA	TAGTTTGAT
151	AGGCGCAGGA	ATTTTCGCC	GCGTGCGGCC	AGCATATCGC	GCCAAACGGC
201	AATTTCTTCG	GCGGAGGGGG	CATCGTCTAT	GCTGCATTcG	TAGAGCAGGA
251	AATCGAGGGT	TTCTTCGATG	ACGGGGATGG	ATTcGGTTTG	GATAAGCTGC
301	TTGAGTTCGG	TCATGACTGT	TCGGATATGG	AAATCGGGAA	CATGCCGTCT
351	GAAAGGGGCT	CAGACGGCAT	CGGGTCATT	GCTGTGCAGG	AAGCGGGTTG
401	CTTCTTCCCA	TTTGCCGGCA	AGGATGTCGG	GTATGGCTTG	CAGGGATTTG
451	CGACCGGCAT	CGTCAATCTG	TCGGCGGTGT	.TCCGTACTG	GGTTTGTTCA
501	GGACATAGCC	GACGACGAGG	TTGCGGTcGC	CCGGGTGGCC	GATGCCGAGG
551	CGCAGGCGGT	AATAGTCTGC	CGTGCCGAGT	TTTGCCTGAA	TGTCTTTCAA
601	GCCGTTGTGT	CCGCCGTTGC	CGCCGCCGAG	TTTGAATTTG	ATCCGTCCGC
651	AGGGAATGTC	GAGTTCGTcG	TGGACGACGA	GGATTCTTC	GGGTTTGATT
701	TTGTAGAAct	GTGCAAGCGC	GGCAACTGCC	TGTCCGGAAC	GGTTCATGAA
751	CGTGGCAGGT	TTGAGCAGCC	AAACGTcGCC	GTCGGGCAGG	GCGGCACGGG

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801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GGCGTGTCTG CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFEKQXVNA CKPQCREQDK AVAWQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISRQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDPAGNV EFVVDDEDF GFDFVELCKR GNCLSGTVHE
251 RGRFEQPNVA VGQGGTG DFAEEFFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHD IFRVSVECLK ASDGMVILL DFERVCGALLW
351 GRSTAGGTLR CGRRRAACRLX L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHS LDRRRNFPPRAA					
g615	MWKRRRRGVGSFEEQRIDAAGKPQCGKQAEAVARQLHAASSSSHVWQILD RRRNLPPRAA					
	10	20	30	40	50	60
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
g615	SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSFM TVRIKSGKCRRLKGL					
	70	80	90	100	110	120
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA					
g615	QTALDYLLCRKRVASSHLPMMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA					
	130	140	150	160	170	180
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNV EFVVDDEDFGFDFVELCKR					
g615	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPASARDVEFVVDDEDFGFDFVELCKR					
	190	200	210	220	230	240
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVAVGQGGTG DFAEEFFFKXSLPFPRQFVEEPKTRIVACLF					
g615	GNRLSGTVHERGRFEQPNIAVGQGGAGNFAEEFFFKRSLPFPRQFVEEPKARIVAGLF					
	250	260	270	280	290	300
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHDFCVXHDIFRVSVECLKASDGMVILLDFERVCGALLWGRSTAGGTLR					
g615	VFFARVAQADNHDFCVRHDI FRVSVECLKASDGMVILLDFERVCGALLWGRSTAGGTLR					
	310	320	330	340	350	360
m615.pep	370					
	CGRRRAACRLX					
g615	CGRRRAACRLX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GCGGCGCGCG CGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCTCC TCGTCCAGCC ACCTTTGGCA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGC GGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTTC TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCAATT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG TTCCGTA CTG GGTTTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTGCG CCGGGTGGCC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCCGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCCGC
651 AGGGAATGTC GAGTTCGTGC TGGACGACGA GGATTCTTTC GGGTTTGATT
701 TTATAAACT GCGCAAGGGC GGCAACTGCC TGTCGGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTC
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTC
901 GTATTCTTTG CCCGGGTGTC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTGG
1051 GGTCGATCAA CAGCGGCGG TACACTTCGA TGCGGTGCGC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPCGKQAE AVARQLHAAS SSSHVWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSTVAAAE FEFDPAGNV EFVVDDEDFE GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQSTGDFE EEEEEFFK*S LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHVWHSIDRRRNFPRAA					
a615	MRKRRRRGVGSFEEQRIDAAGKPCGKQAEAVARQLHAASSSSHVWQILDRRRNLPRAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m615.pep	SISROTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCATSSADGASSMLHSYSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXFRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPAGNVFVVDDEDFGDFEVLCKR					
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPAGNVFVVDDEDFGDFIKLRKG					
	190	200	210	220	230	240
	250	260	270	280	290	300

988

```

m615.pep  GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFFFKXSLFFPRQFVEEPKTRIVACLF
a615       GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFFFKXSLFFPRQFVEEPKTRIVACLF
           250      260      270      280      290      300

           310      320      330      340      350      360
m615.pep  VFFARVAQADNHFDVCVXHDIFRVSVECCLKASDGMVILLDFERVCGALLWGRSTAGGTLR
a615       VFFARVAQADNHFDVCVXHDIFRVSAECLRKASDGMVILLDFERVCGALLWGRSTAGGTLR
           310      320      330      340      350      360

           370
m615.pep  CGRRRAAACRLX
a615       CGRRRAAACRLX
           370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTGGCTGCG TCAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGCGGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGtcggctac
451 gtcttgAAca aaccgagcgc gGagcaccg Ccggcgaatc gacgatgCCG
501 TCGccaaATC CCTgcaggcc gtaccCGACA TcaTTTCCGg caaatgggaa
551 gaggcaacgc gctTCTGCA CAGCAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAAcg gaaTccatcC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgac gaagCaccgt ccgccaaga
751 agtggcacaa TGgcgcgaca tactTGccgc acgcgGcgGC AAATtCCTgc
801 gctgtccaa aatctgcCaa aCGTGGctGG ACgAGGAGGc GGCatgAAgc
851 tGCCGcgcaA CCgcttcaGc ctgctTTCGG CATTGTGGTT TGCCGGCGGc
901 atctATtCgc tgctcttcaA AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTTcgac AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT CGCGCGAGGc
1101 ATGGTTTACC GCAACCGCAA CCGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAAL AQFYKIKPEE ILVHDELDI
101 PCGRIFKFLG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVGY
151 VLNKPSAEAP PANRRCRROI PAGRTRHHFR QMGRGNALPA QQIIQCRLKP
201 FQTAFSRFPY PMSHERTOAA YPNGIHPRHR RNPRFPAVRM QHRRSTVRRR
251 SGTMARHTCR TRQIPAPVQ NLPNVAGRG GMLPRNRFs LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAAHLALFFA QILFLAKAFK TGKLPiPYRS
351 LIAFAFCFAV GSECAQAWFT ATRTGS LGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAACTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCGTG CCGCCCTGCC CGACGGCGAC GTTGGCTGCG TCAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGAT TGCCGCGCTT GCACAGTTCT
251 ACAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCTTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 TCGCTGAACA AACCCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCCG CAAATGGGAA

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551 GAA GCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTT CAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCA AGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GAT TTTCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AAT TGCCGTT TGGCGCGATA TGCTGGCCGC ACGCGGCCGA AAATTCCTGC
801 GCC TATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGC CACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATT TACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCGCCAC CGCCTTTTCC
951 GCA TTTTGAC AAAGTGCGC ACCTCGCCT GTTTTCGCA CAAATCTGGC
1001 TTC TGACCAA AGCATTGAGA ACCGACAACC GCCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATG GTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

```

m616.pep
  1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
 51 VARAALPDGD VWLLKPATFM NRSQGAAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIFKFLG GNGGHNGLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPALRM QHRRCPRLRR
251 NCRRLARYAGR TRRKIPAPIQ TMPDMAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGS LGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

```

m616.pep      10      20      30      40      50      60
MSNTIKMVVGLNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD
|||||
g616          10      20      30      40      50      60
MSNTIKMVVGLNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD

m616.pep      70      80      90     100     110     120
VWLLKPATFMNRSQGAAVALAQFYKIKPEEILVVHDELDIPCGRIKFLGGGNGGHNGLK
|||||
g616          70      80      90     100     110     120
VWLLKPATFMNRSQGAAVALAQFYKIKPEEILVVHDELDIPCGRIKFLGGGNGGHNGLK

m616.pep     130     140     150     160     170     180
DIQAKLGTDYYRLRLGIGHPGDRNLVVGYNLKPSTEXPPTDXRCRRQIPASHTRHPCR
|||||
g616         130     140     150     160     170     180
DIQAKLGTDYYRLRLGIGHPGDRNLVVGYNLKPSEAEPANRRCRRQIPAGRTRHHFR

m616.pep     190     200     210     220     230     240
QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM
|||||
g616         190     200     210     220     230     240
QMGRGNALPAQQIIQCRLKPFQTAFSRFPYPNSHRTQAAAYPNIHPRHRNPRFPVRM

m616.pep     250     260     270     280     290     300
QHRRCPRLRRNCRRLARYAGRTRRKIPAPIQTMPDMAXRGTSMNLPNRNFI LLSALWFAGS
|||||
g616         250     260     270     280     290     300
QHRSTVRRRSGMTARHTCTRTRQIPAPVQNLPNVAGRGGMKLPNRNFI LLSALWFAGG

m616.pep     310     320     330     340     350     360
IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTKAFRTDNRPIPYRSLMVFALCFAL
|||||
g616         310     320     330     340     350     360
IYSLLFKAAETAPPPFPFHDKAAHLALFFAQILFLAKAFKGLPIPYRSLIAFAFCFAV

m616.pep     370     380     390     400
FSECAQAWFTATRTGSLGDVLADLTGAALALFTARAACRPDX
|||||
g616         370     380     390     400
GSECAQAWFTATRTGSLGDVLADLTGAALALFAARSACRPDX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1 ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51 ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAAATG GAAGGCTTCA TTTAAAGAAG AAAAAAATT CTTCCGCGAA
151 GTCGCCCGTG CTACCTGCCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCGG GACAGGCAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCCGAC GGATCAAATT CAAACTCGGC GCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTTCAGACG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCTGTC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACA TGGCGCGACA TACTTGCCGC ACGCGCGGCG AAATTCTGTC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTTCCG CATTGTGGTT TGCCGCGGCG
901 ATCTATTGCG TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAA ACCGAAAAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTGCGCGATA
1151 TGGCAGGTAC GGTCTCGCA CTCTTGCCG CCCGCGCCGC CGACCGCCGC
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1 MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51 VARATLPDGD VWLLKPTTFM NRSQQAVAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHHGLK DIQAKLTAD YYRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPAVRM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GMLPRNRF SLLSALWFAGG
301 IYSLLFKAAD TAPPPPHFD KAAHLALFFA QIWLTKAFK TGKLPIPYRS
351 LMFALCFAL FSECAQA*FT ATRTGLGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	VWLLKPATFMNRSQQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHHGLK					
a616	VWLLKPTTFMNRSGQAVALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHHGLK					
	70	80	90	100	110	120
m616.pep	DIQAKLTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	QMGSRNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPALRM					
a616	QMXRGNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPVRM					
	190	200	210	220	230	240
m616.pep	QMXRGNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPALRM					
a616	QMXRGNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPVRM					
	250	260	270	280	290	300

```

g619.seq
1  ATGCCGCTCTG  AAAAAAATAT  CGGTTTTATG  GCAGGAAGCA  GCCGTCGGTT
51  TCGGGCTCGCC  TTTGCGCTGT  TGCTGGTTTC  TGCACTCTCG  TTTATGACGC
101  GCAACGTCGA  AAGGATTTGG  TGCTGTGTCT  TGCACCTGCG  CTTGACCAAC
151  CTTGCCGCGC  TGCTGATGGT  CGCCTATGCG  GTCGGCGTGT  CCACTCAACT
201  CTTCCAAACG  CTGACCAACA  ACCCGATTCT  GACCCCTFCG  ATTTTGGGTT
251  TCGATTCTGT  GTATTGTGTT  TGCAGACCT  TGGTGgtGTT  TACGTTcgGC
301  GGCCTGGGCT  ATAcatccct  gccgttgacy  gGCAAAATTC  GCTTTGAAC
351  GGTTGTTATG  ATGGCGCGCT  CGCTGCTGCT  GTTTTACACG  CTCATCCGTC
401  AGGCGGGGCG  CGATTGCGC  CACATGATT  TAATCGGCGT  GATTTTCGGG
451  ATTTTGTTC  CGAGCCTTTC  TCTCGTGTCT  TCGCGCATGA  TAGACCCCGA
501  AGAATTATACC  GCCGCGCAGG  CGAATATGTT  TGCCGGATTC  AATACCGTCC
551  GCAGCGAGCT  TTTAGGCATA  GCGCGCGCTG  TCTCTGCTCT  CAGCGCGCGG
601  GTCGTTTGG  ACGAACGCTA  CGCTCGGAG  GTACACCTTT  TGGGCGCGGA
651  CCAAGCCGTC  AATTTGGGCA  TCAGCTACAC  GCGCAACACC  TTATGGATAC
701  TGCTTTGGAT  TCGCGCATTC  GTGGCGGACG  CGACGCCCAT  TGTCGGCCCG
751  GTGAGCTTTT  TCGGGCTTCT  CGCCGCGCTG  CTTGCCCAAC  actTTTCCCC
801  gtCCGTGCGC  CATTCGCTCC  CGCTCGcat  gacggtttGC  gctcgGcgGCA
851  TCCTCTTggt  cggCggacaA  ACCGTATTTC  AACACTTCTT  GGGCATGAag
901  gCggtATTAA  GCGTGGTGGT  cgAATTTCGG  ggcggactcg  TTTTCTCTA
951  TCTCGTTTTA  AAACACAAAA  ATAGA

```

**g619.pap**

1	MPSEKNIGFM	AGSSRPLRVA	FALLLVSCIL	FMTLVNKGDW	DFVLHLRLTK
51	LAALLMVAYA	VGVS <del>T</del> QLFQT	LTNNPILTPS	ILGFDLSLYF	LQTLVLVTFFG
101	GVGYTSLPLT	GKGFELVVM	MGGSLLLFTY	LIRQGGRLDP	HMILIGVIFG
151	ILERSLSLL	SRMIDPEEFT	AAQANMFAG	NTWRELLGI	GALLVLVSAA
201	VVWHERYRSD	VHLLGRDQAV	NLGISYTRNT	LWILLWIAAL	VATATVAVGP
251	VSFFGLLAAS	LANHFSPSVR	HSPRLPMTVC	VGGILLVGGQ	TVFEHFLGMK
301	AVLSVVVEFA	GGLVFLYLVL	KSRK*		

```
m619.seq
1 ATGCCGCTCG AAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCGTT
51 TCGCCGTCGCC TTTCGCGTGT TGTTGGTTTC CTGCGCTCGT TTTATGACGC
101 GTAACGTGCA AGGCGATGTT GATTTTGTTT TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTCTGT GTATGTGTTT TTGCAGACCT TGCTGGTGTG TACGTTCCGG
301 GCGCTGGGCT ATGCTTCCCT GCGGTTGACG GCGAAATTCG CCGTTGAACT
351 GGTCTGTCATG ATGGCGCGCT CGCTGCTGCT GTTCTACACG CTCATCAAAC
401 AGGGCGGGAGC CGATTTGTCT GCGATGATT TAATCGCGCT TCGTTCCGG
451 ATTTTGTTC GCAGCCTGTC CTGCTGCTTT TGCGCATGA TCGATCCCGA
501 AGAATTTACC GCCGCGCAGG CGAATATGTT TCCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA CGCGCGCTGA TTCTGCTGCT CAGCGCGCGG
601 CTCGTTTGCG CGCAACGCTA CCGCTTGGAC GTTTTACCTT TGGGGCGTGA
651 CCAAGCCGTC AATTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTGCGGCCC
751 GTAAGCTTTT TCGGGCTTCT CGCGCGCTCG CTTGCCAAAC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT ATCGGCGGCA
851 TCTCTTGGT CCGCGGACAG ACGGTGTTCT AACACCTGCT CGGTATGCAG
```



901 GCAGTGTGTA GCGTAGTAGT AGAATTGCC GCGGACTCG TTTCTCTCTA  
 951 TCTCGTTTAA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep  
 1 MPSEKNIGFM AGSSRPLWYA FALLLVSCVL FMTLNVKGDW DFVLQRLTK  
 51 LAALLMVAYA VGVSTOLFOT LTNNPILTPS ILGFDSLTVF LQTLVETFG  
 101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRLDS RMILIGVIFG  
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA  
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVGFP  
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ  
 301 AVLSVVVEFA GGLVFLYVL KHKK\*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTOLFOTLTNNPILTPSILGFDSLTVFLQTLVETFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTOLFOTLTNNPILTPSILGFDSLTVFLQTLVETFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGGSLLLFYTLIRQGGRLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVHSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGFPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGFPVSFFGLLAASLANHFSPSVRHSLPMTVCVGGILLVGGQTVFEHLLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYVLKHKKX					
g619	AVLSVVVEFAGGLVFLYVLKHKKX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq  
 1 ATGCCGCTCG AAAAAAATAT CGGTTTATG GCAGGAAGCA GCCGTCCGTT  
 51 GTGGGTGCGC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC  
 101 TCAACGTCAA AGCGGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG  
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGCGGTTT CGACCCAGCT  
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTCG ATTTTGGGTT  
 251 TCGATTGCTG GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTCCGC  
 301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAAC  
 351 GGTCGTTATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAC  
 401 AGGGCGGGCG CGATTGCGG CGTATGATTT TAATCGGCGT GATTTTCGGG  
 451 ATTTTGTTCG GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCCGA  
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC  
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG  
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTACACCTTT TGGGCGCGCA  
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC  
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCGT TGTGGCCCG

993

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7 51 GTAAGCTTTT TCGGGCTTCT CGCCGCTCG CTTGCCAACC ACTTTTCCCC
8 01 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
8 51 TCCTCTTGGT CGGCGGACAG ACCGTATTCTG AACACTTCTT GGGCATGAAG
9 01 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTCTCTCTA
9 51 TCTCGTTTTA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLVNKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLIVF LQTLVFTFG
1 01 GVGYASLPLT GKFGFELVVM MGSLLLLFYT LIKQGRDLR RMILIGVIFG
1 51 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
2 01 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVG
2 51 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
3 01 AVLSVVVEFA GGLVFLYLVL RHKK*

```

m619/a619 97.2% identity in 324 aa overlap

	10	20	30	40	50	60
m619.pep	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLVNKGDWDFVLQRLTKLAALLMVAYA					
a619	MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLVNKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m619.pep	VGVSTQLFQTLTNNPILTPSILGFDSLIVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
a619	VGVSTQLFQTLTNNPILTPSILGFDSLIVFLQTLVFTFGGVGYASLPLTGKFGFELVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m619.pep	MGSLLLLFYTLIKQGRDLRSMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
a619	MGSLLLLFYTLIKQGRDLRPMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m619.pep	NTVHSELLGIGALILLVSAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
a619	NTVHSELLGIGALILLVSAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m619.pep	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
a619	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
	310	320				
m619.pep	AVLSVVVEFAGGLVFLYLVLKHKXX					
a619	AVLSVVVEFAGGLVFLYLVLRHKKX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gttttcgCCT TAAGTCCTG
51  CCGGCaggcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttegggtcgg aCACTAttgc Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAACCC GATCAGCCG TTTGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAG CCTTTACGT
351 CATCGACAGC GCCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCGCGATGCT TACATTTCA AGTAA

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

**This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:**

m620/g620 97.0% identity in 164 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

**This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:**

```
a620.pep
1  MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPWFSTIK QMFGYTKLPE EPKGRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGMGMAED ALFPGNKEQA EKFAKDKGGK
151 VVGFDMPDPT YIFK*
```

995

m620/a 620 100.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pép	MKKTL LAIVAVSALSACRQAE EGPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a620	MKKTL LAIVAVSALSACRQAE EGPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pép	DQP VWFSTIKQMF GYTKLP EEPKGIRVIYVTD MGNVTDW TNP NADTEWMDAKKAFYVIDS					
a620	DQP VWFSTIKQMF GYTKLP EEPKGIRVIYVTD MGNVTDW TNP NADTEWMDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pép	GFIGGMGAEDALPFGNKEQAEKFAKDKGKGKVVGFDDMPDITYIFKX					
a620	GFIGGMGAEDALPFGNKEQAEKFAKDKGKGKVVGFDDMPDITYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

g622.seq

```

1  ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAG ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCCGC ACGCCTTCCG CGTTGCCTGC
301 GGC TTGGATT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAACTCA
401 ATGCCCTGTT CCAAAAACC TTTTCCGTTG CTAAGAAGT CCGTACCGAT
451 ACCGCTGTG GCGAAAATC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GGC GGAACAG ATTTTCCCG ACATCGGCGA TTTGAACGTA TGTATTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAT
601 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTTCAAC GGCGAGCCAG
751 CTTCCGATAG TCGGCAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTATGCG TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTC AACATCG TCCAAAGCG caaggaggca aggcagaaag ccgccgcCgc
951 cgc cgaacg ctggtGTCCG AAAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GaggcttcCG CTGATTAAGG CCTTGCGGGA CGAGGCGGAG
1051 AAAGCGCGCA AGCAGGTGTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaacGGCG GAAGaggttt TGgaacggt gtcctgcCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAACT CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAA GatttGG TTCATGCCgt cGCGCAGAtt tatcatttGG ACAATAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 1992; ORF 622.ng&gt;:

g622.pép

```

1  MQLTAVGLNH QTAPLSIREK LAFAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RAAQEESMG AKLNALFORT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVVGKME RALKRQSMP LFMLDLAVPR DIEAEVGDIN DAYLYTVDDM
301 VNI VQSKEA RQKAAAAET LVSEKVAEFV RQQQGRQSV LKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLRLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHVAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

m622.seq

```

1  ATGCAACTTA CCGCTGTGCG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCCGC ATGCTTTCCG CGTCGCCTGC

```

```

301 GGGCTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTCCGTTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCATG GCTTCGCTT CCGTCAAATT
501 GGC GGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTTGCG AGTGCCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTGAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGCAGGCGA GAGTGTCCCC TTGATTAAGG CGTTGCGGGA CGAGGCGGAG
1051 AAAGCGCGCA AACAGGTGTT GGAATGACC ATGAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCCTA CTGACCAACA
1151 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGTTG TTCATGCCGT CGCGCAGATT TATCATTGG ACAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

```

m622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLRNSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEO IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SLDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMPL FMLDLAVPRD IEAEVGDNDL DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPL IKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

m622.pep	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLRNSNAATEAVILSTCNRTELYCVGD					
g622	:					
	10	20	30	40	50	60
	MQLTAVGLNHQTAPLSIREKLAFAAAALPEAVRNLRNSNAATEAVILSTCNRTELYCVGD					
m622.pep	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	:					
	70	80	90	100	110	120
	SEEIIRWLADYHSLPIEEIRPYLYTLDMEQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
m622.pep	130	140	150	160	170	180
	RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	:					
	130	140	150	160	170	180
	RAAQEESMGAKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
m622.pep	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	:					
	190	200	210	220	230	240
	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
m622.pep	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDLNDAYLYTVDDM					
g622						
	250	260	270	280	290	300
	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDNDLNDAYLYTVDDM					
m622.pep	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622						
	310	320	330	340	350	360
	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
m622.pep	370	380	390	400	410	
	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
g622						
	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1  ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
1 01 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
1 51 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
2 01 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
2 51 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
3 01 GGCTTGGATT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
3 51 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
4 01 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAAGAGGT CCGTACCGAT
4 51 ACTGCCGTCG GCGAAAAC TC GTTTCCATG GCTTCCGCTT CCGTCAAGTT
5 01 GGCAGAGCAG ATTTTCCCGG ACATCGGCGA TTTGAATGTC TTGTTTATCG
5 51 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
6 01 CCCCGGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
6 51 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
7 01 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
7 51 TTGCCCATTT TCGGCAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
8 01 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
8 51 CGGAAGTCGG AGATTGAAC GATGCCTATC TTTATACGGT GGACGATATG
9 01 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
9 51 CGCCGAAACG CTGGTGTCCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
10 01 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
10 51 AAAGCGCGCA AACAGGTCTT GGAAATGCG ATGAAACAGC TTGCCAAAGG
11 01 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
11 51 AGCTGCTGCA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
12 01 AAAGATTGGT TTCACGCCGT CGCGCAGATT TATCATTGGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1  MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEIS PYLYTLGMQE TVRHAFRVAC
1 01 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
1 51 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
2 01 PRIMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILEHY DVVVSSTASQ
2 51 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGDIN DAYLYTVDDM
3 01 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVF LIRALRDEGE
3 51 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLLHSPT QTLNKAGEED
4 01 KDLVHAVAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

```

          10      20      30      40      50      60
m622.pep  MQLTAVGLNHQTAPLSIREKLAFAAALPKAVRNLARSNAATEAVILSTCNRTLYCVGD
          |||
a622      MQLTAVGLNHQTAPLSIREKLAFAAACLPEAVRNLARSNAATEAVILSTCNRTLYCVGD
          10      20      30      40      50      60

          70      80      90      100     110     120
m622.pep  SEEIIRWLADYHSLPIEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          |||
a622      SEEIIRWLADYHSLPIEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV
          70      80      90      100     110     120

          130     140     150     160     170     180
m622.pep  RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          |||
a622      RVAQEESMGKKLNALFQKTFVSAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV
          130     140     150     160     170     180
```

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVOLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq  
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG  
 51 GATAATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTAC  
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATccc cgcgcTTTCa ccgCTGGCTG  
 151 CACcgcGacc gCTATTTCGG CCCGATGGT CATAACTGGG AACAAAACGG  
 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt  
 251 cctgcctcat gatctTTtgg CattTTCccc aacnctgggtg ggctGGGGCG  
 301 GTTTCATCGG TTTTTGTTC CCTTGTCacC ATacggatgt gGcacAGacc  
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep  
 1 MIRYLLIACG GISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL  
 51 HRRHYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPOXWWVGA  
 101 VSSVFCSLVT IRMWRHPES\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq  
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCTCC TACTGTTGGG  
 51 TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC  
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG  
 151 CACCGGCACC GCTATTTCGG CCCGATGGT CATAACTGGG AACAAAACGG  
 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT  
 251 CCTGCCTGAT AATGTTTGG CAGTTTCCC AACGCTGGTG GGTGGGGCG  
 301 GTTTCATCGG TTTTTGTTC CCTTGTCGCC ATATGGATGT GCGCAGGCC  
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep  
 1 MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFYRWL  
 51 HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMEW QFPQRWWVGA  
 101 VSSVFCSLVA IWMWRHPES\*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWAKASPRFYRWLHRRHYFGPMV					
g624	MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWAKASPRFYRWLHRRHYFGPMV					
	10	20	30	40	50	60

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	:     :     :     :     :     :					
g624	HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTCCCT TGCTGTTGGG
51  TATCATCGGC ATTTTTTTGC CGCTGTTGCC GACCACGCCG TTCGTACTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTTGG CAGTTTCCCC AACGCTGGTG GGTCCGGGCG
301 GTTTCATCGG TTTTTTGTTC CCTTGTCGCC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1  MIRYLLIACG CISLLGLIIG IFLLPPTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLGLIIGIFLLPPTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	:     :     :     :     :     :					
a624	MIRYLLIACGCISLLGLIIGIFLLPPTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	:     :     :     :     :     :					
a624	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1  ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCCG
101 CGGTGCTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1  atGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtctTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCCGCG
101 CGGtcgttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gtaa
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
```



1000

51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq  
1 ATGTTTGCAG CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT  
51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC  
101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG  
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCG  
201 TGAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGG ATGTATTCTT  
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGCGGGACGC GCCAAAAACC  
301 AAACCTGAAC GGATGAGGAA GAGCAATGTC CAAAGGCGG TAATTTTGCC  
351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPME ASAVPTASRA  
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
g625	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep  
1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPME ASAVPTASRA  
51 VLSLGVPFKS PQTMPPEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT  
101 KLNGMRKSNV QKAVILP\*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFFSSGRIISIAAPVVPMEASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILEX					
a625	PQTMPPEMVYRASSSRMKGMYSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq  
1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG  
51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA  
101 CCGCCGTATC TATGCCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA  
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTTC TCGGCATCTT  
201 CATCACCATC TTCCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG  
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT  
301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA  
351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GCGGGGCGGC GATGCCCAAG  
401 CCTTAATGAC GGGTCCCCTG TTTTATTcgc TGCTGGCGGT TTCTAtgggT  
451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT

1001

501 GGTcaaggcc aTTGCCGaaC agcgcgGCgt accgaTGCcg actTTCTTcc  
 551 ggtaTAtgat gtggtcggtc gcCTTCCTGa caCCCGTCTT CATcgTACAT  
 601 ACCCTcgtCT TTTTcgTTtt cAAACTACTg taa

This corresponds to the amino acid sequence <SEQ ID 2010; ORF 627.ng>:

g627. pep

1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL ITLTAVSMAI TPKQVRAGNE  
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI  
 101 NTMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGPL FHSLLAVSMG  
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFRYMMWSV AFLTPVFIVH  
 201 TLVFFVFKLL \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2011>:

m627. seq

1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG  
 51 CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA  
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA  
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAACCTCTCC TCGGCATCTT  
 201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG  
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT  
 301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGATAA  
 351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG  
 401 CCTTGATGAC GGGTACCCTG TTTCATTCGC TGCTGGCGGT TTCTATGGGT  
 451 TGGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT  
 501 GGTCAAGGCC ATTGCCGAAC AGCGCGCGCT ACCGATGCCG ACTTCTTCG  
 551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT  
 601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

This corresponds to the amino acid sequence <SEQ ID 2012; ORF 627>:

m627. pep

1 MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE  
 51 FNFEPIAEVG KLFLGIFITI FPVLSILKAG EAGALGGVVS LVHDTAGHPI  
 101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGL FHSLLAVSMG  
 151 SVFMGALTYI GNAPNFMVKA IAEQRGVPMP TFFGYMMWSV AFLTPVFIVH  
 201 TLIFFVFKLL \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m627/g627 97.6% identity in 210 aa overlap

	10	20	30	40	50	60
m627. pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	:					
g627	MSGLWKPEHPGFEILGSRYALQNLVRDVILITLTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m627 . pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
g627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINTMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627 . pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
g627	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627 . pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					
g627	TFFRYMMWSVAFLTPVFIVHTLVFFVFKLLX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2013>:

```

a627 . seq
1  ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
51  CCGTTACGCC CTGCAAAACC TCGTCCGCGA TGTCATCCTG ATTGCATTGA
101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AACTCTTCC TCGGCATCTT
201 CATCACCATC TTTCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
301 AATGTGATGT ATTTTGGAT GAGCGGCATA TTGTCGGCAT TCTTGGATAA
351 CGCGCCCACT TATCTCGTTT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
401 CCTTGATGAC GGGTTCCTCG TTTCATTGCG TGCTGGCGGT TTCTATGGGT
451 TCGGTATTCA TGGGCGCACT GACCTACATC GGCAACGCAC CGAACTTCAT
501 GGTCAAGGCC ATTGCCGAAC AGCGCGGCGT ACCGATGCCG ACTTTCTTCG
551 GCTATATGAT GTGGTCGGTC GCCTTCCTGA CACCCGTCTT CATCGTACAT
601 ACCCTTATCT TTTTCGTTTT CAAACTGCTG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2014; ORF 627.a>:

```

a627 . pep
1  MSGLWKPEHP GFEILGSRYA LQNLVRDVIL IALTAVSMAI TPKQVRAGNE
51  FNFEPIAEVG KLFLGIFITI FVLSILKAG EAGALGGVVS LVHDTAGHP
101 NVMYFWMSGI LSAFLDNAPT YLVFFNMAGG DAQALMTGSL FHSLLAVSMG
151 SVFMGALTYI GNAPNFMVKA IAEQRGVMP TFFGYMMWSV AFLTPVFIVH
201 TLIFFVFKLL *

```

m627/a627 99.5% identity in 210 aa overlap

	10	20	30	40	50	60
m627 . pep	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
a627	MSGLWKPEHPGFEILGSRYALQNLVRDVILIALTAVSMAITPKQVRAGNEFNFEPIAEVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m627 . pep	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
a627	KLFLGIFITIFPVLSILKAGEAGALGGVSVLVHDTAGHPINVMYFWMSGILSAFLDNAPT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m627 . pep	YLVFFNMAGGDAQALMTGTLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
a627	YLVFFNMAGGDAQALMTGSLFHSLLAVSMGVSFVMGALTYIGNAPNFMVKAIAEQRGVMP					
	130	140	150	160	170	180
	190	200	210			
m627 . pep	TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX					

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a627                    TFFGYMMWSVAFLTPVFIVHTLIFFVFKLLX  
                               190            200            210

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2015>:

g628. seq  
 1 ATGTGCGTGC CACTCAAGCC GGCAGGATGC GGGCCGCCAA ATTCATGTGT  
 51 TTCGATATG GCAGCATTTT CAGACGGCAC GTCTGCGCCT GCTGCTTTAC  
 101 ACACATGGAT TTTACGTTTCG GTCAGGCGGC TCAATACCAA CAGGCCGCGT  
 151 TTGAAGTCTT CGGCGGCTTC TTTGATGATG ACCGTAGGGT CGGCAGCCAG  
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCTA  
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTGC GAAGCGCAGT CCATAAGCCT  
 301 GATTGAATCA GGTGCGGCG CACTTTTTCG CTGCTCAATT TTGCCAGCGC  
 351 TTCAGGTacg TAG

This corresponds to the amino acid sequence <SEQ ID 2016; ORF 628.ng>:

g628. pep  
 1 MCVPLKPAGC GPPNSCVSIL AAFSDGTSAP AALHTWILRS VRLNTNRP  
 51 LKSSAASLMM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP  
 101 D\*IRLRRTFS LLNFASASGT \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2017>:

m628. seq  
 1 ATGTGCGTGC CACTCAAACC GGCAGGATGC GGGCCGCCGA ATTCATGTGT  
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCTTAC  
 101 AAACATGGAT TTTGCGTTTCG GTCAAACGGC TCAATACCAA CAGGCCGCGT  
 151 TTGAAATCCT CGGCGGCTTC TTTGATAATG ACCGTAGGGT CGGCAGCCAG  
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA  
 251 CGGCAGGAAT TTTGCTGAAC GGACGGGTGC GCAGCGCAGT CCACAAACCG  
 301 GATTGGATCA GGTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAGCGC  
 351 TTCAGGTGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2018; ORF 628>:

m628. pep  
 1 MCVPLKPAGC GPPNSCVSML AAFSDGTSAP AALQTWILRS VKRLNTNRP  
 51 LKSSAASLIM TVGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP  
 101 DWIRLRRTSS PLKFASASGA \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m628/g628 93.3% identity in 119 aa overlap

	10	20	30	40	50	60
m628. pep	MCVPLKPAGCGPPNSCVSMLAAFS	DGTSAPAAALQ	TWILRSVKRLNTNRP	RLKSSAASLIM		
g628	MCVPLKPAGCGPPNSCVSILAAFS	DGTSAPAAALHTWILRSVRLNTNRP	RLKSSAASLIM			
	10	20	30	40	50	60
	70	80	90	100	110	120
m628. pep	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDWIRLRRTSSPLKFASASGA				
g628	TVGSAASGLVSIALTKMANGSASTAGILLN	GRVRSVHKPDXIRLRRTFSLNFASASGT				
	70	80	90	100	110	120
m628. pep	X					
g628	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2019>:

1004

a628.seq  
 1 ATGTGCGTGC CACTCAAACC GGCCGGATGC GGGCCGCCGA ATTCATGTGT  
 51 TTCGATGTTG GCAGCATTTT CAGACGGCAC GTCTGCGCCA GCTGCCCTTAC  
 101 ACACATGGAT TTTACGCTCG GTCAAACGGC TCAATACCAG CAAACCTCGT  
 151 CTGAAATCCT CGGCGGCTTC TTTGATCACA ACCACAGGGT CTGCCGCCAG  
 201 CGGATTGGTG TCCATCGCAT TGACGAAGAT GGCGAACGGC TCGGCATCGA  
 251 CGGCAGGGAT TTTGCTGAAC GGACGGGTAC GCAGCGCAGT CCACAAACCG  
 301 GATTGGATCA GATTGCGGCG CACTTCTTCG CCGCTTAAGT TTGCCAACCG  
 351 TTCGGGCGCG TAG

This corresponds to the amino acid sequence <SEQ ID 2020; ORF 628.a>:

a628.pep  
 1 MCVPLKPAGC GPNSCVSM LAAFSDGTSAP AALHTWILRS VKRLNTSKPR  
 51 LKSSAASLIT TTGSAASGLV SIALTKMANG SASTAGILLN GRVRSVHKP  
 101 DWIRLRRTSS PLKFANASGA \*

m628/a628 95.0% identity in 120 aa overlap

	10	20	30	40	50	60
m628.pep	MCVPLKPAGCGPNSCVSM LAAFSDGTSAP AALHTWILRSVKRLNTNRPR LKSSAASLIM					
a628	MCVPLKPAGCGPNSCVSM LAAFSDGTSAP AALHTWILRSVKRLNTSKPR LKSSAASLIT					
	10	20	30	40	50	60
m628.pep	TVGSAASGLV SIALTKMANGSASTAGILLN GRVRSVHKPDWIRLRRTSS PLKFASASGA					
a628	TTGSAASGLV SIALTKMANGSASTAGILLN GRVRSVHKPDWIRLRRTSS PLKFANASGA					
	70	80	90	100	110	120

m628.pep X  
 |  
 a628 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2021>:

g629.seq  
 1 ATGACTGCca aacCTTTTTC CCTCAACCTG GCcaaCCTCC TGCTGCCggc  
 51 ggtatTGTTT GCCGTCAGcc tGtcggtTCGG cattgccgat TTCCGCTGGT  
 101 CGGATGTGTT TTCGCTGTCC GACAGCCAGC AAGTGATGTT CATCAGCCGC  
 151 CTGCCGCGCA CGTTTGcgaT TGTGTTGACG GGCgcgtcga tagcgtggtc  
 201 gGGGAtgatt atgcagATTC TGATGCGCAA CcgtTTTGTC GAGCCTtcta  
 251 tggcgGGTGC GGGCCAAAGt gcgGCTTTGG GTttgcttct gAtgtccctg  
 301 ctgctgcctg CcgcGccgct gccggtcaAA ATGTCGGtag Ccgccgttgc  
 351 CGCGCTGATC GGGATGTTGG tctTtatgct gctaaccgc Cgcctgccac  
 401 cgacggcgca gctgatgGTg ccgCTGGTGG Gg.ttATTTT CGGCGGCGTG  
 451 GttgaGGCGG TGGCGACGTT TGTCGCGTAT GAGTTTGAGA TGCTGCAAAAT  
 501 GTTGGGCGTG TGGCAGCAGG GCGACTTTTC AAGCGTGCTG CTGGGGCGGT  
 551 ACGAGCTGCT TTGGATTACG GCGGTTTGG CCGTGTGTTGC CTACCTGATT  
 601 GCCGACCGGC TGACGATTTT GGGGCTGGGC GAGACGGTGA GCGTGAATT  
 651 GGGTTTGAAC CCGACGGCGG TGTGTTGGTC GGGTTTGATT ATTGTGGCAC  
 701 TGATTACATC GCTGGTCATT GTAACGGTCG GCAATATTCC GTTATCGGG  
 751 CTGGTCGTGC CGAATATCGT CAGCCGCTG ATGGGCGACA GGCTGCGCCA  
 801 AAGCCTGCCT GCGGTGCGCC TCTTGGGCGC GTCTTTGGTT TTATTGTGCG  
 851 ACATTATCGG ACGCATGATT GTGTTTCCGT TTGAAATTCC GGTCTCCACG  
 901 GTTTTGGTG TGTGGGTAC GCCTTTGTTT TTGTGGCTTT TGTGAGGAA  
 951 ACCCGCTAT GCCGTCTGA

This corresponds to the amino acid sequence <SEQ ID 2022; ORF 629.ng>:

g629.pep  
 1 MTAKPFSNL ANLLPAVL AVLSVGIAD FRWSDVFSLS DSQQVMFISR  
 51 LPRTFAIVLT GASIAVAGMI MQILMRNRFV EPSMAGAGQS AALGLLLMSL  
 101 LLPAAPLPVK MSVAAVAALI GMLVFMLLR RLPPTAQLMV PLVGXIFGGV

m629.seq

m629.pap

**m629/g629 95.7% identity in 322 aa overlap**

		10	20	30	40	50	60
m629. pep		MTAKPFSLNLTNLLLLAVLFAVSLVSGVADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
		:     :     :     :     :     :     :     :     :     :					
g 629		MTAKPFSLNLANLLLPVLFVAVSLVSGIADFRWSDVFSLSDSQQVMFISRLPRTFAIVLT					
		10	20	30	40	50	60
		70	80	90	100	110	120
m629. pep		GASMAVAGMIMQILMRNRFVEPSMVGASQSAALGLLMTLLLPAAPLPAKMSVAAVAALI					
		:     :     :     :     :     :     :     :     :     :					
g 629		GASIAVAGMIMQILMRNRFVEPSMAGAGQSAALGLLMSLLLPAAPLPVKMSVAAVAALI					
		70	80	90	100	110	120
		130	140	150	160	170	180
m629. pep		GMLVFMLLIRLPPTAQLMVPLVGIIIFGGVIEAVATFIAYENEMQLMLGVWQQGDFSSVL					
		:     :     :     :     :     :     :     :     :					
g 629		GMLVFMLLIRLPPTAQLMVPLVGXIFGGVVEAVATFVAYEEMQLMLGVWQQGDFSSVL					
		130	140	150	160	170	180
		190	200	210	220	230	240
m629. pep		LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI					
		:     :     :     :     :     :     :     :     :					

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```

g629      LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           190      200      210      220      230      240

           250      260      270      280      290      300
m629 .pep VTVGNIPFIGLVVFNIIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VTVGNIPFIGLVVFNIVSRIMGDRLRQSLPAVALLGASLVLLCDIIGRMIVFPFEIPVST
           250      260      270      280      290      300

           310      320
m629 .pep VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g629      VFGVLGTALFLWLLLRKPAYAVX
           310      320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2025>:

```

a629 .seq
1  ATGACTGCCA AACCTTTTTC CCTCAACCTG ACTAACCTCC TGCTGCTGGC
51  GGTGTTGTTT GCCGTCAGCC TGTCGGTGGG CGTTGCCGAT TTCCGCTGGT
101 CGGATGTGTT TTCGCTGTCG GACAGCCAGC AGGTTATGTT CATCAGCCGC
151 CTGCCGCGCA CGTTTGCGAT TGTGTTGACG GCGCGCTCGA TGGCGGTGGC
201 GGGGATGATT ATGCAGATTC TGATGCGTAA CCGTTTGTG GAGCCTTCTA
251 TGGCGGGCGC GGGTCAGAGT GCGGCTTTGG GTTGCTTCT GATGTCCCTG
301 CTGCTGCCTG CCGCGCCGCT GCCGGTCAA ATGTCGGTTG CCGCCGTTGC
351 CGCGTTAATC GGGATGTTGG TGTATATGAT GCTTATCCGC CGCCTGCCGC
401 CGACGGCGCA ACTGATGGTG CCTTGGTGCG GGATTATTTT CGGCGGCGTG
451 GTTGAGGCGG TGGCCACCTT TATTGCGTAT GAAAACGAAA TGCTGCAAAAT
501 GCTGGGCGTG TGGCAACAGG GCGATTTTTC CGGCGTGTTG CTCGGACGGT
551 ATGAAGTGTG GTGGGCAACG GGGATTTTGG CTTTGTGTTG CTATTTGATT
601 GCCGACCAGC TGACGATTTT GGGTTTGGGC GAAACGGTAA GCGTGAACCT
651 GGGGCTGAAC CGGACGGCGA TTCTGTGGTC GGGGCTGATT ATTGTGGCTT
701 TGATTACGTC GCTGGTTATC GTTACGGTCG GCAATATTCC GTTTATCGGG
751 CTGGTCGTGC CGAACATCAT CAGCCGCTG ATAGGCGACA GGCTGCGCCA
801 AAGCCTGCCT GCGGTGGCTT TGCTGGGTGC GTCTTTGGTT TTATTGTGCG
851 ACATTATCGG ACGAGTGATT GTGTTCCGT TTGAAATTCC GGTATCGACC
901 GTCTTCGGCG TATTGGGTAC GCGTTGTTT TTATGGCTTT TGTTAAGGAA
951 ACCTGCTCAT GCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2026; ORF 629.a>:

```

a629 .pep
1  MTAKPFSLNL TNLLLAVLF AVSLSVGVD FRWSDVFSLS DSQQVMFISR
51  LPRTFIVLT  GASMAGMI  MQILMRNRFV EPSMAGAGQS AALGLLMSL
101 LLPAAPLPVK MSVAAVAALI GMLVFMLIR RLPPTAQLMV PLVGIIFGGV
151 VEAVATFIAY ENEMQLMLGV WQQGDFSGVL LGRYELLWAT GILALFAYLI
201 ADQLTILGLG ETVSVNLGLN RTAILWSGLI IVALITSLVI VTVGNIPFIG
251 LVVFNIIISRL IGDRLRQSLP AVALLGASLV LLCDIIGRVI VFPFEIPVST
301 VFGVLGTALF LWLLLRKPAH AV*

```

m629/a629 95.7% identity in 322 aa overlap

```

           10      20      30      40      50      60
m629 .pep MTAKPFSLNLTNLLLAVLFAVSLSVGVD FRWSDVFSLS DSQQVMFISR LPRTFIVLT
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      MTAKPFSLNLTNLLLAVLFAVSLSVGVD FRWSDVFSLS DSQQVMFISR LPRTFIVLT
           10      20      30      40      50      60

           70      80      90      100     110     120
m629 .pep GASMAGMIMQILMRNRFV EPSMAGAGQS AALGLLMSL LPAAPLPVK MSVAAVAALI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      GASMAGMIMQILMRNRFV EPSMAGAGQS AALGLLMSL LPAAPLPVK MSVAAVAALI
           70      80      90      100     110     120

           130     140     150     160     170     180
m629 .pep GMLVFMLIR LRPPTAQLMV PLVGIIFGGV IEAVATFIAY ENEMQLMLGV WQQGDFSSVL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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a629      GMLVFMMLIRRLPPTAQLMVPLVGIIFGGVVEAVATFIAYENEMLQMLGVWQQGDFSGVL
           130      140      150      160      170      180
           190      200      210      220      230      240
m629 - pep  LGRYELLWITGGLAVFAYLIADRLTILGLGETVSVNLGLNRTAVLWSGLIIVALITSLVI
           ||||| || ||:|||||:|||||:|||||:|||||:|||||:|||||
a629      LGRYELLWATGILALFAYLIADQLTILGLGETVSVNLGLNRTAILWSGLIIVALITSLVI
           190      200      210      220      230      240
           250      260      270      280      290      300
m629 - pep  VTVGNIPFIGLVVPNIISRLMGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VTVGNIPFIGLVVPNIISRLIGDRLRQSLPAVALLGASLVLLCDIIGRVIVFPFEIPVST
           250      260      270      280      290      300
           310      320
m629 - pep  VFGVLGTALFLWLLLRKPAYAVX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||
a629      VFGVLGTALFLWLLLRKPAHAVX
           310      320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2027>:

```

g630.seq (partial)
1  aTgatGATTT TGGTGTGGCT ggctttgttt ccccccattgt tttacggcat
51  g tacaacgtc GGCACACAGG CATTGGGTGC CTAAACGCCG GAttgtctgc
101 a acaaaagcat cgcccacgac ggcaattacg ccctcgccaa cgctttgggc
151 a tcaatatgt cccccgaaGc gggcgtgtTg ggcaaaatgc tgttcgGCGC
201 GATTtacttc ctgccgattt acgcgaccgt aTTTATTGTG GGcggcttct
251 g gGaagtCTT GTTCGCATCc gtACGCAAAC ACGAAATCAA CGAAGGTTTC
301 T TCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTGCGCGG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCCG
451 GCCTTCTCTG TCTTCGCCTA CCCCGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGCGCAAC CGCGCTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
701 CTtcttgGCG CATTATTGCC ggCGTGATGA TCGGTatGat tGcgtatTCT
751 t cgctgatta acttcatCGg ttctgacacc aaagctatgt ttgctatgca
801 c ttggtacat ggcacttggg GGAaagatGa ttAtcactca ctgtacatta
851 aa.....

```

This corresponds to the amino acid sequence <SEQ ID 2028; ORF 630.ng>:

```

g630.pep
1  MMILVWLALF PPMFYGMYNV GAQAFGALTP DLLOQSIAMD GNYALANALG
51  I NMSPAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAS VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAHAGADGL KNAVGTQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLINFIGSDT KAMFAMHLVH GTWKKDDYHS LYIK....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2029>:

```

m630.seq
1  ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT
51  GTACAACGTC GGCACACAGG CATTGGGTGC GTTAACGCCG GATTGCTGTC
101 AACAAAACAT CGCCAACGAC TGGCATTACG CCTTTGCCAA CGCTTTGGGC
151 ATCAATATGT CGTCTGAAGC GGGCGTGTG GACAAAATGC TGTTTGGCGC
201 GATTTACTTC CTGCCGATTT ACGCGACTGT ATTTGTTGTG GCGGTTTCT
251 GGGAAGTTT GTTCGCCACC GTGCGCAAC ACGAAATCAA CGAAGGTTTC
301 T TCGTTACTT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT
351 GTGGCAGGCG GCTTTGGGTA TTTCTTTCGG CGTTGTGGTT GCGAAAGAAG
401 TATTGCGCGG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCGT
451 GCCTTCTCTG TCTTCGCCTA CCTGCCAAC TTGAGCGGCG ATGCGGTTTG
501 GACGGCGGTT GACGGCTATT CCGCGCAAC CGCACTGGCG CAATGGGCGG
551 CACACGGTGC AGACGGCCTG AAAACGCCG TAACCGGTCA AACCATCACT
601 TGGATGGACG CGTTATCGG CAAACTGCCC GGCTCCATG GCGAAGTCTC
651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTT GCCCGCATCG
701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TCGGTATGCT
751 TCGTGTTCAT ACTTCATCGG TTCGGACACC AACGTATGT TTGCTATGCC

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801 T TGGTACTGG CACTTGGTGG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA  
 851 T GCGGACCGA CCCTGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG  
 901 T ACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC  
 951 G GCTTACCCC GAAGGCATGA TGTGGCGAT TCTGTTGCC AACCTGTTG  
 1001 C CCGGATTTT CGACTATTTC GTCGCACAAG CGAACATCAA ACGCAGAAAG  
 1051 GCGCGCAGCA ATGGCTAA

This corresponds to the amino acid sequence <SEQ ID 2030; ORF 630>:

m630.pep  
 1 MMILVWLALF PAMFYGMYNV GAQAFGALTP DLLQONIAND WHYAFANALG  
 51 I NMSSEAGVS DKMLFGAIYF LPIYATVFVV GGFWEVLFAT VRKHEINEGF  
 101 F VTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR  
 151 A FLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAVGTQTIT  
 201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS  
 251 S LFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW  
 301 Y GALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIFDYF VAQANIKRRK  
 351 A RSNG\*

m630/g630 93.5% identity in 275 aa overlap

	10	20	30	40	50	60
m630.pep	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQONIANDWHYAFANALGINMSSEAGVS					
g630	MMILVWLALFPAMFYGMYNVGAQAFGALTPDLLQSIADHGNALANALGINMSPEAGVL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m630.pep	DKMLFGAIYFLPIYATVFVVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
g630	GKMLFGAIYFLPIYATVFIVGGFWEVLFASVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m630.pep	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
g630	ALGISFGVVVAKEVFGGTGKNFMNPALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m630.pep	QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
g630	QWAAHGADGLKNAVGTQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m630.pep	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
g630	GVMIGMIAMSSLFNFIGSDTKAMFAM---HLVHGTWKKDDYHSLYIK.					
	250	260	270	280		
	310	320	330	340	350	
m630.pep	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2031>:

a630.seq  
 1 ATGATGATTT TGGTGTGGCT GGCTTTGTTC CCTGCCATGT TCTACGGTAT  
 51 GTACAACGTC GCGGCACAGG CATTGCGTGC GTTAACGCCC GATTGCTGTC  
 101 AACAAAGCAT CGCCAACGAC TGGCATTACG CCCTTGCCAA CGCTTTGGGC  
 151 ATCAATATGT CGTCTGAAGC GGGCGTGTTG GGCAAAATGC TGTTGCGCGC  
 201 GATTTACTTC CTGCCGATTT ACGCGACCGT ATTTATTGTC GGCGGTTTCT  
 251 GGGAAAGTTT GTTCGCCACC GTGCGCAAC ATGAAATCAA CGAAGGTTTC  
 301 TTTGTTACCT CGATTCTGTT TGCCTTAATC GTTCCGCCCA CGCTGCCGCT  
 351 GTGGCAGGCA GCTTTGGGTA TTTCTTTTCG CGTTGTGGTT GCGAAAGAAG  
 401 TATTCGCGCG TACAGGTAAG AACTTCATGA ACCCTGCGCT GGCAGGCCGT  
 451 GCCTTCCTGT TCTTCGCTA CCCTGCCAAC TTGAGCGGCG ATGCGGTTTG  
 501 GACGGCGGTT GACGGCTATT CCGGCGCAAC CGCGCTGGCG CAATGGGCGG  
 551 CACACGGTGC AGACGGCCTG AAAACGCCA TAACCGGTCA AACCATCACT  
 601 TGGATGATG CGTTTATCGG CAAACTGCCC GGCTCCATCG GCGAAGTCTC  
 651 CACTTTGGCA CTCTTAATCG GCGGCGCGTT TATCGTGTTC GCCCGCATCG

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701 CTTCTTGGCG CATTATTGCC GCGGTGATGA TCGGTATGAT TGCCATGTCT
751 TCGCTGTTCA ACTTCATCGG TTCGGACACC AACGCTATGT TTGCTATGCC
801 TTGGTACTGG CATTGCTCG TCGGCGGCTT CGCCATCGGT ATGCTGTTTA
851 TGGCGACCGA CCCCGTTTCC GCTTCCTTTA CCAATGTCGG CAAATGGTGG
901 TACGGCGCAC TGATCGGTGT GATGTGCGTA TTAATCCGCG TGGTCAATCC
951 GGCTTACCCC GAAGGCATGA TGTGCGCAT TCTGTTTGGC AACCTGTTTG
1 001 CCCGATTTT CGACTATTTT GTCGCACAAG CGAACATCAA ACGCAGAAAG
1 051 GCGCGCAGCA ATGGCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2032; ORF 630.a>:

a630.pep

```

1  MMILVWLALF PAMFYGMYNV GAQAFGALT PDLLQOSIAND WHYALANALG
51  INMSSEAGVL GKMLFGAIYF LPIYATVFIV GGFWEVLFAT VRKHEINEGF
101 FVTSILFALI VPPTLPLWQA ALGISFGVVV AKEVFGGTGK NFMNPALAGR
151 AFLFFAYPAN LSGDAVWTAV DGYSGATALA QWAAHGADGL KNAITGQTIT
201 WMDAFIGKLP GSIGEVSTLA LLIGGAFIVF ARIASWRIIA GVMIGMIAMS
251 SLFNFIGSDT NAMFAMPWYW HLVVGGFAIG MLFMATDPVS ASFTNVGKWW
301 YGALIGVMCV LIRVVNPAYP EGMMLAILFA NLFAPIDYF VAQANIKRRK
351 ARSNG*

```

m630/a630 98.3% identity in 355 aa overlap

m630.pep	10	20	30	40	50	60
	MMILVWLALFPAMFYGMYNVGAQAFGALT PDLLQONIAN DWHYAFANALGINMSSEAGVS					
a630	MMILVWLALFPAMFYGMYNVGAQAFGALT PDLLQOSIANDWHYALANALGINMSSEAGVL					
	10	20	30	40	50	60
m630.pep	70	80	90	100	110	120
	DKMLFGAIYFLPIYATVFVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
a630	GKMLFGAIYFLPIYATVFIVGGFWEVLFATVRKHEINEGFFVTSILFALIVPPTLPLWQA					
	70	80	90	100	110	120
m630.pep	130	140	150	160	170	180
	ALGISFGVVVAKEVFGGTGKNFMN PALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
a630	ALGISFGVVVAKEVFGGTGKNFMN PALAGRAFLFFAYPANLSGDAVWTAVDGYSGATALA					
	130	140	150	160	170	180
m630.pep	190	200	210	220	230	240
	QWAAHGADGLKNAVITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
a630	QWAAHGADGLKNAITGQTITWMDAFIGKLP GSIGEVSTLALLIGGAFIVFARIASWRIIA					
	190	200	210	220	230	240
m630.pep	250	260	270	280	290	300
	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
a630	GVMIGMIAMSSLFNFIGSDTNAMFAMPWYWHLVVGGFAIGMLFMATDPVSASFTNVGKWW					
	250	260	270	280	290	300
m630.pep	310	320	330	340	350	
	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
a630	YGALIGVMCVLIRVVNPAYPEGMMLAILFANLFAPIFDYFVAQANIKRRKARSNGX					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2033>:

g635.seq

```

1  ATGACCCGGC GACGGGTCGG CAAGCAAAC CGTATTGCCA TCCACTCCGC
51  GCAATACCGA AAAATGGTCG TCTTGGCGGT ATTTAGATA CACGATGACG
101 GGGATTTCCT ACTGCGCGAG CTGTTGAAA GACAGGCGAT AGCCTTTCGC
151 CTCAAAACCC AAATCGGGCA TAATGCGCG CATATCCTCA AACGACGCGC
201 GCATCTGTTC CTTACCCAGT TTTTCCAACA CTTCTCTTTC CGTCAGCTTT
251 TGCCCGTAAA AATTGTTCAA AAGCGTCGCC ACCGAGCCG CCCCAGGA

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301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCCGCGCGC GCTTTCCAAC  
 351 TCTGCAATTT GATTTTCCG TAAACAACAG GATTATCGTT AACATCGGT  
 401 GCAGCATTCA AACGATAAGA CAAGGGTCTG TACCAGATTA G

This corresponds to the amino acid sequence <SEQ ID 2034; ORF 635.ng>:

m635.pep  
 1 MTRRRVGKQN RIAIHSAYR KMVFAVFI HDDGDFQLRE LFERQGIAR  
 51 LKTQIGHNAP HILKRRALF LTQFFQHFF RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IPPRFPTLQF DFSVNNRIIV KHRCISQITR QGSVPD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2035>:

m635.seq  
 1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC  
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG  
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCCG  
 151 TTCAAACCC AAATCAGGCA TAATGCGCCG CATATCCTCA AACGACGCGG  
 201 GCATCTGCTC CTTATCCAGT TTTTAAACA CGTCTCTTC CGTCAGCTTT  
 251 TGCCCGTAAA AATTGTTCAA AAGCGTCACC ACCGAAGCCG CCCCAGGAG  
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC  
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2036; ORF 635>:

m635.pep  
 1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAR  
 51 EKTQIRHNAP HILKRRGHLI LIQFF\*HVLV RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D\*

m635/g635 80.0% identity in 130 aa overlap

	10	20	30	40	50	60
m635.pep	MTQRRVGKQNRIAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGIARFKTQIRHNAP					
g635	MTRRRVGKQNRIAIHSAYRKMVFAVFIHDDGDFQLRELFERQGIARFKTQIGHNAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m635.pep	HILKRRGHLI LIQFFXHVLF RQLLPVKIVQ KRRHRSRPAG KIQILLYNIE IAPFFPTLHF					
g635	HILKRRALFLTQFFQHFF RQLLPVKIVQ KRRHRSRPAG KIQILLYNIE IPPRFPTLQF					
	70	80	90	100	110	120
	130					
m635.pep	DFSISNRIIVDX					
g635	DFSVNNRIIVKHRCISQITIROGSVPDX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2037>:

a635.seq  
 1 ATGACCCAGC GACGGGTCGG CAAGCAAAAC CGTATTGCCG TCTATACCGC  
 51 GCAATACCGA GAAATGATCA TCCTTGCGGT ATTCAGATA CACGATGACG  
 101 GGGATTTGCA ACTGTGCAAG CTGCTCGAAA GACAGGGCAT AGCCTTTCCG  
 151 CTCAAACCC AAATCAGGCA TGATGCGCCG CATATCCTCA AACGACGCGC  
 201 GCATCTGCTC CTTATCCAGC TTTTCAACA CGTCTCTTC CGTCAGCTTT  
 251 TGCCCGTGAA AATTGTTCAA AAGCGTCGCC ACCGAAGCCG CCCCAGGAG  
 301 AAAATCCAAA TCCTGCTTTA CAATATTGAA ATCGCGCCTT TCTTTCCAAC  
 351 TCTGCACCTT GATTTTCCA TAAGCAACAG GATTATAGTG GATTAA

This corresponds to the amino acid sequence <SEQ ID 2038; ORF 635.a>:

a635.pep  
 1 MTQRRVGKQN RIAVYTAQYR EMILAVFQI HDDGDLQLCK LLERQGIAR  
 51 LKTQIRHDAP HILKRRALHL LIQLFQHVLF RQLLPVKIVQ KRRHRSRPAG  
 101 KIQILLYNIE IAPFFPTLHF DFSISNRIIV D\*

m635/a635 95.4% identity in 131 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----

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m635 - pep      MTQRRVGKQNR IAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHNAP
|||||
a635            MTQRRVGKQNR IAVYTAQYREMIILAVFQIHDDGDLQLCKLLERQGI AFRFKTQIRHDAP
                  10      20      30      40      50      60

                  70      80      90      100     110     120
m635 - pep      HILKRRGHLLLIQFFXHVLF RQLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
|||||
a635            HILKRRGHLLLIQFFXHVLF RQLLPVKIVQKRHRSRPAGKIQILLYNIEIAPFFPTLHF
                  70      80      90      100     110     120

                  130
m635 - pep      DFSISNRIIVDX
|||||
a635            DFSISNRIIVDX
                  130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2039>:

```

g638.seq
1  A TGATTGGCG GACAGTTTAT CGTAGTtgGc attGTAGGCA AAAACGCACT
51  T GCCCGCTTT GTTGATAATA ttgtcGTGAA TAtcGGAATA GTTGACATAG
101 T TGAGCATGA TGCCCTAATC GCGGCTGCCG ACGGCGATAT TGTCGAACAC
151 T TTGAGCCGT TCGGAAAACA TCAGCACATA GCCCATATTG TtgcCCACGG
201 A AATATTGCC GCTGacttcg ctgtcgtTGG TGTACATATA GTGGACGGCG
251 A AACGCAGGT CGCTGAAGCG GTTGTTTTTA TAGGTGTTGT GCGTGCTGGT
301 A TTGAAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG ccgACGACCT
351 G CGCgcccggg CgcgtTCCAA ACGGTAACGC CATTGCCGCG CTCATTACAG
401 C GCAAGGTcg catcgCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 A GAACCATGA AGGTATACGC CGAACGAATT ATCAAAAATA TTGTTGTGTT
501 C AACCAGGGC GCGCGGGGCG GCTTTTTCGA GATAAATACC GGCATCCATT
551 G CTGGCAGGC TCATACCGGA ACGGTAACG GTCAGGTTGC GGAGCGTTAC
601 G TCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCTGTGCC CCTTCGATGG
651 T TGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCGATATAA
701 A GTTTGGTTT GATATACGCC GGAAGCCAGT TTGATCGTAT CGCCCGCCCC
751 G CGCGGGGCA AAAATTTCGG CAAGGTTGTC TTGCGGGGAA ACGTGGACGA
801 C GCGTGCCGA TGCCGTCTGA AAAATGCTGC CGCGGGCAAG TATCAGCAGC
851 G CCTTCAGCC ATATACGGAG CGCGGATGTG TGCATAGTGT CCCTCTGTTT
901 C GTTCGGTAT GGCCGAACAA AATAAGCAT CATTCAAATG TGCCTGTTTT
951 T ATAGCGAAA CCGCTGAAA CCGTACGGCA AGCGGTTTGG CTATAA

```

This corresponds to the amino acid sequence <SEQ ID 2040; ORF 638.ng>:

```

g638.pep
1  MIGGQFIVVG IVGKNALARF VDNIVVNIGI VDIVEHDALI AAADGDIVEH
51  FEPFGKHQHI AHIVAHGNIA ADFAVVGVHI VDGETQVAEA VVFIGVVRAG
101 I GKNVPPFG NUVADDLRAG RVPNGNAIAA LIHAQGRIAD DFILAHHRIG
151 R TMKVYAERI IKNIVVENQ ARGGFFEINT GIHCWQAHTG TGNGQVAERY
201 V RRVYGYGTP ALVPFDGCGT VGRPFNRRNF VDIKFLIYA GSQFDRIAR
251 G AGKNFGKVV LRGNVDDGCR CRLKNAAGGK YQHGLQPYTE RGCVHSVPLF
301 R SVWPNKIKH HSNVPVFIAR PPETVRQAVW L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2041>:

```

m638.seq
1  ATGATTGGCG AAAAGTTTAT CGTAGTGGC ATTATAGGCA AATACGCACT
51  TGCCCTGCC TTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 T TGAGCATAA TGCCCTGATC GCGGCTGCCG ACGGCGATAT TGTCGAATAC
151 T TTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACACG
201 A AATATTGCC GCTGATTTTC GTGTCGTTGG TGTACATATA GTGGACGGCG
251 A AACGCAAAAT CGCTGAAGCG GTTGTTTTTC TAGGTGTTGT GCGTGCTGGT
301 A TTGAAAAAA ATGCCGTCCC GCCCTTTGGA AATGTCGTTG CCGACGACCT
351 G CGCACCGGG TGCGTTCCAA ACGGTAACGC CGTGGCCGCG CTCGTTACAG
401 C GCAAGATCG CGTCGCCGAC GATTTTATTC TCGCGCACCA TCGCATCGGC
451 A GAACCATGC AGATATACGC CGACCGAATT ATCAAAAATA TTGTTGTGTT
501 C AATCAGGGC GCGCGGGGCA GTTCTTCGA GATAAATACC GGCATCCATT
551 G CGGGCAGGC TCATACCGGA ACGGGTAACG GTCAGGTTGC GGAGCGTTAC
601 G TCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTGC CCTTCGATGG
651 T TGCGGAACG GTCGGCAGGC CCTTCAATCG TAATCGGTTT GTCAATGTGA
701 A GTTTGGTTT TATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 G GCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGGTT CGTGA

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This corresponds to the amino acid sequence <SEQ ID 2042; ORF 638>:

m638.pep

```

1  MIGEKFIIVG IIGKYALACL VDNVVVNI GI VDIVEHNALI AAADGDIVEY
51  FEPLGKHQHI AHIVAHGNIA ADFAVVG VHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRTG CVPNGNAVAA LVHAQSRVAD DFILAHHRIG
151 RTMQIYADRI IQNIVVFNQG ARGSF FEINT GIHCGQAHTG TGNQQAERY
201 VRRVYGYGTP APVAFDGC GT VGRPFNRNRF VNVKFGFIYA GSQFERIARP
251 GAGKCGIPIS IIGS*

```

m638/g638 88.2% identity in 254 aa overlap

	10	20	30	40	50	60
m638.pep	MIGEKFIIVG	IIGKYALACL	VDNVVVNI	GI VDIVEHNALI	AAADGDIVEY	FEPLGKHQHI
g638	MIGGQFIVVG	IVGKNALARF	VDNVVVNI	GI VDIVEHDALV	AAADGDIVEH	FEPLGKHQHI

	70	80	90	100	110	120
m638.pep	AHIVAHGNIA	ADFAVVG VHI	VDGETQIAE	AVVFIGVVR	AGIGKNAVPP	FGNVVADDLRTG
g638	AHIVAHGNIA	ADFAVVG VHI	VDGETQVAE	AVVFIGVVR	AGIGKNAVPP	FGNVVADDLRAG

	130	140	150	160	170	180
m638.pep	CVPNGNAVA	ALVHAQSRV	ADDFILAHHR	IGRTMQIYA	DRIIQNIVV	FNQGARGSF FEINT
g638	RVPNGNAIA	ALVHAQSRV	ADDFILAHHR	IGRTMKVYA	ERIKNIVV	FNQGARGGFEINT

	190	200	210	220	230	240
m638.pep	GIHCGQAHT	TGTGNGQVA	ERYVRRVY	GYGTPAPVA	FDGCGTVGR	PFNRNRFVNVKFGFIYA
g638	GIHCWQAHT	TGTGNGQVA	ERYVRRVY	GYGTPALVP	FDGCGTVGR	PFNRNRFVDIKFGLIYA

	250	260
m638.pep	GSQFERIARP	GAGKCGIPIS IIGSX
g638	GSQFDRIARP	GAGKCNFGKVVL RGNVDGCRCLKNAAGGKYQHGLQPYTERGCVHSVPLF

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2043>:

a638.seq

```

1  ATGATTGGCG GACAGTTTAT CGTAGTTGGC ATTGTAGGCA AAAACGCACT
51  TGCCCGCTTT GTTGATAATG TTGTCGTGAA TATCGGAATA GTTGACATAG
101 TTTGAGCATGA TGCCTTGGTC GCGGCTGCCG ACGGCGATAT TGTCAAACAC
151 TTTGAGCCGC TCGGAAAACA TCAGCACATA GCCCATATTG TTGCCACCGG
201 AAATATTGCC GCTGATTTCG CTGTCGTTGG TGTACATATA GTGGACGGCG
251 AAACGCAAT CGCTGAAGCG GTTGTTTTGA TAGGTGTTGT GCGTGTCTGGT
301 ATTGGAAAAA ATGCCGTCCC GCCCTTTGGA AATATCGTTG CCGACGACCT
351 GCGCGCCGGG CGCGTTCCAA ACGGTAACGC CATTGCCGCG CTCGTTACAG
401 CGCAAAGTCG CGTCGCCGAC GATTTTATTC TCCCGCACCA TCGCATCGGC
451 AGAACCATGC AGATAGACGC CGACCGAATT ATCCAAAATA TTATTGTGTT
501 CAATCAGGGC GCGCGGGGCA GTTCTTTCGA GATAAATACC GGCATCCATT
551 GCGGGCAGGC TCATACCGGA ACGGTAACGC GTCAGGTTGC GGAGCGTTAC
601 GTCCGGCGCG TGTACGGCTA TGGTACGCCC GCTCCTGTCT CCTTCGATGG
651 TTGCAGAACG GTCGGCAGGC CCTCAATCG TAATCGGTTT GTCGATGTGA
701 AGTTTGGTTT GATATACGCC GGAAGCCAGT TTGAGCGTAT CGCCCGCCCG
751 GGCGCGGGCA AATGCGGGAT ACCGATCAGC ATAATCGACT CATGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2044; ORF 638.a>:

a638.pep

```

1  MIGGQFIVVG IVGKNALARF VDNVVVNI GI VDIVEHDALV AAADGDIVKH
51  FEPLGKHQHI AHIVAHGNIA ADFAVVG VHI VDGETQIAEA VVFIGVVRAG
101 IGKNAVPPFG NIVADDLRAG RVPNGNAIAA LVHAQSRVAD DFILPHHRIG
151 RTMQIDADRI IQNIVVFNQG ARGSF FEINT GIHCGQAHTG TGNQQAERY
201 VRRVYGYGTP APVSFDGCRT VGRPFNRNRF VDVKFGLIYA GSQFERIARP

```

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251 GAGKCGIPIS IIDSW\*

m638/a638 91.3% identity in 264 aa overlap

	10	20	30	40	50	60
m638 .pep	MIGEKFIVVGIIGKYALACLVNVDNVVNIIGIVDIVEHNLIAAADGDIVEYFEPLGKHQHI					
a638	MIGGQFIVVGIVGKNALARFVDNVVNIIGIVDIVEHDALVAAADGDIVKHFEPLGKHQHI					
	10	20	30	40	50	60
m638 .pep	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFGVVRAGIGKNAVPPFGNVVADDLRTG					
a638	AHIVAHGNIAADFAVVGVIHVDGETQIAEAVVFIGVVRAGIGKNAVPPFGNIVADDLRAG					
	70	80	90	100	110	120
m638 .pep	CVPNGNAVALVHAQSRVADDFILAHHRIGRTMQIYADRIIQNIIVFNQARGSFEEINT					
a638	RVPNGNAIALVHAQSRVADDFILPHHRIGRTMQIDADRIIQNIIVFNQARGSFEEINT					
	130	140	150	160	170	180
m638 .pep	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVAFDGCRTVGRPFNRNRFVNVKFGFIYA					
a638	GIHCGQAHTGTGNGQVAERYVRRVYGYGTPAPVSFDGRTVGRPFNRNRFVDVKFGLIYA					
	190	200	210	220	230	240
m638 .pep	GSQFERIARPGAGKCGIPISIIGSX					
a638	GSQFERIARPGAGKCGIPISIISWX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2045>:

g639-1.seq

```

1  ATGAGCCTGC CAGCAATGGA TGCCGGTATT TATCTCGAAA AAGCCGCCCC
51  GCGCGCCCTG GTTGAACACA ACAATATTTT TGATAATTCG TTCGGCGTAT
101 ACCTTCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GATGCGACCT TGCGCGTGAA TGAGCGCGGC AATGGCGTTA CCGTTTGGAA
201 CGCGCCCGGC GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAACT CCTATAAATA CAACCGCTTC
301 AGCGACCTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAGT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAACGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGATTAG
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAATATTAT
501 CAACAAAGCG GCGAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATGCA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGGAAG
651 CCAGGTCAAA TATGTCAGTA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA CTGGAGCGAC AACAGCCCGT TCGATTTGAA CCGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCGACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGG GCAGGCGCAG TTTCCGCGG TTCTGCCCGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATTC AAACCGGTTA
951 TCAGGCGATG AAGGACGAGT TGCTCAAAGA AGCCGAAACG CGGCAGTCGG
1001 AACGGGCGAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2046; ORF 639-1.ng&gt;:

g639-1.pep

```

1  MSLPAMDAGI YLEKAAPRAL VEHNIFDNS FGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101  SDLRFVHYM YTNDSEVSGN ISVGNMNGYV LMFSERLKVF DNIIVGSRD*
151  GIMLVVNYN DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGMHFTA
201  AIEGTSLHDN SFINNGSQVK YVSTRFLDWS EGGHGNYSWD NSPFDLNGDG
251  FGDSAYRPDG IIDQIIWRAP VSRLMNSPA ISIVKWAQQA FPAVLPGGVV
301  DSKPLMKPYA PKIQTRYQAM KDELLEKET RQSERGRAEN GSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2047>:

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## m639-1.seq

```

1   ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AACTGCCCC
51  GCGCGCCCTG ATTGAACACA ACAATATTTT GGATAATTCG GTCGGCGTAT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GCGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AACGGCGTTA CCGTTTGGAA
201 CGCACCCGGT GCGCAGGTCG TCGGCAACGA CATTTCCTAA GGGCGGGACG
251 GCATTTTTC CAATACCAGC ACGCACAAAC CCTACAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTATTC GACAATATCG CCGTCGGCAG CCGCGATCAG
451 GGCATTATGC TCAACTATGT CAACTATTCC GATATTACG ACAACATTAT
501 CAACAAGGCA GGCAAGTGCG TATTGCTTA TAATGCCAAC TACGATAAAC
551 TTTTCGCCAA TCATTTTGAA AACTGTCAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCTT GCATGACAA TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTCT CGATTGGAGC GAGGCGGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG CCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCGCCC GTATCGCGCC TTTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAAATGGC GCAGGCGCAG TTCCCGCCG TTCTGCCTGG CGGCGTGGTG
901 GACAGCAAAC CGCTGATGAA GCCTTATGCC CCCAAAATC AAACCCGTTA
951 TCAGGCGATG AAGGACGAGC TACTCAAAGA AGTCGAAACG CGGCAGTCGG
1001 AATGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2048; ORF 639-1>:

## m639-1.pep

```

1   MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWNAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 SDLRFVHYM YTNDSEISGN ISVGNNMGYV LMFSERLKVF DNIAGVSRDQ
151 GIMLNYYNYS DIHDNIINKA GKCVFAYNAN YDKLFANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSW SDNSAFDLNGDG
251 FGDSAYRPNG IIDQIIWRAP VSRLLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIOTRYQAM KDELLEKETV RQSEWGRAEN GSLN*

```

g639-1/m639-1 95.9% identity in 344 aa overlap

g639-1.pep	10	20	30	40	50	60
m639-1	10	20	30	40	50	60
g639-1.pep	70	80	90	100	110	120
m639-1	70	80	90	100	110	120
g639-1.pep	130	140	150	160	170	180
m639-1	130	140	150	160	170	180
g639-1.pep	190	200	210	220	230	240
m639-1	190	200	210	220	230	240
g639-1.pep	250	260	270	280	290	300
m639-1	250	260	270	280	290	300
g639-1.pep	310	320	330	340		
m639-1	310	320	330	340		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2049>:

## a639-1.seq

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```

1  ATGAGCCTGC CCGCAATGGA TGCCGGTATT TATCTCGAAG AACTGCCCC
51  GCGCGCCCTG ATTGAACACA ATAATATTTT GGATAATTCG GTCGCGCTCT
101 ATCTGCATGG TTCTGCCGAT GCGATGGTGC GGGAGAATAA AATCGTCGGC
151 GACGCGACTT TGCGCGTGAA CGAGCGCGGC AATGGCGTTA CCGTTTGAA
201 CCGCGCCGGC GCGCAGGTCG TCGGCAACGA TATTTCCAAA GGGCGGGACG
251 GCATTTTTTC CAATACCAGC ACGCACAACA CCTATAAAA CAACCGCTTC
301 AGCGATTTGC GTTTCGCCGT CCACTATATG TACACCAACG ACAGCGAAAT
351 CAGCGGCAAT ATTTCCGTGG GCAACAATAT GGGCTATGTG CTGATGTTTT
401 CCGAGCGGCT CAAAGTGTTT GACAATATCG CCGTCGGCAG CCGCGACCAA
451 GGCATCATGC TCAACTATGT CAACTATTCC GATATTACAG ACAACATTAT
501 CAACAAAGCG GGCAAGTGCG TTTTGCCTA CAATGCCAAC TACGATAAAC
551 TGTCCGCCAA TCATTTTGAA AACTGCCAAA TCGGCATACA CTTTACCGCC
601 GCCATCGAAG GCACGTCCCT GCACGACAAT TCCTTTATCA ACAACGAAAG
651 CCAGGTCAA TACGTCAGCA CGCGCTTTCT CGACTGGAGC GAGGGCGGAC
701 ACGGCAACTA TTGGAGCGAC AACAGCGCGT TCGATTGAA CGGCGACGGC
751 TTCGGAGACA GCGCGTACCG TCCCAACGGC ATCATCGACC AAATCATCTG
801 GCGCGCACCC GTATCGCGCC TCTTGATGAA CAGTCCCGCA ATCAGCATCG
851 TCAAATGGG CAGGCGCAA TTTCCGCGG TTTGCGCTGG CGGCGTGGTG
901 GACAGCAAA CGCTGATGAA GCCTTATGCC CCAAAATTC AAACCGTTA
951 TCAGGCGATG AAGGACGGG TGCTCAAAA AGTCGAAACG CGGCAGTTGG
1001 AATGGGGCAG GCGGAAAAC GGTCTTTGA ACTAG

```

This corresponds to the amino acid sequence <SEQ ID 2050; ORF 639-1.a>:

a639-1.pep

```

1  MSLPAMDAGI YLEETAPRAL IEHNNILDNS VGVYLHGSAD AMVRENKIVG
51  DATLRVNERG NGVTVWVAPG AQVVGNDISK GRDGIFSNTS THNTYKNNRF
101 S DLRFAVHYM YTNDSEISGN ISVGNMGGYV LMFSERLKVF DNIIVGSRDQ
151 GIMLNYVYNS DIHDNIINKA GKCVFAYNAN YDKLSANHFE NCQIGIHFTA
201 AIEGTSLHDN SFINNESQVK YVSTRFLDWS EGGHGNYSWD NSAFDLNGDG
251 FGD SAYRPNG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV
301 DSKPLMKPYA PKIQTRYQAM KDGLLKKVET RQLEWGRAEN GSLN*

```

a639-1/m639-1 98.8% identity in 344 aa overlap

a639-1.pep	10	20	30	40	50	60
	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
m639-1	10	20	30	40	50	60
	MSLPAMDAGIYLEETAPRALIEHNNILDNSVGVYLHGSADAMVRENKIVGDATLRVNERG					
a639-1.pep	70	80	90	100	110	120
	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN					
m639-1	70	80	90	100	110	120
	NGVTVWVAPGAQVVGNDISKGRDGIFSNTSTHNTYKNNRFSDLRFAVHYMYTNDSEISGN					
a639-1.pep	130	140	150	160	170	180
	ISVGNMGGYVLMFSERLKVF DNIIVGSRDQ GIMLNYVYNS DIHDNIINKA GKCVFAYNAN					
m639-1	130	140	150	160	170	180
	ISVGNMGGYVLMFSERLKVF DNIIVGSRDQ GIMLNYVYNS DIHDNIINKA GKCVFAYNAN					
a639-1.pep	190	200	210	220	230	240
	YDKLSANHFENCQIGIHFTA AIEGTSLHDNS FINNESQVK YVSTRFLDWS EGGHGNYSWD					
m639-1	190	200	210	220	230	240
	YDKLFANHFENCQIGIHFTA AIEGTSLHDNS FINNESQVK YVSTRFLDWS EGGHGNYSWD					
a639-1.pep	250	260	270	280	290	300
	NSAFDLNGDGFGDSAYRPNG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV					
m639-1	250	260	270	280	290	300
	NSAFDLNGDGFGDSAYRPNG IIDQIIWRAP VSRLMNSPA ISIVKWAQAF FPAVLPGGVV					
a639-1.pep	310	320	330	340		
	DSKPLMKPYAPKIQTRYQAM KDGLLKKVET RQLEWGRAENGSLN					
m639-1	310	320	330	340		
	DSKPLMKPYAPKIQTRYQAM KDELLEK VET RQSEWGRAENGSLN					



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The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2051>:

```

g640.seq
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGC
51  TATGTCCTGT TTTTCAATCC GCGGTATGTC TCGGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TACCGCCTTT GTCTTTTGA CGGcggcACT GCCCGCTTAT
151 GcggAgcgTc tgcctGATTT TCTGgcgAAA ATacAgcctT CGGAAATTTT
201 TCCGGGTGCG GATCGTTACG GCAAGCCGGA aggcAAGCCT AtggtTGCCC
251 GCGtttACAA AGgcgATGAG CAGCTCGGTT TGGTTTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATCGATA CGCTGATGGC
351 TTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GATCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAAT CGCGTGTGTA TAAGTTCATC
451 GACAAATATA TCGGTCTGAA TTTTATTAAA AATCCGCCGA CCCCAGCGT
501 GCGCCCGGGC GACATCATCA GcggtGCGAC TgttaCACTG ATGGTGGTTA
551 ACGACAGCAT CCAGCGTTCG TACAAGGTCA TTGCCAACCA ATACCGTCTG
601 GGTTCGGACA AGGCCCTTCA GACGGCATCC GCTTCCGATG TTCGGGAAGC
651 CGCGCCTGCG TCAGAAACCC GTCCGCGCCG TATGGCAAAT CCCGACAAGC
701 AGGATATTTT GTCTTGGGAC GAACTTTTGA AACAAAAGGC CGTCGGCCAT
751 CTGCATATCA CGCTCGATCA AATCAACAAA CTGTTTGAGA AAGGCGGCAA
801 GGCCGGCGTG GCCGATCACG CCGAACAGGG CGATCCTGAC GATACCTTTA
851 TTGATTTGTA TGTTCCTTG GTCAGCCAGC CTTCCATCGG TAAAGCCTG
901 CTGGGTGAGG ACGCTGGGG GCATCTGCAA AAACGGCTGA AACCCGGGCA
951 GCAGGCGGTT TTGGTTGCCG GAGAGGGCCG TTATTCTTGG AAAGGTTCCG
1001 GCTATGTGCG CGGCGGTATT TTCGACCGTA TCGAGATGAT TCAGGGGGAG
1051 AACAGCTTCC GTTTTACCGA TGCCCAACAC GAACGCGTCG TCGAGCTGTC
1101 TGCCGCCGAT GCGCCGCGTT TTAAAGAGT TTCTTGGTT ACCATCCCTG
1151 AAGCGTAGC GTTTGACGGT GCGGAGCCGT GGCGGCTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2052; ORF 640.ng>:

```

g640.pep
1  MIHIISILKS IGISGIAMSC FSIRMSAFR ARITAFFTAE VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAN DGTIAGAKLV DHHEPIMLIG IPQSRVDKFI
151 DKYIGLNFIL NPPTPSVAPG DIISGATVTL MVVNSDIQRS YKVIANQYRL
201 GSDKALQTAS ASDVREAAPA SETRPRRMAN PDKQDILSWD ELLKQKAVGH
251 LHITLDQINK LFEKGGKAGV ADHAEQGDPD DTFIDLYVAL VSQPSIGKSL
301 LGEDGWAHLQ KRLKPGQAV LVAGEGRYSW KSGSYVRGGI FDRIEMIQGE
351 NSFRTDAQH ERVVELSAAD APRFKEVSWF TIPEGVAFDG AEPWRL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2053>:

```

m640.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51  CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATTT TCTGGCGAAA ATACAGCCTT CGGAAATTTT
201 TCCGGGTGCG GACCGTTACG GCAAGCCGGA AGGTAAGCCT ATGTTTGCCC
251 GCGTTTACAA AGGCGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGT
351 GTTGGCAAAC GACGGCACGA TAGCCGGGGC GAAACTGGTC GACCATCACG
401 AACCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2054; ORF 640>:

```

m640.pep (partial)
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51  AERLPDFLAK IQPSEIFPGA DRYGKPEGKP MVARVYKGE QLGLVYITTD
101 AVNTRGYSSK PIDTLMVLAN DGTIAGAKLV DHHEPIMLIG IPH...

```

m640/g640 96.5% identity in 143 aa overlap

	10	20	30	40	50	60
m640.pep	MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK					
g640	MIHIISILKSIGISGIAMSCFSIRMSAFRARITAFFTAFVFLTAALPAYAERLPDFLAK					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m64 O.pep  IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
            |||||||||||||||||||||||||||||||||||||||||||||||||||
g64 O      IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAN
            70      80      90      100     110     120

            130      140
m64 O.pep  DGTIAGAKLVDHHEPIMLIGIPH
            |||||||||||||||||||
g64 O      DGTIAGAKLVDHHEPIMLIGIPQSRVDKFDIKYIGLNFINKPPTPSVAPGDIISGATVTL
            130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2055>:

```

a64 O.seq (partial)
1  ATGATTCATA TAATATCAAT ATTAAAGAGT ATCGGTATAT CGGGGATAGT
51 CATGTCCTGT TTTTCAATCA AACGTATGTC CGCGTTTCGG GCGCGGATAA
101 CGGCGTTTTT TGCCGCCTTT GTCTTTTGA CGGCGGCACT GCCCGCTTAT
151 GCGGAGCGTC TGCTGATT TCTGGCGAAA ATACAGCCTT CGGAAATTGT
201 TCCGGGTGCG GACCGTTACA GCAAGCCGGA AGGTAAGCCT ATGGTTGCC
251 CGGTTTACAA AGCGGATGAG CAGTTGGGCT TGGTCTATAT CACGACCGAT
301 GCGGTCAATA CGCGCGGTTA TTCGAGCAAA CCGATTGATA CGCTGATGGC
351 GTTGGCTAAA GACGGTACGA TAGCCGGAGC GAAATTGGTT GATCACCATG
401 AGTCGATTAT GCTGATCGGT ATCCCGCAT...

```

This corresponds to the amino acid sequence <SEQ ID 2056; ORF 640.a>:

```

a64 O.pep (partial) Length: 143
1  MIHIISILKS IGISGIVMSC FSIKMSAFR ARITAFFAAF VFLTAALPAY
51 AERLPDFLAK IQPSEIVPGA DRYSKPEGKP MVARVYKGDE QLGLVYITTD
101 AVNTRGYSSK PIDTLMALAK DGTIAGAKLV DHESIMLIG IPH...

```

m640/a640 96.5% identity in 143 aa overlap

```

            10      20      30      40      50      60
m64 O.pep  MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
            |||||||||||||||||||||||||||||||||||||||||||||||||||
a64 O      MIHIISILKSIGISGIVMSCFSIKMSAFRARITAFFAAVFVFLTAALPAYAERLPDFLAK
            10      20      30      40      50      60

            70      80      90      100     110     120
m64 O.pep  IQPSEIFPGADRYGKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMVLAN
            |||||||||||||||||||||||||||||||||||||||||||||||||||
a64 O      IQPSEIVPGADRYSKPEGKPMVARVYKGDEQLGLVYITTDVNTRGYSSKPIDTLMALAK
            70      80      90      100     110     120

            130      140
m64 O.pep  DGTIAGAKLVDHHEPIMLIGIPH
            |||||||||||||||||||
a64 O      DGTIAGAKLVDHHEPIMLIGIPH
            130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2057>:

```

g64 2.seq
1  ATGCGGTATC CGCGCAATC GCGGTTTTG CAGAATGCCG CGCGTTGCCT
51 TTTGCGCCGC CCGAAATCTG CCGCGCCCG TATTGCCCC CTATCGCAA
101 TATCGGCAGT CCAATATATC TTTGCGGATG TCGTTCAGCA GGAAGGCTGT
151 GGTGCTTCG TGTTCTCTCT GTACGAAGAC AAAAAGTCGG GCGATGATTT
201 TGCCGATGAA GACTTTTTCG AGGGCGCAGG CGTCGGTCAG GGTGTGTTCC
251 TGCAGGAAGC TGCGGATGTC TTCGGGCAAA GCGTAgTcgc gGGCAACGGC
301 GGcaaagcgg ACatcggtTT Gcaeggcgtc gagCAGGGtt tggTTTTTGT
351 CCAACTTAAT GCCTGCTTCT TTTCTTCGG CCGTGGCGCG GACGAACTGG
401 TCGTAAATTT CGGCATAAAG CATATCGTTC GGGCCTTCAA AAATCGTGAA
451 GGGGCGGATA TCGATGGCGA TATTGCCGGC TGGGTGTCCG CGTTCAAAAC
501 CCTTCGCGCC CAAGAGTTTT TGCAACATT GCGCGCGGgc gTAAGTGTAT
551 TCCGTGGCGa ggGTTTTGac gatgTTCGCC TCCATCAATT GATGGGCGac
601 ggGCGcgacg ggCGAAACGG AATGGCAGAC GTAGCGGTAA AGGATTTCGG
651 AAACCTGATG GCGGCGTTGG ATTTGCGCGC GTTCGTAATC GACGAATCTG

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```

701 ATATCGTTGC GGACATATCG GTTCAGGTTG TCAAGGATGT ATTCCATAAT
751 GCCGTGCGTC ATGCCGATCA GTTGCAGGCG GCTGCGGATA AAGATGTTTT
801 GGAACGCGCG CAAACCGGCA GCGTCGCCCC GGGAGAGTTT CATCACGGCG
851 GTTGCAGGCA TTTCGGCATC GATGCGGTTG ACGGCGTAAC GGACGGCGCG
901 CAGGCCTTCG GATGCGAGGG TTTCGCAGCG GATGTATGTT TTGGGGACGA
951 GCAGCAGGTC GATGactttg gcgagtttgC CgtttttgCG ctctttggcg
1001 gcaacgaggA GGAAGTCGCT TTGCGAATTG CCCTGCCAGT ATTTGCGGGC
1051 GttgACGTAA ATGGTttgtt cgtcggtata ttcgtagcag gactgcaTTT
1101 CGCGTGCAAT cgCgcgcgcg gaggtTtcgg gttcggtaAc gcccaaacgg
1151 cggctttcgc ctTTGAAAAT CATGTCCAAA CCTTGTGCGA CTTCGcttc
1201 gccgccgaac tCTTGACAGAG GCTGCAACAC CAGCGCGCCT TCGATGCCGG
1251 TACGCAGCGT AACGGGCACG CCGTAATGCC CCGCAATCCT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2058; ORF 642.ng>:

g642.pep

```

1 MRYPPQSAVL QNAARCLLR PKSACRRICP LSAISAVQYI FADVQQEGC
51 GVVFVLLYED KKSDDDFADE DFLQGAGVGQ GVFLQEAADV FGQSVVAGNG
101 GKADIGLHGV EQGLVFVQLN ACFFFFGGGA DELVVNFGIK HIVRAFKNRE
151 GADIDGDIAG WWSAFKTLRA QEFLQHLRGG VSVFRGEGFD DVRLHLQMGD
201 GRDGRNGMAD VAVKDFGNLM AALDFAAFVI DESDIVADIS VQVVKDVFHN
251 AVRHADQLQA AADKDVLER QTVSVAPGEF HHGGCRHFGI DAVDGVTDGA
301 QAFGCEGFAA DVCFGEQGV DDFGEFAVFA LFGGNEEEVA LRIALPVFRG
351 VDVNGLFVCI FVAGLHFACN RRAGGFGFGN AQTAFAFEN HVQTLCDLRF
401 AAELLQRLQH QRAFDAGTQR NGHVMVRNP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2059>:

m642.seq (partial)

```

1 GCCTGCCGCC GTATTTGCCG GCTACCCGCA ATATCGGCAG TCCAATATAT
51 CTTTGGCGAT GTCGTTGAGC AGGAAGGCTG CCGTGTCTTC GTGTTTCGCC
101 TGTACGAAGA CAAAGAGTCG GCGGATGATT TTGCCGATAA AGACTTTTTG
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCAGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGCT TTGGTTTTTG TCCAACCTCA TGCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAACTG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CCGGCCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CCGTGTGTCC GCGTTCAAAA CCCTTCGCAC CCAAGAGTTT
451 TTGCAACATT TGCAGGCGCG CGTAAGTGTG TTCCGTGGCG AGGGTTTGA
501 CGATGTTTCG CTCATCAGC TGATGGGCGA CGGGGGCAAC AGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GCGGCGCGCG
601 GATTTCGCGG CATTGTAAT CGACGAATTT GATGTCGTG CCGACGTATC
651 GTTCCAGATT TTCAAGGATG TATTCATAA TGCCGTGCGT CATGCCGATC
701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCGGCAT
801 CGATGCGGTT GACGGCGTAA CCGACGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GGCAGATTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTGCGG CATTGACGTA AATGTTTGT
1001 CCGTCGATAT ATTCGTAGTA GGACTGCATT TCGCGTGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CACCCAAACC GCCGCCCTCG CCTTGAAAA
1101 TCATCTCCAA ACCTGCGCG ACTTGCGCTT CATCGCCGAA CTCTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2060; ORF 642>:

m642.pep (partial)

```

1 ACRRICPLPA ISAVQYIFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51 QGAGIGQGVF LQEAADVFRQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFQIKHIV RAFKNREGAD VSDIAGGVS AFKTLRTQEF
151 LQHLRGGVSV FRGEGFDVVR LHQLMGDGGN RRNGMADVAV KNLGNLMAAP
201 DFAAFVIDEF DVVADVSTFI FKDVFNHVR HADQLQAAAD KDVLERATG
251 SVALGEFHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFAVFALFG GNEEEVALRV ALPVFRGVDV NGLSVDIFV GLHFAFNRR
351 GGFVFGNTQT AALAFENHLQ TLRDLRFIAE LLQWLQHQRA FDAGTQRNGH
401 AVMPRNP

```

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m642/g642 90.4% identity in 407 aa overlap

m642.pep				10	20	30
				ACRRICPLPAISAVQYIFADV	VQEGCGVFVFR	LYED
g642	MRYPPQSAVLQNAARCLLRPKSACRRICPLSAISAVQYIFADV	VQEGCGVFVFR	LYED			
	10	20	30	40	50	60
m642.pep	40	50	60	70	80	90
	KESGDDFADKDFLQAGIGQG	VFLQEAADVFRQSVVAGDGGKAGIGLQAVEQGLV	FVQLH			
g642	KKSGDDFADEDFLQAGVGQGVFLQEAADVFRQSVVAGNNGKADIGLHGVEQGLV	FVQLN				
	70	80	90	100	110	120
m642.pep	100	110	120	130	140	150
	ACFFFFGGGADKLVNFGIKHIVRAFKNREGADVSDIAGGVSAFKTLR	TQEF	LQHLRGG			
g642	ACFFFFGGGADELNVNFGIKHIVRAFKNREGADIDGDIAGVWSAFKTLRAQEF	LQHLRGG				
	130	140	150	160	170	180
m642.pep	160	170	180	190	200	210
	VSVFRGEGFDDVRLHQLMGDGNRRNGMADVAVKNLGNLMAAPDFAAFVIDE	FDDVADVS				
g642	VSVFRGEGFDDVRLHQLMGDGRDGRNGMADVAVKDFGNLMAALDFAAFVIDES	DIADIS				
	190	200	210	220	230	240
m642.pep	220	230	240	250	260	270
	FQIFKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVALGEFHHGGCRHFGIDA	VDGVT	DGA		
g642	VQVVKDVFNHNAVRHADQLQAAADKDVLERAQ	TGSVAPGEFHHGGCRHFGIDA	VDGVT	DGA		
	250	260	270	280	290	300
m642.pep	280	290	300	310	320	330
	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRVALPVFRGVDV	NGLSVDI				
g642	QAFGCEGFAADVCFGDEQQVDDFGEFAVFALFGGNEEEVALRIALPVFRGVDV	NGLFVGI				
	310	320	330	340	350	360
m642.pep	340	350	360	370	380	390
	FVVGLHFACNRRAGGFGFGNTQTAAALAFENHLOTLRDLRFIAELLQWLQHQRA	FDAGTQR				
g642	FVAGLHFACNRRAGGFGFGNAQTAAALAFENHVQTLCDLRFIAELLQWLQHQRA	FDAGTQR				
	370	380	390	400	410	420
m642.pep	400					
	NGHAVMPRNP					
g642	NGHAVMPRNPX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2061>:

a642.seq (partial)

```

1  GCCTGCCGCC GTATTGCCCC GCTATCCGCA ATATCGGCAG TCCAATATGT
51  CTTTGCGGAT GTCGTTCCAGC AGGAAGGCTG CGGTGTCTTC GTGTTCCGCC
101 TGTACGAAGA CAAAGAGTCG GGCGATGATT TTGCCGATAA AGACTTTTGT
151 CAGGGCGCAG GCATCGGTCA GGGTGTGTTT CTGCAGGAAG CTGCGGATGT
201 CTTCGGGCAA AGTGTAGTCG CGGGCGACGG CGGCAAAGCG GGCATCGGTT
251 TGCAGGCGGT CGAGCAGGGT TTGGTTTTTG TCCAACTTCA TGCCTGCTTC
301 TTTTCTTCG GCGGTGGCGC GGACAAATG GTCGTAAATT TCGGCATAAA
351 GCATATCGTT CGGGCCTTCA AAAATCGTGA AGGGGCGGAT GTCGATAGCG
401 ATATTGCCGG CGGTGTGTCC GCGTTCAAAA CCCTTCGCGC CCAAGAGTTT
451 TTGCAACATT TGCAGCGCGG CGTAAGTGTA TTCCGTGGCG AGGGTTTTGA
501 CGATGTTTCG CTCCATCAGT TGATGGGCGA CGGGTGCAAC GGGCGAAACG
551 GAATGGCAGA CGTAGCGGTA AAGAATCTCG GAAACCTGAT GGCGGCGCCG
601 GATTTCGCGG CGTTCGTAAT CGACGAATCT GATGTCGTTG CGGACGTATC
651 GTCCAGGTT TTCAAGGGTG TATTCATAA TGCCGTGCGT CATGCCGATC

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1020

```

701 AGTTGCAGGC GGCTGCGGAT AAAGATGTTT TGAACGCGC GCAAACCGGC
751 AGCGTCGCTC TGGGAGAGTT TCATCACGGC GGTTCAGGC ATTTCCGGCAT
801 CGATGCGGTT GACGGCGTAA CGGACGGCGC GCAAGCCTTC GGATGCGAGG
851 GTTTCGCAGC GGATGTATGT TTTGGGGACG AGCAGCAGGT CGATGACTTT
901 GCGGAGTTTG CCGTTTTTGC GCTCTTTGGC GGCAACGAGG AGGAAGTCGC
951 TTTGCGAGTT GCCCTGCCAG TATTTCCGGC CGTTGACGTA AATGGTTTGT
1001 CCGTCGGTAT ATTCTAGTA AGACTGCATT TCTCGGGCAA TCGCCGCGCC
1051 GGAGGTTTCG GGTTCGGTAA CGCCTAAACC GCCGCCCTCG CCTTGAAAA
1101 CCATGTCCAA ACCCTGTGCG ATTTGCGCTT CATCGCCGAA CTCTTGCACT
1151 GGCTGCAACA CCAGCGCGCC TTCGATGCCG GTACGCAGCG TAACGGGCAC
1201 GCCGTAATGC CCCGCAATCC G

```

This corresponds to the amino acid sequence <SEQ ID 2062; ORF 642.a>:

```

a 642 .pep Length: 407
1  ACRRICPLSA ISAVQYVFAD VVQQEGCGVF VFRLYEDKES GDDFADKDFL
51  QGAGIGQGVF LQEAADVFGQ SVVAGDGGKA GIGLQAVEQG LVFVQLHACF
101 FFFGGGADKL VVNFGIKHIV RAFKNREGAD VSDIAGGVS AFKTLRAQEF
151 LQHLRGGVSV FRGEGFDDVR LHQLMGDGCN GRNGMADVAV KNLGNLMAAP
201 DFAAFVIDES DVVADVSFQV FKGVFHNAVR HADQLQAAAD KDVLERAQTG
251 SVALGEFHG GCRHFGIDAV DGVTDGAQAF GCEGFAADVC FGDEQQVDDF
301 GEFVAFALFG GNEEEVALRV ALPVFRGVDV NGLSVGIFVV RLHFSGNRRA
351 GGFGFGNA*T AALAFENHVQ TLCDLRFIAE LLQWLQHORA FDAGTQRNGH
401 AVMPRNP

```

m642/a642 95.8% identity in 407 aa overlap

```

m642 .pep      10      20      30      40      50      60
ACRRICPLPAISAVQYIFADVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||
a 642          10      20      30      40      50      60
ACRRICPLSAISAVQYVFADVQQEGCGVFVFRLYEDKESGDDFADKDFLQAGIGQGVF
|||||

m642 .pep      70      80      90     100     110     120
LQEAADVFRQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLVVNFGIKHIV
|||||
a 642          70      80      90     100     110     120
LQEAADVFGQSVVAGDGGKAGIGLQAVEQGLVFVQLHACFFFGGGADKLVVNFGIKHIV
|||||

m642 .pep     130     140     150     160     170     180
RAFKNREGADVSDIAGGVSAFKTLRTQEFQLHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||
a 642         130     140     150     160     170     180
RAFKNREGADVSDIAGGVSAFKTLRAQEFQLHLRGGVSVFRGEGFDDVRLHQLMGDGCN
|||||

m642 .pep     190     200     210     220     230     240
RRNGMADVAVKNLGNLMAAPDFAAFVIDEFDVVADVSFQIFKDVFNHNAVRHADQLQAAAD
|||||
a 642         190     200     210     220     230     240
GRNGMADVAVKNLGNLMAAPDFAAFVIDESDVVADVSFQVFKGVFNHNAVRHADQLQAAAD
|||||

m642 .pep     250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||
a 642         250     260     270     280     290     300
KDVLERAQTG SVALGEFHGGCRHFGIDAVDGVTDGAQAFGCEGFAADVCFGDEQQVDDF
|||||

m642 .pep     310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVDIFVVGHLHFACNRRAGGFGFGNTQT
|||||
a 642         310     320     330     340     350     360
GEFAVFALFGGNEEEVALRVALPVFRGVDVNGLSVGIFVVRHLHFSGNRRAGGFGFGNAXT
|||||

m642 .pep     370     380     390     400
AALAFENHLQTLRDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||
a 642         370     380     390     400
AALAFENHVQTLCDLRFIAELLQWLQHORA FDAGTQRNGHAVMPRNP
|||||

```

1021

370

380

390

400

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2063>:

g643.seq

```

1   ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGgTcgg CTACGCTGAC
51  gttgtancGt TTGGcaATGt tGaaCagggt gtcgccTTCT ACAACGCGGT
101 GGATGCTGGC ATGGagcGGG GAGGTTTCGG CTTCCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TGCCCGGCGT TtgCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGagaTGTT TCTTCAGCCT GCCGCGCag gTTGTTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTGGGGGGAT
351 GACCTGCGCg aGTGtTGGG TTTGGGTTTC agacgGCATG GCAGTCTGTT
401 TTTcggTTTG a

```

This corresponds to the amino acid sequence <SEQ ID 2064; ORF 643>:

g643.pep

```

1   MVLPLMLLAT IRSATLTLXR LAMLNRVSPS TTRWMLAWSG EVSASPSAAL
51  ATRVSKRARR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFGGMTCA SVAVWVSDGM AVCFSV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2065>:

m643.seq

```

1   ATGGTGTTC CTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCTTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTTCGG CTTCCGCCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAGCGGT
201 ATGTTGCGGA GATGCGGAAA TTTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC GGAGATGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAT
351 GATCTGCGCG AGTGTTCGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2066; ORF 643>:

m643.pep

```

1   MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAAAVCCG DAEILCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGMICA SVAVWVSDGM AVCFSV*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*.

ORF 643 shows 94.9% identity over a 136 aa overlap with a predicted ORF (ORF643.a) from *N. gonorrhoeae*:

m643/g643

```

                                10      20      30      40      50      60
m643.pep  MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAALATRVSKRTRR
          |||
g643       MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEVSASPSAALATRVSKRARR
          |||
                                10      20      30      40      50      60
m643.pep  LPSAAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA
          |||
g643       LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFGGMTCA
          |||
                                70      80      90      100     110     120
m643.pep  SVAVWVSDGMVAVCFVSX
          |||
g643       SVAVWVSDGMVAVCFVSX
          |||
                                130
m643.pep  SVAVWVSDGMVAVCFVSX
          |||
g643       SVAVWVSDGMVAVCFVSX
          |||
                                130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2067>:

1022

```

a643.seq
1  ATGGTGTTC CTTTGATGTT GTTGGCGACA ATCAGGTCGG CTACACTGAC
51  GTTGTAGCGT TTGGCAATGT TGAACAGGGT GTCGCCCTCT ACAACGCGGT
101 GGATGCTGGC ATGGAGCGGG GAGATTTCGG CTTCCGCGTC GGCAGCTTTG
151 GCTACGCGCG TTTCCAAACG TACCCGGCGT TTGCCGTCGG CGGCAACGGT
201 ATGTTGCGGA GATGAGGAAA TGTGTGTTC GGCAACTGTG TCAGGCGTGC
251 CGATGACGGC AGAGATGGTT TCTTCAGCCT GTCGGCGCAG GTTGTTCGG
301 GCAACAAGCT GCATGAGTTC GTCTGCCGCC TGCATGTCGT TTTGGGGGAC
351 GATCTGCGCG AGTGTTCGGG TTTGGGTTTC AGACGGCATG GCGGTCTGTT
401 TTTCGGTTTG A

```

This corresponds to the amino acid sequence <SEQ ID 2068; ORF 643.a>:

```

a643.pep
1  MVLPLMLLAT IRSATLTL*R LAMLNRVSPS TTRWMLAWSG EISASPSAAL
51  ATRVSKRTRR LPSAATVCCG DEEMLCSATV SGVPMTAEMV SSACRRRLFR
101 ATSCMSSSAA CMSFWGTICA SVAVWVSDGM AVCFVS*

```

m643/a643 97.1% identity in 136 aa overlap

	10	20	30	40	50	60
m643.pep	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
a643	MVLPLMLLATIRSATLTLXRLAMLNRVSPSTTRWMLAWSGEISASPSAAL	ATRVSKRTRR				
	70	80	90	100	110	120
m643.pep	LPSAAVCCGDAEILCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGMICA					
a643	LPSAATVCCGDEEMLCSATVSGVPMTAEMVSSACRRRLFRATSCMSSSAACMSFWGTICA					
	130					
m643.pep	SVAVWVSDGMVCFVSX					
a643	SVAVWVSDGMVCFVSX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2069>:

```

g644.seq
1  ATGCCGTCTG AAAGGccgGC GGATTGTTGC CCGGTGCACT TTGTGGTAAA
51  GTTTAGAAAA TTAACCTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CCATGGACAC GGCTGCTTTT TTAAagcaca tcgaatCCGC
201 ATTCCCCCGC ATTTTTTCAG ACGGCATCGA CCTGATGCGA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTGCTGT GCCCTTCCTC
301 GACAAAAAAC ACGGCGGGCG CAAGGGCAGT CAGTTTGAAA TCCAAGAAGT
351 CCTAAGGATT GCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA
401 TCGAAGGCGC GCTGTGTGTT CAGCCTCTGC AAGagttcgg cggcgaagcG
451 CAAGTCGCAC AAGGTTTGA CATGATTTTC AAagggcgaaa gccgcccgtt
501 gggcgTtacc gaacccgaAa cctccggcgc gGcgATTGCA CGCGAAAtgc
551 agtcctgcta cgaatatacc gacgaacAAA CCATTACGT caaCGCCGCG
601 AAATACTGGC AGGCAATTC GCAAAGCGAC TTCCTcctcg ttgccgccaa
651 agagcgcaaaa aacGGcaaac tcgccaaagt CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCCTCG CATCCGAAGG CCTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAACATC TCCCGGGGCG ACGCTGCCGG TTTGCGCGCG TTCCAAAACA
851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACATCC TTGACAACCT GAACCGATAT GTCCGCAACG ATATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCAACG CCGCATCAG GTTTCGAAA
1001 TCCTTTACCG CTACGCTGTC CATTCGTTT CGcccgctgc GCccgTCGCC
1051 CATCAATTGA TGGAGGCGAA catcgTCAAA ACcctCGCCA CGGAATACAC
1101 TTAcgCGGCC GCGCAATGT TGCAAAAACCT CTTGGGCGCG AAGGGTTTGT
1151 AACGCGGACA CCCAGCCGGC AATATCGCCA TCGATATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 CGTCCGCGCC ACCGCCGAAG AAAAAGAAGC AGGCATTAAG TTGGACAAAA
1301 accaaaCCCT Gctcgacgcc gtgCAAaccg atGTCcgctt tgCCGCCGTT
1351 GCCcgGact ACGCTTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCCTGACC GACGCTGCG CCCTGCAAAA AGTCTTCATC GGCAAAATCA

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1023

1451 TCGCCCGACT TTTTGTCTTC GTACAGGAGG AACACGAAGA CACCACAGCC  
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG  
 1551 ATAG

This corresponds to the amino acid sequence <SEQ ID 2070; ORF 644.ng>:

g644.pep

1 MPSEPADCC PVHFVVKFRK LTLNCGRRFD RPPINGNRQR KPMIHTEPSA  
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL  
 101 DKKHGGRKGS QFEIQEVLRI AGHYGVVPTL RTGIEGALVL QPLQEFGEA  
 151 QVAQGLDMIF KGESRRLGVT EPETSGAIIA REMQSYEYT DEQTIYVNAA  
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA  
 251 VRYAVNRIDA EMPATAVMKL SRGDAAGLRA FQNIIFIRSRL QLIGMTHGIM  
 301 EYILDNLNRY VRNDIRFVDY ERREIQRHQ VSEILYRYVC HSVSPVAPVA  
 351 HOLMEANIVK TLAETTYAA AQMLQKLLGA KGFERGHFAG NIAIDIRPFT  
 401 IFEGPNMMLY AEIYDQFVRA TAEKEAGIK LDKNQTL LDA VQTDVRFRAV  
 451 ARDYALPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VQEEHEDTTA  
 501 FLLNDIRKDI LDCRYCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2071>:

m644.seq

1 ATGCCGCTCTG AAAGGTCGGC GGATTGTTGC CCGGCCGCACT TTGTGGTAAA  
 51 GTTTAGAAAA TCAACTCTAA ACTGTGGCAG CGGTTTGAC CGGCCGCCGA  
 101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCCGC  
 151 CAGCCGTCAG CTATGGACAC GGCTGCTTTT TTAAGCACA TCGAATCCGC  
 201 ATTCGCGCGC ATTTTTCAG ACGGTATCGA CCTGATGCGA TACCTGCCCG  
 251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC  
 301 GACAAAAAT ACGGCGGGCG CAAGGCGAGC CAGTTTGAAA TCCAAGAAAT  
 351 CcTGGCGATT CCGGGGCATT ACGGCGTGCC CGTTACGCTG CGTACCGGCA  
 401 TCGAAGCGCG GCTGGTGTG CAGCCACTGC AAGAGTTCCG CGATGAAGCG  
 451 CAAGTCGCGC AAGGTTTGA GATGATTTTC AAAGGCGAGG CCGCGGGTTT  
 501 GGGTGTTACC GAACCCGAAA CCTCCGGCGC GCGGATTGCA CGCGAAATGC  
 551 AGTCCTACTA CGAATATATC GACGGACAAA CCATTTACGT CAACGCCGCG  
 601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCCTCCTCG TTGCCGCCAA  
 651 AGAGCGCAAA AACGGCAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC  
 701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAG CTTCGCCGCC  
 751 GTCCGTTAGC CCGTCAACCG CATCGATGCC GAAATGCGTG CAACCGCCGT  
 801 GATGAACTC TCCAGAGCG ACGCTGCCGG TTTGCCGCGC TTCCAAAACA  
 851 TCTTTATCCG CAGCCGCCCTG CAACTGATCG GCATGACGCA CGGCATTATG  
 901 GAATACATCC TTGAAAATCT GGAACGATAC GTCCGCAACG ACATCAAATT  
 951 CGTCGATTAC GAACGCCGCG AAATCCGCGC CCGCCATCAG GTTCCGAGA  
 1001 TTCTTTACCG CTACGCTGCG CATTCGTTT CGCCTGTTGC CCCCGTCGCC  
 1051 CATCAGCTGA TGGAGGCGAA CATCGTCAA ACCCTCGCCA CGGAATACAC  
 1101 TTACGCCGCC GCGCAATGT TGCAAAACT CTGGGTGCG AAGGGTTTG  
 1151 AACGCCGACA CACCGCCGCG AATATCGCTA TCGACATCCG CCCCTTCACG  
 1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATT ACGACAGTT  
 1251 TGTCGCCGCC ACCGCCGAG AAAAAGAAG AGGCATGAAG TTGGACAAA  
 1301 ACCAAACCTT GCTCGACCGC CTGCAACCG ATGCCCGCTT TGCCGCCGTC  
 1351 GCCCGCGACT ACATTTGACC TGAAGACATC CGCAGCTTCC TGCAGGAACA  
 1401 CACCTGACC GATGCCTGCG CCTGCAAAA AGTCTTTATC GGCAAAATCA  
 1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGA AACACGAAGA CACCGCAGCC  
 1501 TTCCTGCTGA ACGACATCCG CAAAGATATA TTGGACTGCC GATATTGCGG  
 1551 GTAG

This corresponds to the amino acid sequence <SEQ ID 2072; ORF 644>:

m644.pep

1 MPSEPADCC PAHFVVKFRK STLNCGRRFD RPPINGNRQR KPMIHTEPSA  
 51 QPSTMDTAAF LKHIESAFRR IFSDGIDLMR YLPEDKWLAL KQAGLLLPFL  
 101 DKKHGGRKGS QFEIQEVLRI AGHYGVVPTL RTGIEGALVL QPLQEFGEA  
 151 QVAQGLEMIF KEGGGLGVT EPETSGAIIA REMQSYEYI DGQTIYVNAA  
 201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA  
 251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSRL QLIGMTHGIM  
 301 EYILENLERY VRNDIKFVDY ERREIRRHQ VSEILYRYVC HSVSPVAPVA  
 351 HOLMEANIVK TLAETTYAA AQMLQKLLGA KGFERGHFAG NIAIDIRPFT  
 401 IFEGPNMMLY AEIYDQFVRA TAEKEAGMK LDKNQTLDR LQTDARFAAV  
 451 ARDYTLPEDI RSFLQEHILT DACALQKVFI GKIIARLFVF VOAKHEDTAA  
 501 FLLNDIRKDI LDCRYCG\*

m644/g644 94.6% identity in 517 aa overlap

	10	20	30	40	50	60
m644.pep	MPSEPADCCPAHFVVKFRKSTLNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					
g644	MPSEPADCCPVHFVVKFRKLTNCGRRFDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF					



1024

	10	20	30	40	50	60
m644.pep	70	80	90	100	110	120
g644	LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLPFLDKKYGGRKGSQFEIQEVLRI					
	70	80	90	100	110	120
m644.pep	130	140	150	160	170	180
g644	AGHYGVPVTLRTGIEGALVLQPLQEFGEAQVAQGLEMI FKEGGGGLGVTEPETSGAAIA					
	130	140	150	160	170	180
m644.pep	190	200	210	220	230	240
g644	REMQSYEYIDGQTIYVNAAKYWQNSQSDFLVAAKERKNGKLAKVIDLLVPKTYIRC					
	190	200	210	220	230	240
m644.pep	250	260	270	280	290	300
g644	ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNI FIRSRLQLIGMTHGIM					
	250	260	270	280	290	300
m644.pep	310	320	330	340	350	360
g644	EYILENLERYVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLM EANIVK					
	310	320	330	340	350	360
m644.pep	370	380	390	400	410	420
g644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
m644.pep	430	440	450	460	470	480
g644	TAEKEAGMKLDKNQTL DRLQTDARFAAVARDYTL PEDIRSFLOEHTLT DACALQKVFI					
	430	440	450	460	470	480
m644.pep	490	500	510			
g644	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2073>:

```

a644.seq
1  ATGCCGCTCG AAAGGTCGGC GGATTGTTGC CCGGCGCACT TTGTGGTAAA
51  GTTTAGAAAA TCAACTCTAA ACTGTGGCAG GCGGTTTGAC CGGCCGCCGA
101 TTAATGGGAA CCGACAGAGG AAGCCGATGA TACACACCGA ACCGAGCGCG
151 CAGCCGTCAA CTATGGACAC GGCTGCTTTT TTAAAGCACA TCGAATCCGC
201 ATTCCGCCGC ATTTTTCAG ACGGTATCGA CCTGATCGCA TACCTGCCCG
251 AAGACAAATG GCTTGCCTTG AAGCAGGCGG GTTGTCTGTT GCCCTTCCTC
301 GACAAAAAAT ACGGCGGGCG CAAGGCAGC CAGTTTGAAA TTCAGGAAGT
351 CTTGCGGATT GCGGGGCATT ACGGCGTGCC CGTTANNNNN NNNNNNNNNN
401 NNGAAGGCGC GCTGGTGTG CAGCCACTGC AAGAGTTCGG CGATGAAGCG
451 CAAATCGCAC AGGTTTGGGA CATGGTTTTC AAAGGCGAGG GCGCGGGTTT
501 AGGCGTTACC GAACCCGAAA CCTCCGGCGC GGCGATTGCC CGAGAAATGC
551 AGTCTTACTA CGAATATACC GACGGACAAA CCATTACGT CAACGCCCGC
601 AAATACTGGC AGGGCAACTC GCAAAGCGAC TTCTCCTCG TTGCCGCCAA
651 AGAGCGCAAA AACGGCAAAC TCGCCAAAGT CATCGACCTG CTGCTCGTCC
701 CCAAAACATA CATCCGCTGC GAAACCTCG CATCCGAAGG CTTGCGCGCC
751 GTCCGTTACG CCGTCAACCG CATCGATGCC GAAATGCCTG CAACCGCCGT
801 GATGAAACTC TCCAGAGCG ACGTGCCCGG TTTGCGCGCG TTCCAAAACA

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1025

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851 TCTTTATCCG CAGCCGCTG CAACTGATCG GCATGACGCA CGGCATTATG
901 GAATACACCC TTGAAAACCT GGAACGATAC GTCCGCAACG ACATCAGATT
951 CGTCGATTAC GAACGCCGCG AAATCCGGCG CCGCCATCAG GTTTCGAGA
1001 TTCTTTACCG CTACGTCTGC CATTCCGTTT CGCCCGTTGC ACCCGTCGCC
1051 CATCAACTGA TGGAGGCGAA CATCGTCAAA ACCCTCGCCA CGGAATACAC
1101 TTACGCCGCC GCGCAAATGT TGCAAAAACT CTTGGGCGCG AAGGGTTTTG
1151 AACGCGGACA CACCGCCGGC AATATCGCTA TCGACATCCG CCCCTTCACG
1201 ATTTTGAAG GCCCGAACGA TATGCTTTAT GCCGAAATTT ACGACCAGTT
1251 TGTCCGCGCC ACCGCCGAAG AAAAAAGAAG AGGCATGAAG TTGGACAAAA
1301 ACCAAACCCT GCTCGACCGC CTGCAAAACG ATGCCCGCTT TGCCGCCGTC
1351 GCCCGCGACT ACACCTTGCC CGAAGACATC CGCAGCTTCC TGCAGGAACA
1401 CACCTTGACC GATGCCTGCG CCCTGCAAAA AGTCTTTATC GGCAAAATCA
1451 TCGCCCGACT CTTTGTCTTC GTACAGGCGG AACACGAAGA CACCGCAGCC
1501 TTCCTGCTGA ACGACATCCG CAAAGACATA TTGGACTGCC GATATTGCGG
1551 ATAG

```

This corresponds to the amino acid sequence <SEQ ID 2074; ORF 644.a>:

```

a644 .pep
1  MPSERSADCC PAHFVVKFRK STLNCGRFRD RPPINGNRQR KPMIHTEPSA
51  QPSTMDTAAF LKHIESAFRR IFADGIDLMR YLPEDKWLAL KQAGLLLPFL
101 DKKYGGRKGS QFEIQEVLRI AGHYGVPVXX XXXXEGALVL QPLQEFGDEA
151 QIAQGLDMVF KEGGGGLGVT EPETSGAAIA REMQSYEYTD DGQTIYVNAA
201 KYWQNSQSD FLLVAAKERK NGKLAKVIDL LLVPKTYIRC ETLASEGLRA
251 VRYAVNRIDA EMPATAVMKL SQSDAAGLRA FQNIIFIRSR LQLIGMTHGIM
301 EYTLENLERY VRNDIRFVDY ERREIRRRHQ VSEILYRYVC HSVSPVAPVA
351 HQLMEANIVK TLATEYTYAA AQMLQKLLGA KGFERGHTAG NIAIDIRPFT
401 IFEGPNDMLY AEIYDQFVRA TAEKEAGMK LDKNQTLLDR LQTDARFAAV
451 ARDYTELPEDI RSFLQEHTLT DACALQKVFI GKIIARLFVF VQAEHEDTAA
501 FLLNDIRKDI LDCRYCG*

```

m644 /a644 97.3% identity in 517 aa overlap

```

m644 .pep      10      20      30      40      50      60
MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF
|||||
a644           10      20      30      40      50      60
MPERSADCCPAHFVVKFRKSTLNCGRFRDRPPINGNRQRKPMIHTEPSAQPSTMDTAAF

m644 .pep      70      80      90     100     110     120
LKHIESAFRRIFSDGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI
|||||:|||||
a644           70      80      90     100     110     120
LKHIESAFRRIFADGIDLMRYLPEDKWLALKQAGLLLPFLDKKYGGRKGSQFEIQEVLRI

m644 .pep     130     140     150     160     170     180
AGHYGVPVTLRTGIEGALVLQPLQEFGDEAQVAQGLEMIFKGGGGGLGVTEPETSGAAIA
|||||: : |||||||:|||||:|||||:|||||
a644          130     140     150     160     170     180
AGHYGVPVXXXXXEGALVLQPLQEFGDEAQIAQGLDMVFKEGGGGGLGVTEPETSGAAIA

m644 .pep     190     200     210     220     230     240
REMQSYEYIDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC
|||||:|||||:|||||:|||||:|||||
a644          190     200     210     220     230     240
REMQSYEYTDGQTIYVNAAKYWQNSQSDFLLVAAKERKNGKLAKVIDLLVPKTYIRC

m644 .pep     250     260     270     280     290     300
ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSR LQLIGMTHGIM
|||||:|||||:|||||:|||||:|||||
a644          250     260     270     280     290     300
ETLASEGLRAVRYAVNRIDAEMPATAVMKLSQSDAAGLRAFQNIIFIRSR LQLIGMTHGIM

m644 .pep     310     320     330     340     350     360
EYILENLERIVRNDIKFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK
|| |||||:|||||:|||||:|||||:|||||
a644          310     320     330     340     350     360
EYTLENLERYVRNDIRFVDYERREIRRRHQVSEILYRYVCHSVSPVAPVAHQLMEANIVK

```

1026

	310	320	330	340	350	360
	370	380	390	400	410	420
m644 . pep	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
a 644	TLATEYTYAAAQMLQKLLGAKGFERGHTAGNIAIDIRPFTIFEGPNDMLYAEIYDQFVRA					
	370	380	390	400	410	420
	430	440	450	460	470	480
m644 . pep	TAEKEAGMKLDKNQTLDRLOTARFAAVARDYTLPEDIRSFLQEHITLDACALQKVFI					
a 644	TAEKEAGMKLDKNQTLDRLOTARFAAVARDYTLPEDIRSFLQEHITLDACALQKVFI					
	430	440	450	460	470	480
	490	500	510			
m644 . pep	GKIIARLFVVFQAKHEDTAAFLNDIRKDILDCRYCGX					
a 644	GKIIARLFVVFQAEHEDTAAFLNDIRKDILDCRYCGX					
	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2075>:

g645.seq

```

1  ATGATGATGG TGTGGCGTT GGGGATGTCG ATGCCGTTT CGATGATGGT
51  GGAACAGAGC AACACATGTA ATCTTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCACGC AGTTGTCCGT GCGCCACGCC GATACGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTCTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAata cCTGTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTCACG
301 GCGAGGCGGC GGCTCGGTGC AGTGGTAATC AGCGAGAAGT CGCGCAGACC
351 TTCGAGCGCC ATGCTGAGGG TGCGCGGAAT CGGCGTGGCG GTCATGGTTA
401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGTCGCACG
451 CCGAAGCGGT GTTCTTCATC GATAATCAAT AAACCTAAGT TTTGAATTT
501 TATGTCGTCC TGCACCAATT TGTGCGTACC GATAACGATA TCGACAGTAC
551 CGTCCGCCAT GCCTTCGAGC GTGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAGAAGCGT GGTGCGGGCG AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGAAG GGCAGCTTCG
751 GTTTTGCCGA AACCGACATC GCCGCACACA AGTCGGTCCA TCGGCTTCGC
801 CTGCGTCAAA TCTTTAATCA CGGcggcgat ggcggcggc TGGTCTTCGG
851 TTTCTCTCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 2076; ORF 645.ng>:

g645.pep

```

1  MMVVLALGMS MPVSMMEQES NTLNLCKKKS RMTCSSRSR SCPCATPIRA
51  SGRSVSSRSR IFSIVSTSLC RKNTPPRLS SRNTASRLP SLNGLTKVET
101 ARRLGAVVI SEKSRPSSA MLRVRGIVA VMVRMTLAR RRLSCSFCRT
151 PKRCSIIIN KPKFLNFMSS CTNLCVPITI STVPSAMPSS VALVALLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVVGA STATCLPPIT ATNAARRATS
251 VLFKPTSPHT SRSIGFACVK SLITAAMAAA WSSVSS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2077>:

m645.seq

```

1  ATGATGATGG TGTGGCGTT GGGGATATCG ATACCGGTTT CGATGATGGT
51  GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAAGTCG CGCATGACTT
101 GTTCCAGCTC GCGCTCGCGC AGTTGTCCGT GCGCCACGCC GATGCGGGCT
151 TCGGGCAGCA GGGTTTCCAG CCGCTCGCGC ATATTTTCAA TCGTATCTAC
201 TTCATTGTGC AGGAAAAATA CCGTCTCTCC GCGTTTGAGT TCGCGCAACA
251 CCGCTTCGCG CACGCTGCCT TCGCTAAAGG GTTTGACAAA GGTTCACG
301 GCGAGGCGGC GGCTGGGCGC GGTGGTAATC AGCGAGAAGT CGCGCAGTCC
351 TTCCAACGCC ATACTTAAAG TACGCGGAAT CGGCGTGGCG GTCATGGTAA
401 GGATATCAAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTT CTGACGCACG
451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTAAGT TTTGAATTT
501 GATGTCGTCC TGCACCAATT TGTGCGTACC GATAACAATA TCGACCGTGC
551 CGTCTGCCAT GCCTTCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA
601 CGCGAAAGGC TGGCGACTTT CACGGGGAAA TCGGCGAAAC GGTGCGCGAA
651 GTTTTGCGCG TGCTGCTCGA CCAAAAGCGT GGTGCGGAGCA AGTACGGCGA
701 CCTGTTTGCC GCCCATCACC GCCACAAACG CGGCGCGCAG GGCAGCTTCG
751 GTTTTGCCGA AGCCGACATC GCCGCACACA AGGCGATCCA TCGGCTTCGC
801 TTGCGTCAAA TCTTTAATCA CGGCGGGGAT GCGGCGGGCC TGGTCTTCGG

```

851 TTTCTCGTA G

This corresponds to the amino acid sequence &lt;SEQ ID 2078; ORF 645&gt;:

m645.pep  
 1 MMMVLALGIS IPVSMVVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA  
 51 SGSRVSSRSR IFSIVSTSLC RKNTCPPLRS SRNTASRTLP SLKGLTKVLT  
 101 ARRRLGAVVI SEKSRSPSNA ILKVRGIGVA VMVRISTLAR RRLSCSF\*RT  
 151 PKRCSSSIIT KPKFLNLMSS CTSLCVPITI STVPSAMPSS AALVALLLLK  
 201 RERLATFTGK SAKRSKFCF CCSTKSVVGA STATCLPPIT ATNAARRATS  
 251 VLPKPTSPHT RRSIGFACVK SLITAAMAAA WSSVSS\*

m645/g645 93.7% identity in 286 aa overlap

	10	20	30	40	50	60
m645.pep	MMMVLALGISIPVSMVVEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGSRVSSRSR	
g645	MMMVLALGMSMPVSMVVEQSN	TLNRCCKKS	RMTCSSSRSR	SCPCATPMRA	SGSRVSSRSR	
	70	80	90	100	110	120
m645.pep	IFSIVSTSLCRKNTCPPLRSS	RNTASRTLP	SLKGLTKVLT	TARRRLGAVV	ISEKSRSPSNA	
g645	IFSIVSTSLCRKNTCPPLRSS	RNTASRTLP	SLKGLTKVLT	TARRRLGAVV	ISEKSRSPSNA	
	130	140	150	160	170	180
m645.pep	ILKVRGIGVAVMVRISTLAR	RRLSCSF	XRTPKRCSSSIIT	KPKFLNLMSS	CTSLCVPITI	
g645	MLRVRGIGVAVMVRISTLAR	RRLSCSF	XRTPKRCSSSIIT	KPKFLNLMSS	CTSLCVPITI	
	190	200	210	220	230	240
m645.pep	STVPSAMPSSAALVALLLL	KRERLATFT	GKSAKRSKFC	ACCSTKSVVGA	STATCLPPIT	
g645	STVPSAMPSSAALVALLLL	KRERLATFT	GKSAKRSKFC	ACCSTKSVVGA	STATCLPPIT	
	250	260	270	280		
m645.pep	ATNAARRATSVLPKPTSPHT	RRSIGFACVK	SLITAAMAAA	WSSVSSX		
g645	ATNAARRATSVLPKPTSPHT	RRSIGFACVK	SLITAAMAAA	WSSVSSX		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2079>:

a645.seq  
 1 ATGATGATGG TGTGGCGTT GGAATGTCG ATACCGGTTT CGATGATGGT  
 51 GGAACAGAGC AACACGTTAA ATCGTTGCTG CAAAAGTCG CGCATGACTT  
 101 GTTCCAGCTC GCGCTCGGCG AGTTGTCCGT GCGCCACGCC GATGCGGGCT  
 151 TCGGGCAGCA GGGTTTCCAG CCGCTCACGC ATGTTTTCGA TGGTATCCAC  
 201 TTCATTGTGC AGGAAAAATA CTTGCCCGCC GCGTTTGAGT TCGCGCAATA  
 251 CGGCTTCGCG CACGCTGCCT TCGCTGAACG GTTTGACAAA GGTTTTGACG  
 301 GCGAGGCGGC GGCTGGGCGC AGTGGTAATC AGCGAGAAGT CGCGCAGTCC  
 351 TTCCAGCGCC ATACTTAAAG TACGCGGAAT CGGCGTAGCG GTCATGGTAA  
 401 GGATGTCGAC ATTGGCGCGC AGGCGTTTGA GCTGCTCTTT CTGACGCACG  
 451 CCGAAGCGGT GTTCTTCGTC GATAATCACT AAACCTACGT TTTTGAATTT  
 501 TATGTCGTCC TGCACCAAGT TGTGCGTACC GATAACAATA TCGACCGTGC  
 551 CGTCCGCCAT GCCTTCCAGC GCGGCTTTGG TGGCTTTGCT GTTGTGAAA  
 601 CGCGAAAGGC TGGCGACTTT CACGGGAAA TCGGCGAAGC GGTCCGCAAA  
 651 ATTTTGC GCG TGTGCTCGA CCAGAAGCGT GGTGGTGGC AGTACGGCAA  
 701 CTTGTTTGCC ACCCATTACC GCCACAAACG CGGCGCGCAG GGCGACTTCG  
 751 GTTTTGCCGA AACCGACATC GCCGCACACG AGGCGGTCCA TCGGCTTCGC  
 801 CTGCGTCAA TCTTTAATCA CGGCGGCGAT GGCGGCTGCC TGGTCTTCGG  
 851 TTTCTTCGTA G

This corresponds to the amino acid sequence &lt;SEQ ID 2080; ORF 645.a&gt;:

a645.pep  
 1 MMMVLALGMS IPVSMVVEQS NTLNRCCKKS RMTCSSSRSR SCPCATPMRA

1028

```

51  SGRVSSRSR MFSMVSTSLC RKNTCPPLRS SRNTASRTLPSLNGLTQVLT
101 ARRRLGAVVI SEKSRSPSSA ILKVRGIGVA VMVRMSTLAR RRLSCSF*RT
151 PKRCSSSIIT KPTFLNFMSS CTSLCVPITI STVPSAMPSS AALVALLLK
201 RERLATFTGK SAKRSKFCA CCSTRSVGA STATCLPPIT ATNAARRATS
251 VLPKTPSPHT RRSIGFACVK SLITAAMAAA WSSVSS*

```

m645/a645 96.9% identity in 286 aa overlap

```

          10      20      30      40      50      60
m645.pep  MMMVLALGISIPVSMVQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
          |||||:|||||
a645      MMMVLALGMSIPVSMVQSNLTNRCKKSRMTCSSSRSRSCPCATPMRASGSRVSSRSR
          10      20      30      40      50      60

          70      80      90     100     110     120
m645.pep  IFSIVSTSLCRKNTCPRLSSRNATSLPSLKGLTKVLTARRRLGAVVISEKSRSPSNA
          :||:|||||:|||||:|||||:|||||:|||||:|||||
a645      MFSMVSTSLCRKNTCPRLSSRNATSLPSLNGLTQVLTARRRLGAVVISEKSRSPSSA
          70      80      90     100     110     120

          130     140     150     160     170     180
m645.pep  ILKVRGIGVAVMRISTLARRLSCSFXRTPKRCSSSIITKPKFLNLMSSCTSLCVPITI
          |||||:|||||:|||||:|||||:|||||:|||||
a645      ILKVRGIGVAVMRMSTLARRLSCSFXRTPKRCSSSIITKPTFLNFMSSCTSLCVPITI
          130     140     150     160     170     180

          190     200     210     220     230     240
m645.pep  STVPSAMPSSAALVALLLKRRERLATFTGKSAKRSKFACCCSTKSVVGASTATCLPPIT
          |||||:|||||:|||||:|||||:|||||:|||||
a645      STVPSAMPSSAALVALLLKRRERLATFTGKSAKRSKFACCCSTRSVVGASTATCLPPIT
          190     200     210     220     230     240

          250     260     270     280
m645.pep  ATNAARRATSVLPKTPSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          |||||:|||||:|||||:|||||
a645      ATNAARRATSVLPKTPSPHTRRSIGFACVKSLITAAMAAWSSVSSX
          250     260     270     280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2081>:

```

g647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAGGTGTCGA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCT
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAGTAGGCGT AGTTGATGAC ACCGATGCCG
251 AGCGAACGGC GGTCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2082; ORF 647.ng&gt;:

```

g647.pep
1  MQRLAADGIQ IFFVGVGQF ALRINGLVKE RARSVFFGKV CRCFEQVILY
51  GFKGTVGQTE RGTAVADTV FRQIVGVDD TDAERTAVHS RGRGTFYRIS
101 LII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2083>:

```

m647.seq
1  ATGCAAAGGC TCGCCGCAGA CGGCATCCAA ATCTTTTTTG TAAGTGTGCA
51  TGGGCAGTTT GCCTTGCGAA TAAACGGTTT GGTAAAGAG CGTGACGCA
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAACCG TCGCTGTAGC
201 GGACACCGTT TTTCGCCAGA TAATAAGCAT AGTTAATCAC GCCGATGCCG
251 AGCGAACGGC GGCCCATAGT AGAGGTACGC GCGGCTTCTA CCGGATATCC
301 CTGATAATCT AA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2084; ORF 647&gt;:

```

m647.pep
1  MQRLAADGIQ IFFVSDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY

```

1029

51 GFKGTVGQTE RGTAVADTV FRQIISIVNH ADAERTAHS RGRGFYRIS  
101 LII\*

m647/g647 91.3% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	:     :     :     :     :     :					
g647	MQRLAADGIQIFFVSDGQFALRINGLVKERARSVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	:     :     :     :     :     :					
g647	RGTAVADTVFRQIVGVDDTDAERTAVHSRGRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2085>:

a647.seq  
1 GTGCAAAGGC TCGTTACACA CAGCGTCCAA GTCTTTTGTG TAGGTGTCGA  
51 TGGGCAGTTT GCCTTGGCAA TAAACGGTTT GGTAAAGAG CGTGCACGCA  
101 CCGTATTCTT TGGCAAGGTT TGCCGATGCT TTGAGCAGGT AATACTGTAT  
151 GGCTTCAAAG GTACGGTGGG TCAGACCGAG CGCGGAGCCG TCGCTGTAGC  
201 GGACACCGTT TTTGCCAAA TAATACGCAT AGTTGATCAC GCCGATACCG  
251 AGCGAACGGC GGCCCATAGT GGAGGTACGC GCGGCTCTA CCGGATATCC  
301 CTGATAATCT AA

This corresponds to the amino acid sequence <SEQ ID 2086; ORF 647.a>:

a647.pep  
1 VQRLVTHSVQ VFFVGVDGQF ALRINGLVKE RARTVFFGKV CRCFEQVILY  
51 GFKGTVGQTE RGAVAVADTV FRQIIRIVDH ADTERTAHS GGTRGFYRIS  
101 LII\*

m647/a647 87.4% identity in 103 aa overlap

	10	20	30	40	50	60
m647.pep	MQRLAADGIQIFFVSDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	:    : :   :     :     :     :     :					
a647	VQRLVTHSVQVFFVGVDGQFALRINGLVKERARTVFFGKVCRCFEQVILYGFKGTVGQTE					
	10	20	30	40	50	60
	70	80	90	100		
m647.pep	RGTAVADTVFRQIISIVNHADAERTAHSRGRGFYRISLIIX					
	:     :     :     :     :     :					
a647	RGAVAVADTVFRQIIRIVDHADTERTAHSGGTRGFYRISLIIX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2087>:

g648.seq  
1 ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT  
51 CGACGTTTTG AATGTAGATG CGCCCGGTCC CGGCACGCTC CTGCATCAGC  
101 GTGGAAAACA GGTCCGCAGC CGGAATGATA CGCTTGCCTA TGTTCGGGTC  
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGTCTTGG TCGGCAAAAA  
201 ACGCTTCGTA CAACCCCGAA ACCTCGTTGG GCGAAAACAG CGTAATGTTG  
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATTT GCACGCCATA  
301 ATCAAGCTGG CGGATACGGT TGTCTTCCAC GCCCGGTTG TTTTCAACA  
351 CCAGCAGGCT TTCGGCTTCA ATATGCCACA AGGGGTAGAA CAAGGTTGCC  
401 GCGCCGCGCG GCACGCCACC TTGCGAACAA GATTGACCG CCGCCTGAAA  
451 CATCTTAAAG AAGGGAATGC AGCCGGTATG CCGGGCTTCA CCGCCCGGA  
501 TTTCCTGTC CAGCCGCGG ATACGTCCGG CATTGATGCC GATGCCCGCG  
551 CGTTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC  
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2088; ORF 648.ng>:

g648.pep

1030

```

1   MNRRNARIER AVRIAVIDVL NVDAPGPGTL LHQRGKQVGS RNDTLAYVRV
51  LLVFRIEPLK FVLVGKKRFV QPRNLVGRKQ RNVAAALNQAG VQQAVIDLHAI
101 IKLADTVVFH APVVFQHQQA FGFNMPQGV FGCRAAAHAT LRTFRDRLK
151 HLKEGNAAGM PGFTAPDFAV QPADTSGIDA DARALGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2089>:

```

m648.seq
1   ATGAACAGGC GCGACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTCCAC ACCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCGCC TTGCGAACAG GATTGACCG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGCGCTTCG CCGCCCGGA
501 TTTCGCTGTC CAAACCGCGG ATACGTCGGG CATTGATGCC GATGCCGCA
551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCAT TGATGGAATC
601 CAAACTATCG TCGCATTCAA TCAGCACACA GCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2090; ORF 648>:

```

m648.pep
1   MNRRDARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV
51  LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAAALNQAG VQQAVIDLHAI
101 IKLTDTVVFH TAVVFQHQQA FGFDMPPQGV FGCRAAAHAA LRTGFDRRLK
151 HFKEGNAAGM PRFAAPDFAV QTADTSGIDA DARTLGNVFH NRAGSGIDGI
201 QTIVAFNQHT A*

```

m648/g648 91.5% identity in 211 aa overlap

	10	20	30	40	50	60
m648.pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGSRNDALADIRVLLVFRIEPLK					
	:     :     :     :     :     :     :     :     :     :					
g648	MNRRNARIERAVRIAVIDVLNVDAPGPGTLLHQRGKQVGSRNDTLAYVRVLLVFRIEPLK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m648.pep	FVLVGKKRFVQSRNLVGRKQNRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
	:     :     :     :     :     :     :     :     :					
g648	FVLVGKKRFVQPRNLVGRKQNRNVAALNQAGVQQAVIDLHAIKLTADTVVFHAPVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648.pep	FGFDMPPQGVQGCRAAAHAALRTGFDRRLKHFKEGNAAGMPRFAAPDFAVQTADTSGIDA					
	:     :     :     :     :     :     :     :     :					
g648	FGFNMPQGVQGCRAAAHATLRTFRDRLKHLKEGNAAGMPGFTAPDFAVQPADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648.pep	DARTLGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	:     :     :     :     :     :     :     :					
g648	DARALGNVFHNRAGSGIDGIQTIVAFNQHTAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2091>:

```

a648.seq
1   ATGAACAGGC GCAACGCGCG GATCGAACGG GCTGTGCGTA TTGCAGTGAT
51  CGACGTTTGG AATGTAGATG CGCCCGGTTT CGGCACGCTC CTGCATCAGC
101 GTGGAAAACA GGTCCGCAGC CGGAATGATG CGCTTGCGGA TATCAGGGTC
151 TTGCTCGTAT TTCGTATAGA GCCGCTCAAA TTCGCTTGG TCGGCAAAAA
201 ACGCTTCGTA CAATCCCGGA ACCTCGTTGG GCGAAAACAG CGTAATGTTG
251 CCGCCCTTAA TCAGGCGGGT GTACAGCAGG CGGTTGATT GCACGCCGTA
301 ATCAAGCTGA CGGATACGGT TGTCTCCAC GCCCGGTTG TTTTCAACA
351 CCAGCAGGCT TTCGGCTTCG ATATGCCACA AGGGGTAGAA CAAGGTTGCC
401 GCGCCGCCGC GCACGCCACC TTGCGAACAG GATTGACTG CCGCCTGAAA
451 CATTTTAAAG AAGGGAATGC AGCCGGTATG CCGTCTTCG CCGCCCGGA

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501 TTTCGCTGTC CAGTCCGCGG ATACGTCCGG CATTGATGCC GATGCCCCGA  
 551 CGCTGGGAAA CGTATTTCAC AATCGCGCTG GTAGTGGCGT TGATGGAATC  
 601 CAGGCTGTCTG TCGCATTCTGA TCAATACGCA GCTTGA

This corresponds to the amino acid sequence <SEQ ID 2092; ORF 648.a>:

a648 . pep  
 1 MNRRNARIER AVRIAVIDVL NVDAPGSGTL LHQRGKQVGS RNDALADIRV  
 51 LLVFRIEPLK FVLVGKKRFV QSRNLVGRKQ RNVAALNQAG VQQAVIDLHAV  
 101 IKLTDTVVFH APVVVFQHQQA FGFDMPQGV E QGCRAAAHAT LRTGFDCLRK  
 151 HFKEGNAAGM PCFAAPDFAV QSADTSGIDA DARTLGNVFH NRAGSGVDGI  
 201 QAVVAFDQYA A\*

m648/a648 93.8% identity in 211 aa overlap

	10	20	30	40	50	60
m648 . pep	MNRRDARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
a648	MNRRNARIERAVRIAVIDVLNVDAPGSGTLLHQRGKQVGS	RNDALADIRVLLVFRIEPLK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m648 . pep	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHTAVVFQHQQA					
a648	FVLVGKKRFVQSRNLVGRKQRNVAALNQAGVQQAVIDLHAVIKLTDTVVFHAPVVVFQHQQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m648 . pep	FGFDMPQGV E QGCRAAAHATLRTGFDRLKHFEKNAAGMPRFAAPDFAVQTADTSGIDA					
a648	FGFDMPQGV E QGCRAAAHATLRTGFDCLRKHFKEGNAAGMPCFAAPDFAVQSADTSGIDA					
	130	140	150	160	170	180
	190	200	210			
m648 . pep	DARTLGNVFHN RAGSGIDGIQTIVAFNQHTAX					
a648	DARTLGNVFHN RAGSGVDGIQAVVAFDQYAAAX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2093>:

g649 . seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATACTG GGA CTGGTAT CAACA ACTGC  
 51 CGTGCCCGGT ACGTCAGAAC CCGCCACCG ACATACCAA CATATCAGCA  
 101 AGGCAAAACAA GCAGATGCTG CACCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCCGGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCACCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGG  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2094; ORF 649.ng>:

g649 . pep  
 1 MLAILLSAIL GLVSTTAAAG TSEPAHRHTK HISKANKQML HPECKRYLER  
 51 RAAWYRSQGN VQELRENKKA RKAFRTL PYA EQKIQCAAAY EAFDDFDGGR  
 101 FRR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2095>:

m649 . seq  
 1 ATGCTTGCCA TACTGTTGTC TGCAATATTG GGA CTGGTAT CGACA ACTGC  
 51 CGTGCCCGGT ACGTCAGAAC CCGCCACCG CGATACCAA CATATCCGCA  
 101 AGGCAAAACAA GCAGATGCTG CACCCGAAT GCAGGAAATA TTTGGAACGC  
 151 CGTGCCCGGT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TGCGCGAAAA  
 201 CAAAAAGGCG CGCAAAGCAT TCCGCTCCCT GCCTTATGCG GAACAGAAAA  
 251 TCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCGGCAGT  
 301 TTCCGCCGTT AA

This corresponds to the amino acid sequence <SEQ ID 2096; ORF 649>:

m649 . pep



1032

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1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYA EQKIQCAAAY EAFDDFDGGS
101 FRR*

```

m649/g649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
g649           MLAILLSAILGLVSTTAAAGTSEPAHRHTKHISKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX
              |||||
g649           VQELRENKKARKAFRTLPHYAEQKIQCAAAYEAFDDFDGGRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2097>:

```

a649.seq
1  ATGCTTGCCA TACTGTGTC TGCAATATTG GGACTGGTAT CGACAACTGC
51  CGCTGCCGGT ACGTCAGAAC CCGCCCACCG CGATACCAA CATATCCGCA
101 AGGCAAACAA GCAGATGCTG CACCCCGAAT GCAGGAAATA TTTGGAACGC
151 CGTGCCCGCT GGTACCGATC GCAAGGCAAC GTGCAGGAAT TCGCGGAAAA
201 CAAAAGGCGC CGCAAAGCAT TCCGCTCCCT GCCTTATAAG GAACAGAAAA
251 CCCAATGCCG GCGGCTTAT GAGGCTTTCG ATGATTTCGA CGGCAGCAGG
301 TTCCGCCGTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2098; ORF 649.a>:

```

a649.pep
1  MLAILLSAIL GLVSTTAAAG TSEPAHRDTK HIRKANKQML HPECRKYLER
51  RAAWYRSQGN VQELRENKKA RKAFRSLPYK EQKTQCAAAY EAFDDFDGSR
101 FRR*

```

m649/a649 96.1% identity in 103 aa overlap

```

              10      20      30      40      50      60
m649.pep      MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              |||||
a649           MLAILLSAILGLVSTTAAAGTSEPAHRDTKHIRKANKQMLHPECRKYLERAAWYRSQGN
              10      20      30      40      50      60

              70      80      90      100
m649.pep      VQELRENKKARKAFRSLPYAEQKIQCAAAYEAFDDFDGGSFRRX
              |||||
a649           VQELRENKKARKAFRSLPYKEQKTQCAAAYEAFDDFDGSRFRRX
              70      80      90      100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2099>:

```

g650.seq
1  ATGTCCAAAC TCAAACCAT CGCCCTGACC GCATCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATATGCCC AAAACACCTC ATCACACCAA GTCGGTTTAG
101 CGATTATGCG GTTAACTCT TCAATACTCG ACCTGCCACC GACAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGGACGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAAGCCGAG CTATTTGAC AGGGTCGTCA ACCGGAGCCG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCCG
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACAGC
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGCTACCGG CAGGCATTAC
451 GGCTTGGAAG AAACaccgGT TTACGacggc aggcacGacy TTtacgcaGc
501 taccgatgcc gcacTCAACT AtctGcaATA TCTCTatggA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAAC TGGGTGAAGG CAACGTCGGA
601 CGCGCCGTCA ACCGCGCCCG CGACCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACC CCCCAATCTT TCGGCATGAA TATCAGCGAC

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1033

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751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGGCC GTCCGCTCGA
801 caacGAagcC ATGCGCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCTGAATCC TGCATTCAAC GTCCCCGgt tcatCCCCAA AAacaaacgc
901 aaacTGCTGC TTCCTGTCGC GTCCGTCCAA ACCTTccaaa gcaACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAGAC CCTTCATACG GCATCGGAat
1151 ccGTCGTTTC CATCGACATC GACAATACGC CcgacacCTa ccgttccaat
1201 ATGCGggcag gcaCGGTGAA CGTCAGCATT gccCgaatcc aacCCgccgc
1251 cgcaCAGACA gcggacatta ccgtcgcacc tttgccgcaa gaaaccgtcc
1301 gtacgggaac ccgatccct tgtccgcaTt accgaaccgc ccctTGCAGC
1351 AGCCGCAGCG CaacctCAAA ccgAAAAACA GACTGCCATG CcgtctGA

```

This corresponds to the amino acid sequence <SEQ ID 2100; ORF 650.ng>:

```

g650.pep
1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ VGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWDE LRQGFMRGEV NPFLVRRHES KFIASRSYFD RVNRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAVNRARDQG LEPTYENLRM PNERNYVVK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFOAV EPGRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKNKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLHT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVSI ARIQPAAAQT ADITVAPLPQ ETVRTGTRSP CPHYRTRPCD
451 SRSATSNRKT DCHAV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2101>:

```

m650.seq
1 ATGTCCAAAC TCAAAACCAT CGCTCTGACC GCATCAGGTC TGTCCGTTTG
51 TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTAAACTCT TCAATACTCG ACCTGCCCCC GACAAAACAA
151 TATTTCGAAT CCGCAGCCT GTGGGGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTTCATCG
251 CAAGGCACAG CTATTTCAAC AGGGTCATCA ACCGGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCCG CCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGCGTTCGT CACCAAAGCC AAATCACAGC
401 TCGGCGCATC AGGATTATGG CAGTTTATGC CCGTACCAGC CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGAGC TTACGCGCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT TGCCCTTGCC GCCTACAAC TGGGGTGAAG CAACGTCGGA
601 CGCGGCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTCCCCAAG CTGCTCGCCG
701 TGCGCAACAT TATTGCCACT CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCTATTT TCAGGCAGTC GAACCGGATC GTCCGCTCGA
801 CAACGAAGCC ATGCGCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCGCGGT TTATCCCCAA AAGCAAACGC
901 AAAGTCTGCT TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951 CAACGCCGCA CCCGACAGCC TGTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CCTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTTC CATCGACATC GACAATACGC CCGACACCTA CCGTTCCAAT
1201 ATGCGCGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCGCG
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTGCGCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCTT TGTCGTATT GCCGAACCTG CCCTTGCAGC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2102; ORF 650>:

```

m650.pep
1 MSKLKTIALT ASGLSVCPGF LYAQTSSHQ IGLAIMRLNS SILDLPPTKQ
51 YFQSGSLWGE LRQGFMRGEV NPFLVRRHES KFIASHSYFN RVINRSRPYM
101 YHIANEVKKR NMPAEAALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151 GLEKTPVYDG RHDVYAATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201 RAINRARAQG LEPTYENLRM PNERNYVVK LLAVRNIIAT PQSFGMNISD
251 IDNKPYFOAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301 KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351 DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPDITYRSN
401 MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451 SRSATSNRKT DRHAV*

```

m650/g650 96.1% identity in 465 aa overlap

1034

m650.pep	10	20	30	40	50	60
	MSKLTIALTASGLSVCPGFLYAQNTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
g650	MSKLTIALTASGLSVCPGFLYAQNTSSHQVGLAIMRLNSSILDLPPTKQYFQSGSLWGE					
	10	20	30	40	50	60
m650.pep	70	80	90	100	110	120
	LRQGRMGEVNPVLVRRHESKFIAHSYFNRVINRSRPYMYHIANEVKKRNMPAEAAALLP					
g650	LRQGRMGEVNPVLVRRHESKFIAHSYFDRVVNRSRPYMYHIANEVKKRNMPAEAAALLP					
	70	80	90	100	110	120
m650.pep	130	140	150	160	170	180
	FIESAFVTAKSHV GASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
g650	FIESAFVTAKSHV GASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG					
	130	140	150	160	170	180
m650.pep	190	200	210	220	230	240
	LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
g650	LFGDWPLAFAAYNWGEENVGRAVNRARDQGLEPTYENLRMPNETRNYVPKLLAVRNIAT					
	190	200	210	220	230	240
m650.pep	250	260	270	280	290	300
	PQSGFMNISDIDNKPYPQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKSKR					
g650	PQSGFMNISDIDNKPYPQAVEPGRPLDNEAIARLAGITQSELLALNPAFNVPAFIPKNKR					
	250	260	270	280	290	300
m650.pep	310	320	330	340	350	360
	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
g650	KLLLPVASVQTFQSNYLNAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG					
	310	320	330	340	350	360
m650.pep	370	380	390	400	410	420
	NLVNAGRSILVAKNGKTLQTASESVVSDIDNTPDTPYRSNMPAGTVNVGIARIRPAAAQT					
g650	NLVNAGRSILVAKNGKTLHTASESVVSDIDNTPDTPYRSNMPAGTVNVSIARIQPPAAAQT					
	370	380	390	400	410	420
m650.pep	430	440	450	460		
	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
g650	ADITVAPLPQETVTRTGRSPCPHYTRPCDSRSATSNRKTDCHAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2103>:

```

a650.seq
1   ATGTCCAAAC TCAAAACCAT CGCCCTGACC GCGTCAGGTC TGTCCGTTTG
51  TCCGGGTTTC CTATACGCCC AAAACACCTC ATCACACCAA ATCGGTTTGG
101 CGATTATGCG CTTAAACTCT TCAATACTCG ACCTGCCACC GACAAAACAA
151 TATTTCCAAT CCGGCAGCCT GTGGAGCGAG CTGCGCCAAG GCTTCCGGAT
201 GGGCGAAGTC AATCCCGAAC TGGTACGCCG CCACGAAAGC AAATTCATCG
251 CAAGCCACAG CTATTTCAAC AGGTCATCA ACCGAGTAG ACCCTATATG
301 TACCATATCG CCAACGAAGT CAAAAACGC AATATGCCC GCGAAGCCGC
351 CCTGCTTCCC TTCATCGAAA GCGGTTTCGT CACCAAGGCC AAATCAGACG
401 TCGGCGCATC GGGCCTGTGG CAGTTCATGC CCGTACCGG CAGGCATTAC
451 GGCCTGGAAA AAACACCGGT TTACGACGGC AGGCACGACA TTTACGCCGC
501 CACCGATGCC GCACTCAACT ATCTGCAATA CCTCTATGGA CTGTTCCGGC
551 ACTGGCCGCT CGCCTTTGCC GCCTACAACT GGGGTGAAGG CAACGTCGGA
601 CGCGCCATCA ACCGCGCCCG CGCCCAAGGG CTCGAACCGA CCTACGAAAA
651 CCTGCGTATG CCCAACGAAA CGCGCAACTA TGTTCCCAAG CTGCTCGCCG
701 TGCGCAACAT CATTGCCGCC CCCCAATCTT TCGGCATGAA TATCAGCGAC
751 ATAGACAACA AACCCTATTT TCAGGCAGTC GAACCGGACC GTCCGCTCGA
801 CAACGAAGCC ATCGCCCGGC TTGCCGGCAT CACGCAAAGC GAGCTGCTCG
851 CCCTAAACCC CGCATTCAAC GTCCCCGCGT TCATCCCAA AAGCAAACGC

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1035

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901  AAACTGCTGC TTCCTGTCGC GTCCGTACAA ACCTTCCAAA GCAACTACCT
951  CAACGCCGCA CCCGACAGCC TGTTTTTCATG GGAAGTCTAT ACGCCTGCCG
1001 CCAAAACCAG CTTGTCCGAC ATCTCGACGG CAACCGGCAT GAGCATTGCC
1051 GACATCAAAC GCCTCAACAA CCTGAACGGC AACCTTGTC ACGCAGGACG
1101 CAGCATCCTT GTCGCCAAGA ACGGCAAAAC CCTTCAGACG GCATCGGAAT
1151 CCGTCGTTC CATCGACATC GACAATACGC CCAACACCTA CCGTTCCAAT
1201 ATGCCGGCAG GCACGGTGAA CGTCGGCATT GCCCGAATCC GACCCGCCGC
1251 CGCACAGACA GCGGACATTA CCGTCGCACC TTGCGCGCAG AAAACCGTCC
1301 GTACGG.AAC CCGATCCCCT TGTCCGTATT GCCGAACCTG CCCTTGCGAC
1351 AGCCGCAGCG CAACCTCAAA CCGAAAAACA GACCGCCATG CCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2104; ORF 650.a>:

```

a650 .pep
  1  MSKLKTIALT ASGLSVCPGF LYAONTSSHQ IGLAIMRLNS SILDLPPTKQ
 51  YFQSGSLWSE LRQGRMGEV NPELVRRES KFIASHSYFN RVINRSRPMY
101  YHIANEVKKR NMPAEALLP FIESAFVTKA KSHVGASGLW QFMPATGRHY
151  GLEKTPVYDG RHDYIATDA ALNYLQYLYG LFGDWPLAFA AYNWGEENVG
201  RAINRARAQG LEPTYENLRM PNETRNVPK LLAVRNIIAA PQSFGMNISD
251  IDNKPYFQAV EPDRPLDNEA IARLAGITQS ELLALNPAFN VPAFIPKSKR
301  KLLLPVASVQ TFQSNYLNAA PDSLFSWEVY TPAAKTSLSD ISTATGMSIA
351  DIKRLNNLNG NLVNAGRSIL VAKNGKTLQT ASESVVSIDI DNTPTYRSN
401  MPAGTVNVGI ARIRPAAQT ADITVAPLPQ KTVRTXTRSP CPYCRTCPCD
451  SRSATSNRKT DRHAV*

m650/a650  99.1% identity in 465 aa overlap

      10      20      30      40      50      60
m650 .pep  MSKLKTIALTASGLSVCPGFLYAONTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWGE
          |||
a650       MSKLKTIALTASGLSVCPGFLYAONTSSHQIGLAIMRLNSSILDLPPTKQYFQSGSLWSE
          |||
      10      20      30      40      50      60

      70      80      90     100     110     120
m650 .pep  LRQGRMGEVNPELVRRESKFIASHSYFNRVINRSRPMYHIANEVKKRNMPAEALLP
          |||
a650       LRQGRMGEVNPELVRRESKFIASHSYFNRVINRSRPMYHIANEVKKRNMPAEALLP
          |||
      70      80      90     100     110     120

      130     140     150     160     170     180
m650 .pep  FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDVYAATDAALNYLQYLYG
          |||
a650       FIESAFVTKAKSHVGASGLWQFMPATGRHYGLEKTPVYDGRHDIYAATDAALNYLQYLYG
          |||
      130     140     150     160     170     180

      190     200     210     220     230     240
m650 .pep  LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVPKLLAVRNIIAT
          |||
a650       LFGDWPLAFAAYNWGEENVGRAINRARAQGLEPTYENLRMPNETRNVPKLLAVRNIIAA
          |||
      190     200     210     220     230     240

      250     260     270     280     290     300
m650 .pep  PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR
          |||
a650       PQSFGMNISDIDNKPYFQAVEPDRPLDNEAIARLAGITQSELLALNPAFNVPAPFIPKSKR
          |||
      250     260     270     280     290     300

      310     320     330     340     350     360
m650 .pep  KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||
a650       KLLLPVASVQTFQSNYLNAAAPDSLFSWEVYTPAAKTSLSDISTATGMSIADIKRLNNLNG
          |||
      310     320     330     340     350     360

      370     380     390     400     410     420
m650 .pep  NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPDYRSNMPAGTVNVGIARIRPAAQT
          |||
a650       NLVNAGRSILVAKNGKTLQTASESVVSIDIDNTPTYRSNMPAGTVNVGIARIRPAAQT
          |||

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1036

	370	380	390	400	410	420
	430	440	450	460		
m650 - pep	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
a650	ADITVAPLPQKTVRTXTRSPCPYCRTCPCDSRSATSNRKTDRAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2105>:

```

g652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
51  GACTTTGGCG GTCTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGTCCGAT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGTAAAG GCTTCCCGAC CACAGTCGCG GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAAGCGGCCG
401 AAGCCGCCGG CTACAAGGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCGTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATACTTGGAA GGCCTGGTTA
551 ACGAATTCCC GATTATTTC ATTGAAGACG GGATGGACGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GGCAAAAAG TTCAATTGGT
651 CGGCGACGAC TTGTTCGTAA CCAATCCGAA AATCTTGCC GAAGGCATCG
701 AAAAAGCGT AGCAAACGCA TTGCTGGTCA AAGTCAACCA AATCGGTACT
751 TTAAGCGAAA CCCTGAAAGC cgtcgatctg gCAAAATGCA accgctacGc
801 cagCGTGATG AGCCACcgct ccggCGAAAC CGAAGACAGT Accattgccc
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TTA AAAAccgG TTCTTTGAGC
901 cgtTCCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCcgctACT ACCCGGCA AGCCGCATTC TACCAACTGG
1001 GCAATAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2106; ORF 652.ng>:

```

g652.pep
1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EAAEAAGYKA GEDVLFALDC
151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW
201 EGVKLLTEKL GKQVQLVDD LFVTNPKILA EGIEKGVANA LLVKVNIQGT
251 LSETLKAVDL AKCNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS
301 RSDRMAKYNQ LLRIEELAE AAYYPGKAFF YQLGK*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2107>:

```

m652.seq
1  ATGATCGAAT TGGACGGTAC TGAAAACAAA GGCAATTTGG GTGCGAATGC
51  GACTTTGGCG GTTCTATGG CGGTTGCACG CGCCGCTGCC GAAGACTCAG
101 GCCTGCCGCT TTACCGCTAC TTGGGGGGCG CAGGCCCAGT GTCCCTGCCC
151 GTACCGATGA TGAACGTCAT CAACGGCGGC GAACACGCCA ACAACAGCCT
201 GAACATCCAA GAGTTTATGA TTATGCCCGT CGGCGCAAAA TCTTTCCGCG
251 AAGCGTTGCG CTGCGGTGCG GAAATTTTCC ACGCCTTGAA AAAACTGTGC
301 GACAGCAAAG GCTTCCCGAC CACAGTCGCG GACGAAGGCG GTTTCGCCCC
351 CAACCTGAAC AGCCACAAAG AAGCCCTGCA ACTGATGGTC GAGGCGACCG
401 AAGCCGCCGG CTACAAAGCG GGCGAAGACG TATTATTCGC ATTGGACTGC
451 GCCTCCAGCG AGTTCTACAA AGACGGCAAA TACCACTTGG AAGCCGAAGG
501 CCGCTCCTAC ACCAACGCGG AATTTGCCGA ATATCTGGAA GGCCTGGTCA
551 ACGAGTTCCC CATCATCTCC ATCGAAGACG GCATGGATGA AAACGACTGG
601 GAAGGCTGGA AACTGCTGAC CGAAAAATG GGCGGTAGAG TTCAATTGGT
651 TGCGGACGAC TTGTTCGTAA CCAATCCAAA AATCTTGCC GAAGGCATCG
701 AAAAAGCGT AGCAAACGCA TTGCTGGTCA AAGTCAATCA AATCGGTACT
751 TTGAGCGAGA CCCTGAAAGC CGTCGACTTA GCCAAACGCA ACCGCTACGC
801 CAGCGTAATG AGCCACCGCT CCGGCGAAAC CGAAGACAGC ACCATTGCCG
851 ACTTGGCAGT CGCCACCAAC TGTATGCAGA TCAAAACCGG TTCTTTGAGC
901 CGTTCGACC GCATGGCGAA ATACAACCAa ctGCTGCGTA TCGAGGAAGA
951 ATTGGCGGAA GCGCGCGACT ACCCCAGCAA AGCCGCATTC TACCAACTGG
1001 GCAATAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2108; ORF 652>:

```

m652.pep
1  MIELDGTENK GNLGANATLA VMAVARAAA EDSGLPLYRY LGGAGPMSLP
51  VPMNVINGG EHANNSLNIQ EFMIMPVGAK SFREALRCGA EIFHALKKLC
  
```

1037

101 DSKGFPTTVG DEGGFAPNLN SHKEALQLMV EATEAAGYKA GEDVLFALDC  
 151 ASSEFYKDGK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW  
 201 EGWKLLETKL GGRVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNIQIGT  
 251 LSETLKAVDL AKRNRYASVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAP YQLGK\*

m652/g652 98.2% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
g652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGGAGPMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
g652	EHANNSLNIEFMIMPVGAKSFREALRCGAEIFHALKKLCDSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
g652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFIISIEDGMDENDWEGWKLLTEKLGGRVQLVGDDLFVTNPKILAEGIEKGVANA					
g652	GLVNEFFIISIEDGMDENDWEGWKLLTEKLGKVKQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNIQIGTILSETLKAVDLAKRNRYASVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
g652	LLVKVNIQIGTILSETLKAVDLAKCNRYASVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAYNQLLRIEELAEAAADYPSKAAPYQLGKX					
g652	RSDRMAYNQLLRIEELAEAAAYYPGKAAPYQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2109>:

a652.seq

1	ATGATCGAAT	TGGACGGTAC	TGAAAACAAA	GGCAATTGGG	GTGCGAATGC
51	GACTTTGGCG	GTTTCTATGG	CGGTTGCACG	CGCCGCTGCC	GAAGACTCAG
101	GCCTGCCGCT	TTACCGCTAC	TTGGGCGGCG	CAGGCCCGAT	GTCCCTGCCC
151	GTACCGATGA	TGAACGTCAT	CAACGGCGGC	GAACACGCCA	ACAACAGCCT
201	GAACATCCAA	GAGTTTATGA	TTATGCCCGT	CGGCGCAAAA	TCTTTCCGCG
251	AAGCGTTGCG	CTGCGGTGCG	GAAATTTTCC	ACGCCTTGAA	AAAACGTGTC
301	GACAGCAAAG	GCTTCCCGAC	CACAGTCGGC	GACGAAGCGG	GTTTCGCCCC
351	CAACCTGAAC	AGCCACAAAG	AAGCCCTGCA	ACTGATGGTC	GAGGCGACCG
401	AAGCCGCCGG	CTACAAAGCG	GGCGAAGACG	TATTATTGCG	ATTGGACTGC
451	GCGTCCAGCG	AGTTCTACAA	AGACGGCAAA	TACCACTTGG	AAGCCGAAGG
501	CCGCTCCTAC	ACCAACGCGG	AATTTGCCGA	ATATCTGGAA	GGCCTGGTCA
551	ACGAGTTCCC	CATCATCTCC	ATCGAAGACG	GGATGGATGA	AAACGACTGG
601	GAAGGCTGGA	AACTGCTGAC	CGAAAAACTG	GGCGGCAAA	TCCAACTCGT
651	TGGCGACGAC	CTCTTCGTGA	CCAACCCGAA	AATCCTTGCC	GAAGGCATTG
701	AAAAAGGCGT	GGCAAACGCA	CTATTGGTCA	AAGTCAACCA	AATCGGTACT
751	TTGAGTGAAA	CCCTGAAAGC	CGTCGACTTA	GCCAAACGCA	ACCGCTACGC
801	CAGCGTAATG	AGCCACCGCT	CCGGCGAAAC	CGAAGACAGC	ACCATTGCCG
851	ACTTGGCAGT	CGCCACCAAC	TGTATGCAGA	TCAAACCGG	TTCTTTGAGC
901	CGTTCCGACC	GCATGGCGAA	ATACAACCAA	CTGCTGCGTA	TCGAGGAAGA
951	ATTGGCGGAA	GCCGCCGACT	ACCCAGCAAA	AGCCGCATTG	TACCAACTGG
1001	GCAAATAA				

This corresponds to the amino acid sequence <SEQ ID 2110; ORF 652.a>:

a652.pep

1	MIELDGTENK	GNLGNATLA	VSMVARAAA	EDSGLPLYRY	LGGAGPMSLP
51	VPMNVINGG	EHANNSLNQ	EFMIMPVGAK	SFREALRCGA	EIFHALKKLC
101	DSKGFPTTVG	DEGGFAPNLN	SHKEALQLMV	EATEAAGYKA	GEDVLFALDC

1038

151 ASSEFYKD GK YHLEAEGRSY TNAEFAEYLE GLVNEFFIIS IEDGMDENDW  
 201 EGWKLLETKL GGVQLVGDD LFVTNPKILA EGIEKGVANA LLVKVNQIGT  
 251 LSETLKAVDL AKRNRYSVM SHRSGETEDS TIADLAVATN CMQIKTGSLS  
 301 RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGK\*

m652/a652 99.7% identity in 335 aa overlap

	10	20	30	40	50	60
m652.pep	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGAGFMSLPVPMNVINGG					
a652	MIELDGTENKGNLGNATLAVSMAVARAAEDSGLPLYRYLGAGFMSLPVPMNVINGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652.pep	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
a652	EHANNSLNIQEFMIMPVGAKSFREALRCGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652.pep	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
a652	SHKEALQLMVEATEAAGYKAGEDVLFALDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m652.pep	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
a652	GLVNEFFIISIEDGMDENDWEGWKLLETKLGGVQLVGDDLFVTNPKILAEGIEKGVANA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m652.pep	LLVKVNQIGTILSETLKAVDLAKRNRYSVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
a652	LLVKVNQIGTILSETLKAVDLAKRNRYSVM SHRSGETEDSTIADLAVATNCMQIKTGSLS					
	250	260	270	280	290	300
	310	320	330			
m652.pep	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
a652	RSDRMAYNQ LLRIEELAE AADYPSKAAF YQLGKX					
	310	320	330			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2111>:

g652-1.seq

```

1   ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GTGCGGCCGT ACCGAGCGGC GCATCCACCG GTCAGAAAGA AGCTTTGGAA
151 CTTCGCGACG GCGACAAATC CCGCTATTCC GGCAAGGCG TATTGAAGGC
201 CGTCGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATC GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAGG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TCTCTATGGC
351 GGTGACACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGGGGCGC AGGTCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGGCGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCGCTC GCGCAAAAT CTTTCCGCGA AGCGTTGCGC TCGGTTGCGG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGTAAAGG CTTCCCGACC
601 ACAGTCGCGC ACGAAGGCGG TTTCGCCCCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AAGCGGCCGA AGCCGCCGGC TACAAGGCGG
701 GCGAAGACGT ATTATTGCGA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAAAT ACCACTTGGG AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TACTTGGAAG GCTTGGTTAA CGAATTCCTG ATTATTTCCT
851 TTGAAGACGG GATGGACGAA AACGACTGGG AAGGCTGAA ACTGCTGACC
901 GAAAAATTGG GCAAAAAAGT TCAATTGGTC GGCACGACT TGTTTCGTAAC
951 CAATCCGAAA ATCTTGCCG AAGGCATCGA AAAAGGCGTA GCAAACGCAT
1001 TGCTGGTCAA AGTCAACCAA ATCGGTACTT TAAGCGAAAC CCTGAAAGCC
1051 GTCGACTGG CAAATGCAA CCGCTACGCC AGCGTGATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGTA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT TAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCTACTA
1251 CCCCGCAA GCGCATTCT ACCAATTGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2112; ORF 652-1.ng>:

1039

## g652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEAEAAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAR YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKRVQLV GDDLFTVNPV ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEAAAYPGK AAFYQLGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2113>:

## m652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCG GAAATTTTGG ACTCAGCGCG
51  CAACCCACAC GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAAGA GGCTTTGGAA
151 CTTGCGCAGC GCGACAAATC CCGTTATTCT GCGAAGGGCG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAACAAAG GCAATTTGGG TCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCGACGC GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCGCGA AGCGTTGCGC TCGGTTGCCG
551 AAATTTTCCA CGCCTTGAAA AAATGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGGCG ACGAAGGCGG TTTCGCCCGC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGCGACCGA AGCCGCGGCG TACAAAGCGG
701 CGGAAGACGT ATTATTGCGA TTGGACTGCG CCTCCAGCGA GTTCTACAAA
751 GACGCGAAAT ACCACTTGA AGCGGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCTC ATCATCTCCA
851 TCGAAGACGG CATGGATGAA AACGACTGGG AAGGCTGGAA ACTGCTGACC
901 GAAAAACTGG GCGGTAGAGT TCAATTGGTT GCGGACGACT TGTTCGTAAC
951 CAATCCAAAA ATCTTGGCGG AAGGCATCGA AAAAGGCGTA GCAACGCAT
1001 TGCTGGTCAA AGTCAATCAA ATCGGTACTT TGAGGAGAC CCTGAAAGCC
1051 TCGCACTTAG CCAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCCGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2114; ORF 652-1>:

## m652-1.pep

```

1  MSAIVDIFAR EILDSRGNPT VECDVLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYG GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGNANA TLAVSMAVAR AAAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNLSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLCDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAR YLEGLVNEFP IISIEDGMDE NDWEGWKLLT
301 EKLGGKRVQLV GDDLFTVNPV ILAEGIEKGV ANALLVKVNO IGTLSETLKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/g652-1 98.6% identity in 428 aa overlap

	10	20	30	40	50	60
m652-1	MSAIVDIFAREILDSRGNPTVECDVLESGVMGRAAVPSGASTGQKEALELRDGDKSRYG					
g652-1	MSAIVDIFAREILDSRGNPTVECDVLESGVMGRAAVPSGASTGQKEALELRDGDKSRYG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
g652-1	GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNANATLAVSMAVAR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNNGGEGHANNLSLNIQEFMIMPVGAKSREALR					
g652-1	AAAEDSGLPLYRYLGGAGPMSLPVPMNNGGEGHANNLSLNIQEFMIMPVGAKSREALR					
	130	140	150	160	170	180



1040

	190	200	210	220	230	240
m652-1	CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA					
g652-1	CGAEIFHALKKLDSKGFPTTVGDEGGFAPNLNSHKEALQLMVEAAEAAGYKAGEDVLFA					
	190	200	210	220	230	240
m652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT					
g652-1	LDCASSEFYKDGKYHLEAEGRSYTNAEFAEYLEGLVNEFPIISIEDGMDENDWEGWKLLT					
	250	260	270	280	290	300
m652-1	EKLGGRRVQLVGDDLFTVNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA					
g652-1	EKLGGKVQLVGDDLFTVNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKCNRYA					
	310	320	330	340	350	360
m652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEEEAADYPSK					
g652-1	SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEEEAAYYPGK					
	370	380	390	400	410	420
m652-1	AAFYQLGKX					
g652-1	AAFYQLGKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2115>:

a652-1.seq

```

1  ATGAGCGCAA TCGTTGATAT TTTCGCCCGC GAAATTTTGG ACTCACGCGG
51  CAACCCACCA GTCGAGTGTG ATGTATTGCT CGAATCCGGC GTAATGGGAC
101 GCGCAGCCGT ACCGAGCGGC GCGTCCACCG GTCAAAAGA GGCTTTGGAA
151 CTTGCGGACG GCGACAAATC CCGTTATTCG GGCAAGGCGG TATTGAAGGC
201 GGTGGAACAC GTCAACAACC AAATCGCCCA AGCCCTCATT GGTATCGATG
251 CCAACGAGCA ATCTTATATC GACCAATCA TGATCGAATT GGACGGTACT
301 GAAAACAAAG GCAATTTGGG TGCGAATGCG ACTTTGGCGG TTTCTATGGC
351 GGTTCACGCG GCCGCTGCCG AAGACTCAGG CCTGCCGCTT TACCGCTACT
401 TGGGCGGCGC AGGCCCGATG TCCCTGCCCG TACCGATGAT GAACGTCATC
451 AACGGCGGCG AACACGCCAA CAACAGCCTG AACATCCAAG AGTTTATGAT
501 TATGCCCGTC GCGCAAAAT CTTTCCGCGA AGCGTTGCCG TCGGTTGCCG
551 AATATTTCCA CGCCTTGAAA AAAGTGTGCG ACAGCAAAGG CTTCCCGACC
601 ACAGTCGCGG ACGAAGCGCG TTTGCCCGCC AACCTGAACA GCCACAAAGA
651 AGCCCTGCAA CTGATGGTCG AGGCGACCGA AGCCGCGGCG TACAAGCGCG
701 GCGAAGACGT ATTATTCGCA TTGGACTGCG CGTCCAGCGA GTTCTACAAA
751 GACGGCAAT ACCACTTGGA AGCCGAAGGC CGCTCCTACA CCAACGCGGA
801 ATTTGCCGAA TATCTGGAAG GCCTGGTCAA CGAGTTCCCC ATCATCTCCA
851 TCGAAGACGG GATGGATGAA AACGACTGGG AAGGCTGAA ACTGCTGACC
901 GAAAACTGG GCGGCAAAGT CCAACTCGTT GCGGACGACC TCTTCGTTAC
951 CAACCCGAAA ATCCTTGCCG AAGGCATTGA AAAAGGCGTG GCAAACGCAC
1001 TATTGGTCAA AGTCAACCAA ATCGGTACTT TGAGTGAAAC CCTGAAAGCC
1051 GTCGACTTAG CCAAACGCAA CCGCTACGCC AGCGTAATGA GCCACCGCTC
1101 CGGCGAAACC GAAGACAGCA CCATTGCCGA CTTGGCAGTC GCCACCAACT
1151 GTATGCAGAT CAAAACCGGT TCTTTGAGCC GTTCCGACCG CATGGCGAAA
1201 TACAACCAAC TGCTGCGTAT CGAGGAAGAA TTGGCGGAAG CCGCGGACTA
1251 CCCCAGCAAA GCCGCATTCT ACCAACTGGG CAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2116; ORF 652-1.a>:

a652-1.pap

```

1  MSAIVDIFAR EILDSRGNPT VECVLLLESG VMGRAAVPSG ASTGQKEALE
51  LRDGDKSRYS GKGVLKAVEH VNNQIAQALI GIDANEQSYI DQIMIELDGT
101 ENKGNLGAHA TLAVSMAVAR AAEDSGLPL YRYLGGAGPM SLPVPMNVI
151 NGGEHANNSL NIQEFMIMPV GAKSFREALR CGAEIFHALK KLDSKGFPT
201 TVGDEGGFAP NLNSHKEALQ LMVEATEAAG YKAGEDVLFA LDCASSEFYK
251 DGKYHLEAEG RSYTNAEFAE YLEGLVNEFP IISIEDGMD NDWEGWKLLT
301 EKLGGKVQLV GDDLFTVNP KILAEGIEKV ANALLVKVNQ IGTLSLTKA
351 VDLAKRNRYA SVMSHRSGET EDSTIADLAV ATNCMQIKTG SLRSRDRMAK
401 YNQLLRIEEE LAEADYPSK AAFYQLGK*

```

m652-1/a652-1 99.8% identity in 428 aa overlap

10 20 30 40 50 60

1041

```

m652-1      MSAIVDIFAREILDSRGNTVECDVLLSGVMGRAAVPSGASTGQKEALELRDGDKSRY
a652-1      MSAIVDIFAREILDSRGNTVECDVLLSGVMGRAAVPSGASTGQKEALELRDGDKSRY
              10      20      30      40      50      60

              70      80      90      100     110     120
m652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
a652-1      GKGVLKAVEHVNNQIAQALIGIDANEQSYIDQIMIELDGTENKGNLGNATLAVSMAVAR
              70      80      90      100     110     120

              130     140     150     160     170     180
m652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
a652-1      AAAEDSGLPLYRYLGGAGPMSLPVPMNVINGGEHANNSLNIQEFMIMPVGAKSFREALR
              130     140     150     160     170     180

              190     200     210     220     230     240
m652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
a652-1      CGAEIFHALKKLDCSKGFPTTVGDEGGFAPNLNSHKEALQLMVEATEAAGYKAGEDVLFA
              190     200     210     220     230     240

              250     260     270     280     290     300
m652-1      LDCASSEFYKDGKYHLEAGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
a652-1      LDCASSEFYKDGKYHLEAGRSYTNAEFAEYLEGLVNEFPPIISIEDGMDENDWEGWKLLT
              250     260     270     280     290     300

              310     320     330     340     350     360
m652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
a652-1      EKLGGRVQLVGDDLFVTNPKILAEGIEKGVANALLVKVNQIGTLSETLKAVDLAKRNRYA
              310     320     330     340     350     360

              370     380     390     400     410     420
m652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
a652-1      SVMSHRSGETEDSTIADLAVATNCMQIKTGSLSRSDRMAYNQLLRIEEELAEADYPSK
              370     380     390     400     410     420

              429
m652-1      AAFYQLGKX
a652-1      AAFYQLGKX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2117>:

```

g653.seq
1  ATGGCGGcg aaccgatgcg gAtgcggag gtaAcgtaCG GTTTTCCGG
51  ATCGTTCGGG ATGGCGTTTT TGTtgacggT GATGTGCGCt ttgcccAAG
101 CGGCTtcggc ggctttgcCg gtgaTTTTCA TCGGTTGCAG GtcgacgaGG
151 AAAacgTGGC TTTCGGTGCG GCCGGAaacy atgcgCaaac cgCGTttaac
201 caactcttcc gcCATGACGG CAGCATTGAT TTCACTTGT TTTGCGTATT
251 GTTTGAactC GGGTTGcaac gcttctTTAA acgctACGGC TttgCGCGCG
301 ATAACGTgca tcaACGGAcc gCCTTGCAGG CTTGGAAGA TGGAAGAGTT
351 CAGCGCTTTT TCGTGGGTAT TGTCACGGCA CAAATCACA CCGCCGCGAG
401 GGCCGCGTAG GGTTTGTGG GTGGTAGTgG ttACgaaGtc GCAGAatgyc
451 ACGGGgttag gatattcgcc gccGGCAACC AgtccgGCAT Ag

```

This corresponds to the amino acid sequence <SEQ ID 2118; ORF 653.ng>:

```

g653.pep
1  MAAEPMRME VTYGFSGSFG MAFLLTMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMTAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCINGPPCR LGMEEFSAF SWVLSRHKIT PPRGPRRLV VVVVTKSQNG
151 TGLGYSPPAT SPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2119>:

```

m653.seq
1  ATGGCAGCGG AGCCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCGTTCGGA ATGGCGTTTT TGTtgacggT GATGTGCGCt TTGCCCAAG
101 CGGCTTCGGC GGCTTGCCTG GTAATTTCA TCGGTTGCAG GTCAACGAGG

```

1042

```

151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACCTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGACC GCCTTGCAAG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TCACGAAGTC GCAGAACGGC
451 ACCGGGTTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2120; ORF 653>:

```

m653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/g653 96.9% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
g653          10      20      30      40      50      60
MAAEPMRMPEVTYGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90      100     110     120
MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
g653          70      80      90      100     110     120
MRKPRLTNSSAMTAALIFTCFAYCLNSGCNASLNATALAAITCINGPPCRLGKMEEFSAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
g653          130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATSPAX
|||||

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2121>:

```

a653.seq
1  ATGGCGGCGG AACCGATGCG GATGCCGGAG GTAACGAAGG GTTTTCCGG
51  ATCATTCCGG ATGGCGTTT TGTGACAGT GATGTGCGCT TTGCCCAAAG
101 CAGCTTCGGC GGCTTGCCG GTAATTTCA TCGGTTGCAG GTCAACGAGG
151 AAAACGTGGC TTTCGGTGCG GCCGGAAACG ATGCGCAAAC CGCGTTTAAC
201 CAACTCTTCC GCCATGGCGG CTGCATTGAT TTTCACCTGT TTTGCGTATT
251 GTTTGAACCTC GGGTTGCAAT GCTTCTTTAA ACGCCACGGC TTTGGCGGCG
301 ATAACGTGCA TCAGCGGGCC ACCTTGCAAG CTTGGGAAGA TGAAGAGTT
351 CAACGCTTTT TCGTGGGTAT TGTCGCGGCA CAAAATTACG CCGCCGCGAG
401 GACCGCGCAG GGTTTTGTGG GTGGTGGTGG TAACGAAGTC GCAGAACGGC
451 ACGGGATTGG GATATTCGCC GCCGGCAACC AGACCGGCAT AG

```

This corresponds to the amino acid sequence <SEQ ID 2122; ORF 653.a>:

```

a653.pep
1  MAAEPMRMPE VTKGFSGSFG MAFLLTVMCA LPKAASAALP VIFIGCRSTR
51  KTWLSVRPET MRKPRLTNSS AMAAALIFTC FAYCLNSGCN ASLNATALAA
101 ITCISGPPCR LGKMEEFNAF SWVLSRHKIT PPRGPRLVW VVVVTKSQNG
151 TGLGYSPPAT RPA*

```

m653/a653 100.0% identity in 163 aa overlap

```

m653.pep      10      20      30      40      50      60
MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||
a653          10      20      30      40      50      60
MAAEPMRMPEVTKGFSGSFGMAFLLTVMCALPKAASAALPVIFIGCRSTRKTWLSVRPET
|||||

m653.pep      70      80      90      100     110     120
MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||
a653          70      80      90      100     110     120
MRKPRLTNSSAMAAALIFTCFAYCLNSGCNASLNATALAAITCISGPPCRLGKMEEFNAF
|||||

m653.pep      130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||
a653          130     140     150     160
SWVLSRHKITPPRGPRRLVWVVVTKSQNGTGLGYSPPATRPAX
|||||

```

130                      140                      150                      160

g656. seq

1	ATGCCCGCTT	TCTCCGGTTC	GATTTCTTCG	ATGATTTCCA	TCGCGCGGAC
51	TTTTggcGCG	CCGGAGAGTG	TGCcggcagg	gaAGGTGGCG	GCGAGGATGT
101	CCATATTGGT	AACCGACTCT	TTCAAACAGC	ctTCGACGTT	GGAAACGATG
151	TGCATCACAT	GGGAGTATTT	TTCAATCACC	ATTTTGTCGG	TGACTTTGAC
201	TTCGCCTGTT	TTGCTGATGC	GTCCGACATC	GTTGCGCCCC	AAATCGATAA
251	GCATAACGTG	TTCGGCgatt	TCTTTGGCGT	CGCTTAACAA	ATCTTGTTTCG
301	TTGGCAAAGT	CTTCGGCGGG	GGTTTTCGCC	CGCAGGCGCG	TGCCGGCGAT
351	GGGGCGGACG	ATGACGTCat	CGCGTTTCGCG	CGCGGACGAGG	ATTTTCGGGCG
401	AGGAACCGAC	GATGTGGAAA	TCGCCGAAAT	CGTAG	

g656.ppep

1	MPRFGSGSISS	MISIARTFGA	PESVPAGKVA	ARMSILVTPS	FKQPSTLETM
51	CITWEYFSIT	ILSVTLTSPV	LLMRPTSLRP	KSISITCSAI	SLASLNKSCS
101	LARSSAGVLP	RRRVAMPGR	MTSSRSRRTR	ISGEEPTMWK	SPKS*

```
m656.seq
  1  ATGCCGCGTT  TGCTCGGTTT  GACTTCTTCG  ATGATTTCCT  TGGCGCGGAC
51  TTTGGGTGCG  CCGGAGAGTG  TGCCGGCAGG  GAAGGTAGCG  GCGAGGATGT
101 CCATGTTGGT  CATCGCGTCT  TTCAGACGGC  CTTTCGACGT  GGAACATGAT
151 TGCATTACAT  GGGAGTATTT  TCAATCACC  ATTTTGTCTG  TAACTTTGAC
201 TTCGCCGGTT  TTAATGATGC  GGCCGACGTC  GTTGCCTCCT  AAGTCAATCA
251 ACATGACGTG  TTCGGCGATT  TCCTTGGCAT  CGCTTAACAA  ATCTTGTTCT
301 TTGGCAAGGT  CTTCCGGCGG  GGTTTGTCCG  CGCAGGCGCG  TGCCGGCGAT
351 GGGCGCGACG  ATAACCTCGT  TCGCTTCGCG  TCGGACGAGG  ATTTTCGGCG
401 AGGAGCCGAC  GATGTGGAAT  TGCCCGAAT  CGTAG
```

```
m656.pep
  1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
 51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSNIMTCSAI SLASLNKSCS
101  LARSSAGVLP RRRVPAMGRT ITSLSRRRTR ISGEEPTMWK SPKS*
```

### Homology with a predicted ORF from *N. gonorrhoeae*

```

      10      20      30      40      50      60
m656.pep  MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSLVMPFSFRPSTLETMCITWEYFSIT
          |||: || |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g656      MPRFSGSISSMISIARTFGAPESVPAGKVAARMSILVTPSFKQPSTLETMCITWEYFSIT
          10      20      30      40      50      60

      70      80      90      100     110     120
m656.pep  ILSVTLTSPVLLMRPTSLRPK SINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR
          |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g656      ILSVTLTSPVLLMRPTSLRPK S IITCSAISLASLNKSCSLARSSAGVLP RRRVPAMGR
          70      80      90      100     110     120

      130     140
m656.pep  ITSLRSRRTRISGE EPTMWKSPK SX
          :|| |||||:||||:||||:||||:||||:||||:||||
g656      MTSSRSRRTRISGE EPTMWKSPK SX
          130     140

```

1044

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2127>:

```
a656.seq
1  ATGCCCGGTT TGCTCGGTTG GACTTCTTCG ATGATTTCCTA TGGCGCGGAC
51  TT TGGGTGCG CCGGAGAGTG TGCCGGCAGG GAAGGTAGCG GCGAGGATGT
101 CCATGTTGGT CATGCCGTCT TTCAGACGGC CTTGACGTT GGAACGATG
151 TGCAATACAT GGGAGTATTT TTCAATCACC ATTTGTCTCG TAACTTTGAC
201 TTCGCGGTT TACTGATGC GGCCGACGTC GTTGCCTCT AAGTCAATCA
251 ACATGACGTG TTCGGCGATT TCTTTGGCAT CGCTTAACAA ATCTTGTTCG
301 TTGGCAAGGT CTTGCGCGGG GGTTCGCGG CGCAGGCGCG TGCCGGCGAT
351 GGGGCGGACG ATGACATCGT CGCGTTCGCG GCGGACGAGG ATTTGCGGCG
401 AGGAGCCGAC GATGTGGAAA TCGCCGAAAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2128; ORF 656.a>:

```
a656.pep
1  MPRLLGSTSS MISMARTLGA PESVPAGKVA ARMSMLVMPs FRRPSTLETM
51  CITWEYFSIT ILSVTLTSPV LLMRPTSLRP KSINMTCSAI SLASLNKSCS
101 LARSSAGVLP RRRVPAMGRT MTSSRSRRT R ISGEEPTMWK SPKS*
```

m656/a656 98.6% identity in 144 aa overlap

	10	20	30	40	50	60
m656.pep	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
a656.	MPRLLGSTSSMISMARTLGAPESVPAGKVAARMSMLVMPsFRRPSTLETMCITWEYFSIT					
	10	20	30	40	50	60
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
a656	ILSVTLTSPVLLMRPTSLRPKSINMTCSAISLASLNKSCSLARSSAGVLP RRRVPAMGRT					
	70	80	90	100	110	120
m656.pep	ITSLRSRRT R ISGEEPTMWKSPKSX					
a656	MTSSRSRRT R ISGEEPTMWKSPKSX					
	130	140				
m656.pep	ITSLRSRRT R ISGEEPTMWKSPKSX					
a656	MTSSRSRRT R ISGEEPTMWKSPKSX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2129>:

```
g657.seq
1  ATGAACACAC CCCCCATCCT TCCTCCCGCC ATGCTCGGCA TCCTCGGCGG
51  CGGACAATTa ggcagAATGT TTGCCGTTGC CGCTAAACC ATGGGCTACA
101 AAGTAACCGT TCTCGATCCC GACCCGAATG CGCCGGCGGC GGAATTTGCC
151 GACCGCCATT TGTGCGCGCC GTTTGACGAC CGGGCCCGCT TGGACGAATT
201 GGCAAAATGC GCGGCGGTTa cgACCGAATT TGAAAacgtc aaTGCCGACG
251 CGATGCGCTC TCTGGCAAAG CATACCAACG TTTCCCCCAG CGGCGACTGC
301 GTGTCCATTG CACAAAACCG CATTCAGGAA AAAGCGTGGA TACGCAAAGC
351 AGGCTTGCAA ACCGCGCCGT ATCAGGCGGT TTGCAAGGCC GAAGACATTA
401 CTGAAGCAAG CGCGCAATTT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG
451 GGCTACGACG GCAAAGGTCA AATCCGCGTC AAAACGTTGG ACGAACTCAA
501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG
551 TGGACTTGCG CGGCGAGATT TCCGTGATCG TATGCGCTCT GAACGATGAA
601 AACGTGCAAA CCTTCGACCC CGCCGAAAAC ATCCACGAAA ACGGCATCTT
651 GGCTTattcc ATCGTccccg CGCGGCTGAG TGCCGACGTG CAGCAACAGG
701 CGCGGCAGAC GCGCAACGc tTGGCGGACG AATTGGATTA TGTGCGGcgt
751 TTGGCGGTAG AAATGTTTGT TGTGCGGAC ACACATGAAT TGCTCGTCAA
801 TGAAACCGCC CCGCGCACGC ACAATTCCGG CCACCATACG ATAGATGCCT
851 GCGCCGCGA CAGTTCCAA CAGCAGGTAC GCATTATGTG CAacctGCCG
901 cccGccgACA CCAAATTATT aTCCCcttgC TGTATGGCGA ATATTTTGg
951 CGACGTTTGG CAGGAAGATG GCGGCGAACC GGATTGGCTG CCGTTGCAAA
1001 GCCGCGCGAA TGCACACCTG CACCTATACG GAAAAAAAAC CGCACAGAAA
1051 GGTGCGAAAA TGGGACACTT TaccgTTTGG ACCACCGATT CGGACaccgC
1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA
```

This corresponds to the amino acid sequence <SEQ ID 2130; ORF 657.ng>:

1045

g657 - pep

1	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGYKVTVLDP	DPNAPAAEFA
51	DRHLCAPFDD	RAALDELAKC	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC
101	VSIAQNRIQE	KAWIRKAGLQ	TAPYQAVCKA	EDITEASAQF	LPGILKTATL
151	GYDGKGQIRV	CTLDELKAAF	AEHGGVDCVL	EKMVDLRGEI	SVIVCRLNDE
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADV	QQQARQTAQR	LADEL DYGV

1046

251 LAVEMFVVD THELLVNETA PRTHNSGHHT IDACAAADQFQ QQVRIMCNLP  
 301 PADTKLLSPC CMANILGDVW QEDGGEPDWL PLQSRPNAHL HLYGKKTAQK  
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2131>:

m657. seq  
 1 ATGAAAAACA TATCTCTTTC TCCGCCCGCC ATGCTTGCCA TCCTCGGCGG  
 51 CGGACAATTA GGCAGAATGT TTACCGTTGC CGCCAAAACC ATGGGCTACA  
 101 AAGTAACCGT TCTCGACCCC GATCCGGACG CGCCGGCAGC AGAATTGTC  
 151 GACCGCCATT TGTGCGCGCC GTTTAACGAC CAAGCTGCTT TGGACGAATT  
 201 GGCAAAATGC GCGGCGGTGA CCACTGAATT TGAAAACGTC AATGCCGATG  
 251 CGATGCGCTT TTTGGCAAAA CATACCAATG TTTCCCTAG CGGCGATTGT  
 301 GTGGCGATTG CACAAAACCG CATTCAAGAA AAGGCATGGA TACGCAAAGC  
 351 GGGATTGCAA ACCGCGCCGT ATCAAGTGGT TTGTAAGGCT GAAGACATCA  
 401 CTGAAGCAAG CGCGCAATT TTGCCCGGCA TCCTGAAAAC GGCTACGTTG  
 451 GGCTACGACG GCAAAGGTCA AATCCGCGTA AAAACATTGG ATGAACTCAA  
 501 AGCCGCGTTT GCCGAACACG GCGGCGTGGA TTGCGTTTGG GAAAAAATGG  
 551 TGGATTGCG CAGTGAAATT TCCGTAATCG TATGCCGTTT GAACAATGAC  
 601 AACGTGCAA CTTTCGACCC TGCCGAAAAC ATCCACGAAA ACGGCATCTT  
 651 GGCTTATCC ATCGTCCCG CGCGACTGAG TGCCGACGTG CAGCAACAGG  
 701 CGCGGCAGAT GCGCAACGC TTGGCGGACG AATTGGATTA TGTCGGCGTA  
 751 TTGGCGGTAG AAATGTTTGT TGTCGGTGAC ACGCATGAAT TGGTCGTCAA  
 801 CGAAATCGCC CCGCGCCCGC ACAATTCCGG ACACCATACG ATAGATGCCT  
 851 GCGCAGCAGA CCAGTTCCAG CAGCAGGTAC GCATTATGTG CAACCTGCCG  
 901 CTGCCGATA CCAAATTACT GAGTTCTTGC TGTATGGCAA ATATTTTGGG  
 951 CGACGTTTGG CAGGAAGACG GCGGCGAACC GGATTGGCTG CCCTTGCAAA  
 1001 GCCATCCGAA TGCACACCTG CACCTTTACG GCAAAAAAAC CGCGCACAAA  
 1051 GGGCGGAAAA TGGGACACTT TACCGTTTGA ACCACCGATT CGGACACCGC  
 1101 ATTTCAAGAA GCAAAAAAAC TGCATCAGTC CCTATAA

This corresponds to the amino acid sequence <SEQ ID 2132; ORF 657>:

m657. pep  
 1 MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGKVTVLDP DPDAPEAEFA  
 51 DRHLCAPFND QAALDELAKE AAVTTEFENV NADAMRFLAK HTNVSPSGDC  
 101 VAIAQNRIQE KAWIRKAGLQ TAPYQVCKA EDITEASQF LPGILKTATL  
 151 GYDGKGQIRV KTLDELKAAF AEHGGVDCVL EKMVDLRSEI SVIVCRLNND  
 201 NVQTFDPAEN IHENGILAYS IVPARLSADV QQARQMAQR LADELQYVGV  
 251 LAVEMFVVD THELVVNEIA PRPHNSGHHT IDACAAADQFQ QQVRIMCNLP  
 301 PADTKLLSSC CMANILGDVW QEDGGEPDWL PLQSHNAHL HLYGKKTAHK  
 351 GRKMGHFTVL TTDSDTAFQE AKKLHQSL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m657/g657 93.9% identity in 378 aa overlap

	10	20	30	40	50	60
m657. pep	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGKVTVLDP	DPDAPEAEF	ADRHLCAPFND
g657	MNTPPILPPA	MLGILGGGQL	GRMFAVAAKT	MGKVTVLDP	DPNAPAEF	ADRHLCAPFDD
	10	20	30	40	50	60
	70	80	90	100	110	120
m657. pep	QAALDELAKE	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC	VAIAQNRIQE	KAWIRKAGLQ
g657	RAALDELAKE	AAVTTEFENV	NADAMRSLAK	HTNVSPSGDC	VSIAQNRIQE	KAWIRKAGLQ
	70	80	90	100	110	120
	130	140	150	160	170	180
m657. pep	TAPYQVCKA	EDITEASQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
g657	TAPYQAVCKA	EDITEASQFL	PGILKTATL	GYDGKGQIRV	KTLDELKAAF	AEHGGVDCVL
	130	140	150	160	170	180

1047

	190	200	210	220	230	240
m657 . pep	EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQQARQMAQR					
g657	EKMVDLRGEISVIVCRLNDENVQTFDPAENIHENGILAYSIVPARLSADVQQQARQTAQR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m657 . pep	LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP					
g657	LADEL DYVGV LAVEMFVVGDTHELLVNETAPRTHNSGHHTIDACAADQFQQQVRIMCNLP					
	250	260	270	280	290	300
	310	320	330	340	350	360
m657 . pep	PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHRNAHLHLYGKKTAKHGRKMGHFTVL					
g657	PADTKLLSPCCMANILGDVWQEDGGEPDWLPLQSRPNAHLHLYGKKTAKHGRKMGHFTVL					
	310	320	330	340	350	360
	370	379				
m657 . pep	TTDSDTAFQEAKKLHQSIX					
g657	TTDSDTAFQEAKKLHQSIX					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2133>:

a657 . seq

1	ATGAAAAACA	TATCTCTTTC	TCCGCCCGCC	ATGCTCGGCA	TTCTTGGCGG
51	CGGACAATTA	GGCAGAAATG	TTACTGTTGC	TGCCAAAACC	ATGGGCTACA
101	AAGTAACCGT	ACTCGATCCC	AACCCGAATG	CGCCCGCAGC	GGAATTTGCC
151	GACCGCCATT	TGTGTGCGCC	GTTTGACAAC	CAAACCGCTT	TGGAAGAATT
201	GGCAAAATGT	GCGGCTGTTA	CGACCGAGTT	CGAAAACGTC	AATGCCGATG
251	CGATGCGTTT	TCTCGCCAAA	CATACCAATG	TTTCCCCCAG	CGGCGACTGC
301	GTTGCCATCG	CGCAAAACCG	CATTCAGGAA	AAGGCATGGA	TACGCAAAGC
351	AGGCCTGCAA	ACCGCGCCGT	ATCAAGCAAT	TTGCAAAGCC	GAAGACATCA
401	CTGAAGAAAG	CATACAATTT	CTGCCCGGCA	TCCTGAAAAC	CGCTACATTG
451	GGCTATGACG	GCAAAGGCCA	AATCCGCGTC	AAAACGGTGG	ATGAACTCAA
501	AGCCGCGTTT	GCCGAACACC	GCGGCGTGGA	TTGCGTTTTG	GAAAAAATGG
551	TGGACTTGCG	CGGCGAAATT	TCCGTTATCG	TATGCCGCTCT	GAACAATGAC
601	AACGTGCAAA	CTTTCGATCC	TGCCGAAAAC	ATTCACGAAA	ACGGTATCCT
651	CGCCTACTCC	ATCGTCCCAG	CCCGACTGAG	TGCCGACATT	CAGCAACAGG
701	CGCGACAAAT	GGCGCAGCGT	TTGGCCGATG	AATTGAACTA	CGTCGGCGTA
751	TTGGCGGTAG	AAATGTTTGT	TGTCGGCGAC	ACGCATGAAT	TGGTCGTCAA
801	CGAAATCGCG	CCGCGTCCGC	ACAATTCCGG	CCACCATAAC	GTCGACGCCCT
851	GCGCGGCAGA	CCAATTCCAG	CAACAGGTCC	GCCTGATGTG	CAACCTGCCA
901	CCTGCTGACA	CCAAATTGCT	GAGTTCCTGC	TGTATGGCGA	ATATTTTGGG
951	CGACGTTTGG	CAGGAAGACG	GCGGCGAACC	GGATTGGTTT	CCCCTGCAAA
1001	GCCGGCCGGA	CGCGCACCTG	CACCTTTACG	GCAAAAAAAC	CGCGCACAAA
1051	GGGCGGAAAA	TGGGACACTT	TACCATTTTA	AGCACCGATT	CGGACACCGC
1101	ATTCAAGAA	GCAAAAAAAC	TGCATCAGTC	CCTATAA	

This corresponds to the amino acid sequence <SEQ ID 2134; ORF 657.a>:

a657 . pep

1	MKNISLSPPA	MLGILGGGQL	GRMFTVAAKT	MGYKVTVLDP	NPNAPAAEFA
51	DRHLCAPFDN	QTALEELAKC	AAVTTEFENV	NADAMRFLAK	HTNVSPSGDC
101	VAIAQNRIQE	KAWIRKAGLQ	TAPYQAICKA	EDITEESIQF	LPGILKTATL
151	GYDGKGQIRV	KTVDELKAAF	AEHRGVDCVL	EKMVDLRGEI	SVIVCRLNND
201	NVQTFDPAEN	IHENGILAYS	IVPARLSADI	QQQARQMAQR	LADELNYVGV
251	LAVEMFVVGDT	THELVVNEIA	PRPHNSGHHT	VDACAADQFQ	QQVRLMCNLP
301	PADTKLLSSC	CMANILGDVW	QEDGGEPDWF	PLQSRPDAHL	HLYGKKTAKH
351	GRKMGHFTIL	STDSDTAFQE	AKKLHQSIL*		

m657/a657 94.2% identity in 378 aa overlap

	10	20	30	40	50	60
m657 . pep	MKNISLSPPA MLGILGGGQL GRMFTVAAKT MGYKVTVLDP DPDAFAAEFADRHLCAFPND					



1048

```

|||||
a657  MKNISLSPPAMLGILGGGQLGRMFTVAAKTMGYKVTVLDPNPNAPAAEFADRHLCAPFDN
      10      20      30      40      50      60

      70      80      90      100     110     120
m657 . pep  QAALDELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
      |||||
a657  QTALEELAKCAAVTTEFENVNADAMRFLAKHTNVSPSGDCVAIAQNRIQEKAWIRKAGLQ
      70      80      90      100     110     120

      130     140     150     160     170     180
m657 . pep  TAPYQVVKAE DITEASAQFLPGILKTATLG YDGKGQIRVKTLD ELKAAFAEHGGVDCVL
      |||||
a657  TAPYQAICKAE DITEESIQFLPGILKTATLG YDGKGQIRVKTLD ELKAAFAEHGRVDCVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m657 . pep  EKMVDLRSEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADVQQARQMAQR
      |||||
a657  EKMVDLRGEISVIVCRLNNDNVQTFDPAENIHENGILAYSIVPARLSADIQQARQMAQR
      190     200     210     220     230     240

      250     260     270     280     290     300
m657 . pep  LADEL DYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTIDACAADQFQQQVRIMCNLP
      |||||
a657  LADEL NYVGV LAVEMFVVGDTHEL VVNEIAPRPHNSGHHTVDACAADQFQQQVRLMCNLP
      250     260     270     280     290     300

      310     320     330     340     350     360
m657 . pep  PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSHPNALHLHYGKKTAAHKGRKMGHFTVL
      |||||
a657  PADTKLLSSCCMANILGDVWQEDGGEPDWLPLQSRPDAHLHLHYGKKTAAHKGRKMGHFTIL
      310     320     330     340     350     360

      370     379
m657 . pep  TTSDS TAFQEAKKLHQSLX
      :|||||
a657  STDS D TAFQEAKKLHQSLX
      370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2135>:

```

g658 . seq
1  ATGGTGGCCG GAATTGTGCG TGC GCGGGGCG GGTTCATTG ACGAGCAATT
51  CATGTGTGTC GCCGACAACA AACATTTCTA CCGCCAAtac GCCGACATAA
101 TCCAATTCGT CCGCCAagcG TTGCGCCGTC TGCCGCGCCT GTTGCTGCAC
151 GTCGGCACTC AGCCGCGcgg gGACGATGga atAAGCCAAG ATGCCGTTT
201 CGTGGATGTT TTCGGCGGGG TCGAAGGTTT GCACGTTTTC ATCGTTCAGA
251 CGGCATACGA TCACGGAAAT CTCGCCGCGC AAGTCCACCA TTTTTCCAA
301 AACGCAATCC ACGCCGCCGT GTTCGGCAAA CGCGGCTTTG AGTTCGTCCA
351 ACGTTTTGAC GCGGATTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGTT
401 TTCAGGATGC CGGGCAAAAA TTGCGCGCTT GCTTCAGTAA TGTCTTCGGC
451 CTTGCAAACC GCCTGATACG GCGCGGTTTG CAAGCCTGCT TTGCGTATCC
501 ACGCTTTTTC CTGAATGCGG TTTTGTGCAA TGGACACGCA GTCGCCGCTG
551 GGGGAAACGT TGGTATGCTT TGCCAGAGAG CGCATCGCGT CGGCAttgac
601 gtTTTCAAAT TCGGTcgtaA CCGCCGCGCA TTTTGCCAAT TCGTCCAACG
651 CGGCCCGGTC GTCAAACGGC GCGCACAAAT GGCGGTCGGC AAATCCGCC
701 GCCGGCGCAT TCGGGTCGGG ATCGAGAACG GTTACTTTGT AGCCCATGTT
751 TTTAGCGGCA ACGGCAAACA TTctgcctAA

```

This corresponds to the amino acid sequence <SEQ ID 2136; ORF 658.ng>:

```

g658 . pep
1  MVAGIVRARG GFIDEQFMCV ADNKHFYRQY ADIIQFVRQA LRLRLPRLLLH
51  VGTQPRGDDG ISQDAVFVDV FGGVEGLHVF IVQTAYDHGN LAAQVHHFFQ

```

1049

101 NAIHAAVFGK RGFEFVQRF ADLTFVVAQ RSRFQDAGQK LRACFSNVFG  
 151 LANRLIRRGL QACFAYPRFF LNAVLCNGHA VAAGGNVGM L CQRAHRVGID  
 201 VFKFGRNRRR FCQFVQRGPV VKRRAQMAVG KFRRRRIRVG IENGYFVAHG  
 251 FSGNGKHS\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2137>:

m658 . seq  
 1 ATGGTGTCCG GAATTGTGCG GGCGCGGGGC GATTTCGTTG ACGACCAATT  
 51 CATGCGTGTC ACCGACAACA AACATTCTA CCGCCAATAC GCCGACATAA  
 101 TCCAATTCGT CCGCCAAGCG TTGCGCCATC TGCCGCGCCT GTTGCTGCAC  
 151 GTCGGCACTC AGTCGCGCGG GGACGATGGA ATAAGCCAAG ATGCCGTTTT  
 201 CGTGGATGTT TTCGGCAGGG TCGAAAGTTT GCACGTGTG ATTGTTCAAA  
 251 CGGCATACGA TTACGGAAAT TTCACTGCGC AAATCCACCA TTTTTCCTAA  
 301 AACGCAATCC ACGCCGCCGT GTTCGGCAA CGCGGCTTTG AGTTCATCCA  
 351 ATGTTTTTAC GCGGATTGA CCTTTGCCGT CGTAGCCCAA CGTAGCCGT  
 401 TTCAGGATGC CGGGCAAAA TTGCGCGCTT GCTTCAGTGA TGTCTTCAGC  
 451 CTTACAAACC ACTTGATACG GCGCGGTTTG CAATCCCGCT TTGCGTATCC  
 501 ATGCCTTTTC CTGAATGCGG TTTTGTGCAA TCGCCACACA ATCGCCGCTA  
 551 GGGGAAACAT TGGTATGTTT TGCCAAAAG CGCATCGCAT CGGCATTGAC  
 601 GTTTTCAAAT TCAGTGGTCA CCGCCGCGCA TTTTGCCAAT TCGTCCAAG  
 651 CAGCTTGGTC GTTAAACGCG GCGCACAAAT GGCGGTCGGC AAATTCTGCT  
 701 GCCGCGCGCT CCGGATCGGG GTCGAGAACG GTTACTTTGT AGCCCATGGT  
 751 TTTGGCGGCA ACGGTAAACA TTCTGCCTAA

This corresponds to the amino acid sequence <SEQ ID 2138; ORF 658>:

m658 . pep  
 1 MVSGIVRARG DFVDDQFMRV TDNKHFYROY ADIIQFVROA LRHLPRLLH  
 51 VGTQSRGDDG ISQDAVFVDV FGRVESLHV IVQTAYDYG N FTAQIHFFQ  
 101 NAIHAAVFGK RGFEFIQCFY ADLTFVVAQ RSRFQDAGQK LRACFSDVFS  
 151 LTNHLIRRGL QSRFAYPCLF LNAVLCNRHT IAARGNIGMF CQKAHRIGID  
 201 VFKFSGHRRR FCQFVQSSLV VKRRAQMAVG KFCCRRVRIG VENG YFVAHG  
 251 FGGNGKHS\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m658/g658 82.2% identity in 259 aa overlap

	10	20	30	40	50	60
m658 . pep	MVSGIVRARGDFVDDQFMRVTDNKHFYROYADIIQFVROALRHLPRLLHVG	VTQSRGDDG				
g658	MVAGIVRARGGFIDEQFMCVADNKHFYROYADIIQFVROALRRLPRLLHVG	TPRGDDG				
	10	20	30	40	50	60
m658 . pep	ISQDAVFVDVFGGRVESLHVIVQTAYDYG N FTAQIHFFQNAIHA	AVFGKRGFEFIQCFY				
g658	ISQDAVFVDVFGGVEGLHVFIVQTAYDHGNLAAQVHHFFQNAIHA	AVFGKRGFEFVQRF				
	70	80	90	100	110	120
m658 . pep	ADLTFVVAQSRFQDAGQKL	LRACFSDVFS	LTNHLIRRGLQSRFAYPCLF	LNAVLCNRHT		
g658	ADLTFVVAQSRFQDAGQKL	LRACFSNVFGLANRLIRRGLQACFAYPRFF	LNAVLCNGHA			
	130	140	150	160	170	180
m658 . pep	IAARGNIGMF	CQKAHRIGIDVFKFSGHRR	AFQFVQSSLVVKRRAQMAVG	KFCCRRVRIG		
g658	VAAGGNVGM	LQRAHRVIGIDVFKFGRNRR	AFQFVQRGPVVKRRAQMAVG	KFRRRRIRVG		
	190	200	210	220	230	240
m658 . pep	VENG YFVAHG	FGGNGKHS				
g658	VENG YFVAHG	FGGNGKHS				
	250	260				
m658 . pep	VENG YFVAHG	FGGNGKHS				

```

:|||||||:|||||
IENGYFVAHGFSNGKHSAX
      250      260

```

a658.seq

1	ATGGTGGCCG	GAATTGTGCG	GACGCGGCGC	GATTCGTTG	ACGACCAATT
51	CATGCGTGTC	GCCGACAACA	AACATTCTA	CCGCCAATAC	GCCGACGTAG
101	TTCAATTCTC	CGGCCAAACG	CTGCGCCATT	TGTCGCGCCT	GTTGCTGAAT
151	GTCGGCACTC	AGTCGGGCTG	GGACGATGTA	GTAGGCGAGG	ATACCGTTTT
201	CGTGAATGTT	TTCCGCGAGG	TCGAAAGTTT	GACAGTTGTC	ATTGTTTCAG
251	CGGCATACGA	TACCGGAAAT	TTCCGCGCGC	AAGTCACCA	TTTTTCCAA
301	AACGCAATCC	ACGCCCGCGT	GTTCCGCAAA	CGCGGCTTTG	AGTTTCATCCA
351	CCGTTTTGAC	GCGGATTTGG	CCTTTGCCGT	CATAGCCCAA	TGTAGCGGTT
401	TTTCAGGATG	CGGGCAGAAA	TTGATGTCTT	TCTTCAGTGA	TGTCTTCGGC
451	TTTGCAAATT	GCTTGATACG	GCGCGGTTTT	CAGGCCGTGCT	TTGCGTATCC
501	ATGCGCTTTT	CTGAATTCGG	TTTTGCGCGA	TGGCAACGCA	GTCGCGCGTC
551	GGGGAACAT	TGGTATGTTT	GGCGAGAAAA	CGCATCGCAT	CGGCATTGAC
601	GTTTTCGAAC	TCGGTCGTAA	CAGCCGCACA	TTTTGCCAAT	TCTTCCAAAG
651	CGGTTTGGTT	GTCAACACGG	GCACACAAAT	GGCGGTGCGC	AAATTCGCGT
701	GCCGGCGCAT	TCGGTGTGGG	ATCGAGTACG	GTTACTTTGT	AGCCCATGGT
751	TTTGGCAGCA	ACAGTAAACA	TTTGCCTTAA		

a658.pap

1	1	MVAGIVRTRR	DFVDDQFMRV	ADNKHFFYRQY	ADVVQFIGOT	LRHLSRLLLN
51		VGTSQGWDDG	VGEDTFEVNV	EGRIESLHVQ	IVGTAYDNGN	FAAQVHHFFQ
101		NAIHAAVFDG	RGFETFRHFD	ADLAFVAHQ	CSGFQDAQQK	LYAFFSDVFG
151		FANCLIRRLG	QACFAYPCLF	LNAVLRDNGA	VAAAGNIGMF	GKTHTRIGID
201		VFELGRNSRT	FCQFFQSGLV	VKRRTQMAVG	KFRCRRIRVG	IYGYFVAHG
251		EGSNSKSHA*				

m658/a658 75.3% identity in 259 aa overlap

	10	20	30	40	50	60
m658.pep	MVSGIVRARGDFVDDQFM	RVTDNKNHFYRQYADII	QFVRQALRHLPRLLLL	HHVGTQSRGDDG		
a658	MVAGIVRTRRDFVDDQFM	RVADNKNHFYRQYADV	VQFQIGQTLRHL	SRLLLLNVGTQSGWDDG		
	10	20	30	40	50	60
m658.pep	ISQDAVFVDVFG	RVESLHVIVQTAYDYGN	FTAQIHFFQNAI	HAAVFGKRGFEFI	QC	FY
a658	VGEDTVFVN	VFGRIESLHVIVQTAYD	NGNFAAQVHHFFQNAI	HAAVFGKRGFEFI	HR	FD
	70	80	90	100	110	120
m658.pep	ADLTFAVVAQSR	SFQDAGQKL	RACFSDFSLTNHL	IRRG	LSRFAYPCLFL	NAVLCNRHT
a658	ADLAFAVIAQCS	GFQDAGQKLYAFF	SDVFGFANCLIR	RGLQACFAYPCLFL	NAVLRD	GNA
	130	140	150	160	170	180
m658.pep	IAARGNIGMFCQ	KAHRIGIDVFKFSG	HRRAF	CQFVQSSLVVK	RRQA	MAVGKFCRRVRIG
a658	VAAGGNIGMFEK	THRIGIDVFLGRNS	RTFCQFFQSG	LVVKRTQ	MAVGKFCRRIR	VG
	190	200	210	220	230	240
m658.pep	VENGYFVAHG	FGGNGKHSAX				
a658	IEYGYFVAHG	FGSNSKHSAX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2141>:

g661.seq  
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT  
 51 GGCGGGCATT GCCGACAAAC CCTTCCGCCG CCTCTGTCGG GCGTTTGGCG  
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGGCCA GCGATCCGAC GCTCAGGAAT  
 151 ACCGGAAAAA CCTgcaccg cagtgaTTTt gccgatgaag gCGGCATCGT  
 201 TGCCGTGCAG ATTGCCGGCA GCGACCcga acaGATGGCG Gatgcggcgc  
 251 gttacAACGT CGGACTCGGG GCGCAGGTCA TCGACATcaa TATGGGCTGC  
 301 cccgccaaga AAGTGTGCAA CGTCCAAGCC GGTAGCGCgc tGATGCAGGA  
 351 CGAGccgctg gttgcCgcca tTTtggaggc ggtggtcAAG GCGGCGGgcy  
 401 TACCCGTTAC cctCAAAACc cgtTtgggtt ggcacgacga cgatcaaaac  
 451 ctgcCcgccg tcgccaat cgcgaagat tgcggcattg ccgccCttgc  
 501 cgttccacgg ggcCGCgcgC ACGCCAATGT ACAAAGGCGA GGCgcGTTAC  
 551 Gaactcatcg CCGAGACCAA AAGccgTCTG AACATCCCG cctGggtCAA  
 601 CGGCGACATC actTCgccc AAAAAGCCGC CGccgTCCTC AAACAAACCG  
 651 CCGCCGACGG CATCATGATA GGGCGCGCG CGCAAGGCAG GCCGTGGTTT  
 701 TTCCGCGATT TGAAGCATT TCGCGAACAC GGCCTTTTAC CGCCTGCCTT  
 751 GAGTTTGGCA GAATGCAGAG CCGCATTTT GAACCACATC CGCGCCATGC  
 801 ACGCGTTTTA TGGTGAGACC GTCGGTGTGC GCATCGCACG CAAACACATA  
 851 GGCTGGTACA TCGCGAAAT GCCCGACGGC GAACAGGCGC GCGGTGA

This corresponds to the amino acid sequence <SEQ ID 2142; ORF 661.ng>:

g661.pep  
 1 MHIGGYFIDN PIALAPMAGI ADKPFRRLCR AFGAGWAVCE MLASDPTLRN  
 51 TGKTLHRSDF ADEGGIVAVQ IAGSDPEQMA DAARYNVGLG AQVIDINMGC  
 101 PAKKVCNVQA GSALMQDEPL VAAILEAVVK AAGVPVTLKT RLGWHDHDDQN  
 151 LPAVAKIAED CGIAALAVPR ARAHANVQRR GALRTHRRDQ KPSEHPGLGQ  
 201 RRHHFAAKSR RRPQTNRRRR HHDRARRARQ AVVFRFEAL CRTRRFTACL  
 251 EFGRMQSRHF EPHPRHARVL WDRRCARHT QTHRLVHRRN ARRTTGAA\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2143>:

m661.seq  
 1 ATGCACATCG GCGGTTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT  
 51 GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG  
 101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT  
 151 ACTAGAAAAA CCTTGACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT  
 201 TGCCGTGCAG ATTGCCGGAA GCGATCCGCA GCAGATGGCG GATGCCGCGC  
 251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT  
 301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA  
 351 CGAGCCGCTG GTTGCCGCCA TTTTGAAGC CGTCGTCCGT GCGGCAGGCG  
 401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC  
 451 CTGCCCCTCA TCGCCAAAAT CGCCGAAGAT TCGGCATCG CCGCCCTTGC  
 501 CGTCC.ACGG ACGCACGCGT ACGCAAATGT ACAAAGGCGA AGCGCGTTAC  
 551 GAACTCATCG CCGAAACCAA ATGCCGTCTG AACATCCCG TCTGGGTCAA  
 601 CGGCGACATT ACTTCGCCGC AAAAAGCCCA AGCCGTCTCT AAACAAACCG  
 651 CCGCCGACGG CATTATGATA GGGCGCGCG CGCAAGGCAG GCCGTGGTTC  
 701 TTCCGCGATT TGAACATTA TGCCGAACAC GGTGTTTTGC CGCCTGCCTT  
 751 GAGTTTGGCA GAATGCGCG CCGCTATTTT GAACCACATC CGCGCCATAC  
 801 ACGCGTTTTA CCGCGACACC GCCGGTGTGC GCATCGCACG CAAACACATA  
 851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

This corresponds to the amino acid sequence <SEQ ID 2144; ORF 661>:

m661.pep  
 1 MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN  
 51 TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC  
 101 PAKKVCNVQA GSALMQNEPL VAAILEAVVR AAGVPVTLKT RLGWHDHDDQN  
 151 LPVIAKIAED CGIAALAVXR THAYANVQRR SALRTHRRNQ MPSEHPGLGQ  
 201 RRHYFAAKSP SRPQTNRRRR HYDRARRARQ AVVLPRFETL CRTRCFAACL  
 251 EFGRMRRRYF EPHPRHTRVL RRHRRCAHRT QTHRLVHRRN ARRTDTS\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m661/g661 88.5% identity in 295 aa overlap

1052

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					
g661	MHIGGYFIDNPIALAPMAGIADKPFRRLCRAFGAGWAVCEMLASDPTLRNTGKTLHRSDF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m661.pep	ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEPL					
g661	ADEGGIVAVQIAGSDPEQMADAARYNVGLGAQVIDINMGCPAKKVCNVQAGSALMQDEPL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m661.pep	VAAILEAVVRAAGVPVTLKTRLGWHDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR					
g661	VAAILEAVVKAAGVPVTLKTRLGWHDHDDQNLPVAKIAEDCGIAALAVPRARAHANVQRR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m661.pep	SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHDRARRARQAVVLPFRFETL					
g661	GALRTHRRDQKPSEHPGLGQRRHHFAAKSRRRPQTNRRRRHDRARRARQAVVFPFRFEAL					
	190	200	210	220	230	240
	250	260	270	280	290	299
m661.pep	CRTRCFAACLEFGMRMRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX					
g661	CRTRRFTACLEFGMRQSRHFEPHPRHARVLWDRRCARHTQTHRLVHRRNARRRTGAAX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2145>:

```

a661.seq
1  ATGCACATCG GCGGCTATTT TATCGACAAC CCCATCGCAC TTGCGCCGAT
51  GGCGGGCATT ACCGACAAAC CGTTCCGCCG ACTTTGCCGA GATTTTGGCG
101 CAGGTTGGGC GGTGTGCGAA ATGCTGACCA GCGACCCGAC GCTCAGAAAT
151 ACTAGAAAAA CCTTGCACCG CAGCGATTTT GCCGATGAAG GCGGCATTGT
201 TGCCGTGCAG ATTGCCGGA GCGATCCGCA GCAGATGGCG GATGCCGCGC
251 GTTACAACGT CAGCCTTGGG GCGCAGCTTA TCGACATCAA CATGGGCTGT
301 CCCGCTAAAA AAGTCTGCAA TGTCCAAGCC GGTAGCGCGC TGATGCAGAA
351 CGAGCCGCTG GTTGCCGCCA TTTTGGAGGC GGTGGTCAA GCGGCGGGCG
401 TACCCGTTAC CCTCAAAACC CGTTTGGGTT GGCACGACGA CCATCAAAAC
451 CTGCCCGTCA TCGCCAAAAT CGCCGAAGAT TGCGGCATTG CCGCCCTTGC
501 CG.TCCACGG ACGCAGCGC ACGCAAATGT ACAAAGGCGA AGCGGCTTAC
551 GACCTGATTG CCGAAACCAA ATGCCGTCTG AACATCCCGG TCTGGGTCAA
601 CGGCGACATT ACCTCGCCGC AAAAAGCCCA AGCCGTCTC AAACAAACCG
651 CCGCAGACGG CATTATGATA GGGCGCGCGC CGCAAGGCAG ACCGTGGTTC
701 TTCCGCGATT TGAAACATTA CGCCGAACAC GGTGTTTTAC CGCCTGCCTT
751 GAGTTTGGCA GAATGTACCG CCACTATTTT GAACCATATC CGAGCCATGC
801 ACGCGTTTTA CGGCGACACC GCCGGTGTGC GCATCGCAGC CAAACACATA
851 GGCTGGTACA TCGACGAAAT GCCCGACGGC GAACAGACAC GTCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2146; ORF 661.a>:

```

a661.pep
1  MHIGGYFIDN PIALAPMAGI TDKPFRRLCR DFGAGWAVCE MLTSDPTLRN
51  TRKTLHRSDF ADEGGIVAVQ IAGSDPQOMA DAARYNVSLG AQLIDINMGC
101  PAKKVCNVQA GSALMQNEPL VAAILEAVVK AAGVPVTLKT RLGWHDHQN
151  LPVIAKIAED CGIAALAXPR THAHANVQRR SGLRPDCRNQ MPSEHPGLGQ
201  RRYLAAKSP SRPQTNRRRR HYDRARRARQ TVVLPFRFETL RRTRCFTACL
251  EFGRMYRHYF EPHPSHARVL RRHRRCAHRT QTHRLVHRRN ARRTDTS*

```

m661/a661 94.6% identity in 298 aa overlap

	10	20	30	40	50	60
m661.pep	MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF					

1053

```

a661      MHIGGYFIDNPIALAPMAGITDKPFRRLCRDFGAGWAVCEMLTSDPTLRNTRKTLHRSDF
           10      20      30      40      50      60

           70      80      90      100     110     120
m661.pep  ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEFL
           |||||
a661      ADEGGIVAVQIAGSDPQOMADAARYNVSLGAQLIDINMGCPAKKVCNVQAGSALMQNEFL
           70      80      90      100     110     120

           130     140     150     160     170     180
m661.pep  VAAILEAVVRAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAVXRTHAYANVQRR
           |||||:|||||
a661      VAAILEAVVKAAGVPVTLKTRLGWHDDHQNLPVIAKIAEDCGIAALAXPRTHAHANVQRR
           130     140     150     160     170     180

           190     200     210     220     230     240
m661.pep  SALRTHRRNQMPSEHPGLGQRRHYFAAKSPSRPQTNRRRRHYDRARRARQAVVLPREFETL
           |:| |||||:|||||
a661      SGLRPDCRNQMPSEHPGLGQRRHYLAAKSPSRPQTNRRRRHYDRARRARQTVVLPREFETL
           190     200     210     220     230     240

           250     260     270     280     290     299
m661.pep  CRTRCFAACLEFGRMRRRYFEPHPRHTRVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           |||||:|||||:|||||
a661      RRTRCFACLEFGRMYRHYFEPHPSHARVLRHRRCAHRTQTHRLVHRRNARRRTDTSX
           250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2147>:

```

g663.seq
1  ATGTGTACCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGGCCTGATC GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGGA CGAAGAAAAG CGTAAACCG TGTGAAACA
201 GCATTTCAAA CACATGGCAA AACTGATGCT CGAATACGGC TTATATTGGT
251 ACGCGtctGC CAAATGCCTG AAATCGCTGG TGCCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTACCC
351 GCACTTTACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATGTCC
401 CGCTGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAg gccgcaACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAagggctg cgCGCCctcg TCAAACAGTT CCGCAAAAGC AGTGCGCCGT
551 TCCTGTATCT GCCCGATCAG GATTCGGAC GCAACAATTC GGTTTTTGTG
601 GATTTTTTCG GCATtcagac GGCAACGATT ACGGCTTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCCGC CATTCCCCTC CGCGAGGCGG
701 ACAATACGGT TACATTGCAA TTCTATCCCG CTGGAAATC CTTTCCGAGT
751 GAAGACGCGC AAGCCGACGC GCAACGTATG AACCGCTTA TCGAAGAACG
801 CGTGCCGCAA CACCCGGAAC AATATTCTG GCTGCACAAG CGTTTCAAAA
851 CCCGTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2148; ORF 663.ng>:

```

g663.pep
1  MCTEMKFIFF VLYVLOFLPF ALLHKIAGLI GSLAYLLVKP RRRIGEINLA
51  KCFPEWDEEK RKTVLKQHFH HMAKLMLEYG LYWYASAKCL KSLVRYRNKH
101 YLDDALAAGE KVILYPHFT AFEMAVYALN QDVPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRRNSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAIPV READNTVTIQ FYPAWSFPS
251 EDAQADAQRM NREIEERVRE HPEQYFWLHK RFKTRPEGSP DEFY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2149>:

```

m663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51  TCTGCCGTTT GCGCTGCTGC ACAAGATTGC CGACCTGACG GGTTCGCTTG
101 CCTACCTTCT GGTCAAACCG CGCCGCCGTA TCGGCGAAAT CAATTGGCA
151 AAATGTTTTT CCGAATGGAG TGAGGAAAAG CGTAAACCG TGTGAAACA

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1054

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201 GCATTTCAAA CACATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACGCGCCTGC CGGACGTTTG AAATCGCTGG TCGCTACCG CAATAAGCAT
301 TATTTGGACG ACGCGCTGGC GCGGGGGGAA AAAGTCATCA TCCTGTATCC
351 GCACTTCACC GCGTTCGAGA TGGCGGTGTA CGCGCTTAAT CAGGATATCC
401 CGCTGATCAG TATGTATTCC CATCAAAAAA ACAAGATATT GGACGAACAG
451 ATTTTGAAAG GCCGCAACCG CTATCACAAC GTCTTCCTTA TCGGGCGCAC
501 CGAAGGGCTG CGCGCCTCG TCAAACAGTT CCGCAAAGC AGCGCGCCGT
551 TTCTGTATCT GCCCGATCAG GATTCGGAC GCAACGATTG GGTTTTGTG
601 GATTTTTTCG GTATTCAGAC GGCAACGATT ACCGGATTGA GCCGCATTGC
651 CGCGCTTGCA AATGCAAAAG TGATACCGC CATTCCCGTC CGCGAGGCAG
701 ACAATACGGT TACATTGCAT TTCTACCCTG CTTGGAAATC CTTTCCGGGT
751 GAAGACGCGA AAGCCGACGC GCAGCGCATG AACCGTTTTA TCGAAGACAG
801 GGTGCGCGAA CATCCGGAAC AATATTTTG GCTGCACAAG CGTTTAAAAA
851 CCCGTCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2150; ORF 663>:

```

m663.pep
1  MCIEMKFIFF VLYVLQFLPF ALLHKIADLT GLLAYLLVKP RRRIGEINLA
51 KCFSEWSEEK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDIPLISMYS HQKNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGRNDSVFV
201 DFFGIQTATI TGLSRIAALA NAKVIPAI PVREADNTVT LH FYPAWSFPG
251 EDAKADAQRM NRFIEDRVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m663/g663 94.9% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKIADLTGLLAYLLVKP RRRIGEINLAKCFSEWSEEK					
g663	MCTEMKFIFFVLYVLQFLPFALLHKIAGLIGSLAYLLVKP RRRIGEINLAKCFPEWDEEK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHYLDDALAAGEKVIILYPHFT					
g663	RKTVLKQHFHMAKLMLEYGLYWYASAKCLKSLVRYRNKHYLDDALAAGEKVIILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDIPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
g663	AFEMAVYALNQDVPLISMYS HQKNKILDEQILKGRNRYHN VFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
g663	SAPFLYLPDQDFGRNDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LQ					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
	FYPAWSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
g663	FYPAWSFPGEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2151>:

```

a663.seq
1  ATGTGTATCG AGATGAAATT TATATTTTTT GTACTGTATG TTTTGCAGTT
51 TCTGCCGTTT GCGCTGCTGC ACAAACCTGC TGATCTGACA GGCTTGCTCG
101 CCTACCTTTT GGTCAAACCC CGCCGCCGTA TCGGCGAAAT CAATTTGGCA

```

```

151 AAA.TGCTTTC CCGAGTGGGA CGGAAAAAAG CGTAAACCG TGTGAAACA
201 GCA.TTTCAA CATATGGCGA AACTGATGTT GGAATACGGT TTATATTGGT
251 ACG.CGCCCCG CGGGCGTTTG AAATCACTGG TCGCTACCG CAACAACAT
301 TAT.TTGGACG ACGCTCTGGC GGCAGGGGAA AAAGTCATCA TCCTGTATCC
351 GCA.CTTACCC GCGTTCGAGA TGGCGGTGTA CGCGCTCAAT CAGGATGTTT
401 CGC.TGATCAG TATGTATTCC CACCAAAAAA ACAAGATATT GGACGAACAG
451 ATT.TTGAAAG GCCGCAACCG CTATCACAAAC GTTTTCCTTA TCGGGCGCAC
501 CGA.AGGGCTG CGCGCCCTCG TCAAACAGTT CCGCAAAAGC AGCGCGCCGT
551 TTC.TGTATCT GCCCGATCAG GATTTCGGAC GCAACGATTG GGTTTTGTG
601 GAT.TTCTTCG GTATTTCGGAC GGCAACGATT ACCGGCTTGA GCCGCATTGC
651 CGC.GCTTGCA AATGCAAAAG TGATACCCGC CATCCCTGTC CGCGAGGCGG
701 ACA.ATACGCT TACATTGCAT TTCTACCCCTG CTTGGGAATC CTTTCCGAGT
751 GAA.GATGCCG AGGCCGACGC GCAGCGCATG AACCCTTTTA TCGAGGAACG
801 CGT.GCGCGAA CATCCCGAGC AGTATTTTGT GCTGCACAAG CGTTTCAAAA
851 CCC.GTCCGGA AGGCAGCCCC GATTTTACT GA

```

This corresponds to the amino acid sequence <SEQ ID 2152; ORF 663.a>:

a663.pep

```

1 MCIEMKFIFF VLYVLQFLPF ALLHKLADLT GLLAYLLVKP RRRIGEINLA
51 KCFPEWDGKK RKTVLKQHFH HMAKLMLEYG LYWYAPAGRL KSLVRYRNKH
101 YLDDALAAGE KVIILYPHFT AFEMAVYALN QDVPLISMYS HQNKILDEQ
151 ILKGRNRYHN VFLIGRTEGL RALVKQFRKS SAPFLYLPDQ DFGNRDSVFV
201 DFFGIRTATI TGLSRIAALA NAKVIPAI PV READNTVT LH FYPWESFSP
251 EDAQADAQRM NRFIEERVRE HPEQYFWLHK RFKTRPEGSP DFY*

```

m663/a663 96.2% identity in 293 aa overlap

m663.pep	10	20	30	40	50	60
	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFSEWSEEK					
a663	MCIEMKFIFFVLYVLQFLPFALLHKLADLTGLLAYLLVKPRRRIGEINLAKCFPEWDGKK					
	10	20	30	40	50	60
m663.pep	70	80	90	100	110	120
	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYDDALAAGEKVIILYPHFT					
a663	RKTVLKQHFHMAKLMLEYGLYWYAPAGRLKSLVRYRNKHLYDDALAAGEKVIILYPHFT					
	70	80	90	100	110	120
m663.pep	130	140	150	160	170	180
	AFEMAVYALNQDPLISMYS HQNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
a663	AFEMAVYALNQDPLISMYS HQNKILDEQILKGRNRYHNVFLIGRTEGLRALVKQFRKS					
	130	140	150	160	170	180
m663.pep	190	200	210	220	230	240
	SAPFLYLPDQDFGNRDSVFVDFFGIQTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
a663	SAPFLYLPDQDFGNRDSVFVDFFGIRTATITGLSRIAALANAKVIPAI PVREADNTVT LH					
	190	200	210	220	230	240
m663.pep	250	260	270	280	290	
	FYPAWKSFPGEDAKADAQRMNRFIEDRVREHPEQYFWLHKRFKTRPEGSPDFYX					
a663	FYPAWESFSEDAQADAQRMNRFIEERVREHPEQYFWLHKRFKTRPEGSPDFYX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2153>:

g664.seq

```

1 ATGATACATC CGCACCCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT
51 AGAAATTGTT CATCTCCTCA TAGCTGAcgg gCGGCACCGG ATGGGCGGTC
101 GGGCCTGCGT CTTGGGGGAA CTGGTTCTGG CGCAGCAGGC GGATGTTCTC
151 GATGCGGCGC ACGGCGCGGC CGGCGCGGTC GCCGAAAAAC TCTTGGTCGC
201 GGAACACGGT CAGCCCTTCC TTCAGCGAAA GCTGGAACCA GTCGCGGCAG
251 GTTACGCGGT TGCCCGTCCA GTTGTGAAA TATTCTGTGC CGACCACGGA
301 TTCAATGCCT TCGAAATCGG TATCGGTGGC GGTGCGGCTG TCGCGGAGGA
351 CGAACTTGGT GTTAAAAATG TTCAAACCTT TGTTTTCCAT CGCGCCATA
401 TTGAAATCGC CTACGGCGAC GACCATGAaa atatccaagt cataTTCcaa
451 cCgaagcgc gtttcgtcCc acttcacgc gTTTTTCAA cgaTTCACG
501 GCAAAGCCGA CCTTGGGTTT GTCCGCTTCG GTGGTGTAaa ACTCGATTTT

```



g664.pcp

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2155>:

**m664.seq**

**This corresponds to the amino acid sequence <SEQ ID 2156; ORF 664>:**

m664.pcp

1 VIHPHYFRAF FINGHGV EIV HLLIAGGAHR MGGRACVFGE LVLAQQADV F  
51 DAAHGAAGAV AGKFLVAEHG QPFLQRKLEP VAAGYAVARP VVEILVSDHG  
101 FDAFEIGIGG GAAVGKDELG VKDVQTLVFH RAHIEIAHGD DHENIQVVFQ  
151 TEARFVPFHR VFXTIPQSR PWACPLRWCK TRF\*

**Computer analysis of this amino acid sequence gave the following results:**

### Homology with a predicted ORF from *N. gonorrhoeae*

**m664/g664 91.8% identity in 183 aa overlap**

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2157>:

a664.seq

1 GTGATACATC CGCACCACCTT CCGCGCCTTT TTCATAAACG GTCATGGTGT  
51 AGAAATTGTT CATCTCCTCA TATCGGGCGG GCGCACCAGG ATGTGCCGTC  
101 GGACCTGCGT CTTGCGGGAA CTGGTGCTGG CGCAGCAGGC GGATGTTTTT  
151 GATACGGCGC ACGGCGCGGC TGGCGCGGTC GCCGAAAAAT TCTTGTCGCG

```

2 01 GGAACACGGT CAACCCTTCC TTCACGAAA GCTGGAACCA GTCGCGGCAG
2 51 GTCACGCGGT TGCCCGTCCA GTTGTGAAA TATTCGTGTC CGACCACGGA
3 01 TTCGATGCCT TCAAAATCGG TATCGGTGGC GGTACGGCTG TCGGCAAGGA
3 51 CGAACTTGGT GTTAAAGATG TTCAAACCCT TGTTTTCCAT CGCACCATA
4 01 TTGAAATCGC CCACGGCGAC GACCATGAAA ATATCCAAGT CGTATTCCAA
4 51 ACCGAAGCGC GTTTCGTCCC ACTTCATTGC GTTTTT.CAG CGATTCCACG
5 01 GCAAAGCCGA CCTTGGGCTT GTCCGCTTCG GTGGTGTAAA ACTCGATTTT
5 51 GA

```

This corresponds to the amino acid sequence <SEQ ID 2158; ORF 664.a>:

```

a664.pep
1  VIHPHHFRAF FINGHGVEIV HLLISGGAHR MCGRTCVEGE LVLAQQADV
51  DTAHGAAGAV AGKFLVAEHG QPFLQKLEP VAAGHAVARP VVEIFVSDHG
101 FDAFKIGIGG GTAVGKDELG VKDVQTLVFH RTHIEIAHGD DHENIQVVFQ
151 TEARFVPLHC VFXAIPRQSR PWACPLRWCK TRF*

```

m664/a664 92.9% identity in 183 aa overlap

```

m664.pep      10      20      30      40      50      60
VIHPHYFRAFFINGHGVEIVHLLIAGGAHRMGRACVFGELVLAQQADVFDAHGAAGAV
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a664          10      20      30      40      50      60
VIHPHHFRAFFINGHGVEIVHLLISGGAHRMCGRTCVEGE LVLAQQADVFDTAHGAAGAV

m664.pep      70      80      90     100     110     120
AGKFLVAEHGQPFLQKLEPVAAGYAVARPVVEILVSDHGFDAFEIGIGGGAAGVKDELG
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a664          70      80      90     100     110     120
AGKFLVAEHGQPFLQKLEPVAAGHAVARPVVEIFVSDHGFDAFKIGIGGGTAVGKDELG

m664.pep     130     140     150     160     170     180
VKDVQTLVFHRAHIEIAHGDDHENIQVVFQTEARFVPFHRVEXTIPQRSRPWACPLRWCK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a664         130     140     150     160     170     180
VKDVQTLVFHRTHEIAHGDDHENIQVVFQTEARFVPLHCVFXAIPRQSRPWACPLRWCK

m664.pep      TRFX
||||
a664          TRFX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2159>:

```

g665.seq
1  atgaagtGg acgaaacgcg cttcgGgttg GAAatgact tggatatttt
51  CATGGTCGTC GCCGTAGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT TTTTAACACC AAGTTCGTCC TCGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCGAAGG CATTGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAGTT TTCCGGCGAC
301 CGCGCCGGCC GCGCCGTGCG CCGCATCGAG AACATCCGCC TGCTGCGCCA
351 GAACCACTTC CCCGAAGACG CAGGCCCGAC CGCCCATCCG GTGCGCcccg
401 TCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGGCGGAT GTATCATACC CTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGC ATGAAGCTAT ATTTcCaacg CCACGACGGA CAGGCAGTGA
551 CCTGCGACGA TTTCCGCGCG GCGatggcgg ATGCGAACGG CATCAATCTC
601 GACCACTTCG CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAAGC
651 CGAAGGCCGT CTGAAAAACA ATGTTTTTGA GTTAACCATT AAACAAACCG
701 TGCCGCCAC GCCCGATATG GCGGACAAAC AGCCGATGAT GATTCCCGTC
751 AAAGTCGGGC TTCTGAACCG CAACGGCGAA GCGGTGGCAT TCGATTATCA
801 GGGCAAAACG GCAACCGAAG CCGTGTTCCT GATGACCGAA GCCGAACagg
851 CCTTCCCGCT CGAAGGTGTA ACCGAAGCGG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCAGTGTA TCTGAACAT CCGTACAGCG ACGACGACCT
951 GCTGCTCCTG CTCGCCACG ACAGCGACG TTTACAGTGC TGGGAAGCCG

```

```

10 01 CCAAACGCT CTACCGTCGC GCCGTCGCG CCAACCTTGC CGCGCTTTCA
10 51 GACGGCATCG GGTGCCGAA ACACGAAAA CTGCTTGCCG CCGTCGAAAA
11 01 AGTCATTTC GACGACCTCT TGGACAACGC CTTCAAAGCC CTGCTTTTGG
11 51 GCGTGCCGTC CGAAGCCGAA ctGTGGGACG GCACGAAAA CATcgaCCCG
12 01 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGtcCG
12 51 CttcctgcCG AAATGGCAGC AATTGGaccg tcaggcggcg aagCaggaaa
13 01 accaaagtTA CGAATACAGC CCCGAAACCG CCGACTGGCG CACGCTGCGC
13 51 AACGTCTGCC GCGCCTtcgt cctGCGCGCC GACCCGCGC acatcgAAAC
14 01 TGTGCCGAA Aaatacggcg AAATGGCGCA AAACATGACC CACGAATGGG
14 51 GCATCCTGTC CGCCGTCAAC GGCAACGAAA GCGATACGCG CAACTGCCTG
15 01 CTGGCGCAGT TTGCCGacaa gTtttcAGAC GACGCGCTGG TGATGGACAA
15 51 ATATTTCCGCC CTTATCGGCT CAAGccgccc cagCGACACC CTGCAACAGG
16 01 TTCAAACCGC CTTGCAGCAT CCGAAATTCA GTCTCGAAAA CCCCAACAAA
16 51 GCCCGTTTCG TCATCGGCAG CTTGAGCCGC AACGTCCCGC ATTTTCACGC
17 01 ACAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
17 51 ACCGCTTCAA cCCGcAggtc gccGCCCGCC TGGTGCAGGC GTTCAACCTC
18 01 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TTgGTGAAAC AAGAATTGCA
18 51 GTGCATTCCG GCGCAGGAAG GATTGTCGAA AGacGTGGGC GAaatcgtCG
19 01 GCAAGATTTT GGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2160; ORF 665.ng>:

g665.pep

```

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFLVADSRTA
51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RAGRAVRRIE NIRLLRQNF PEDAGPTAHP VRPVSYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNVFELTI KQTVPTTDPD ADKQPMPIPV
251 KVGILLNRNGE AVAFDYQGRK ATEAVLLMTE AEQAFPLEGV TEAVVPSLLR
301 GFSAPVYLYN PYSDDDLLLL LAHDSDAFTC WEAQTLYRR AVAANLAALS
351 DGIGLPKHEK LLAAVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGTENIDP
401 LRYHQAREAL LDTLAVRFLP KWHELDROAA KQENQSYEYS PETADWRTLRL
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNMH HEWGILSAVN GNESDTRNCL
501 LAQFADKFSF DALVMDKYFA LIGSSRRSDT LQQVQTALQH PKFSLENPNK
551 ARSLIGSFSR NVPHFHAQDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQELQCIR AQEGLSKDVG EIVGKILG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2161>:

m665.seq

```

1 ATGAAATGGG ACGAAACGCG CTCGGTTTG GAATACGACT TGGATATTTT
51 CATGGTCGTC GCCGTGGGCG ATTTCAATAT GGGCGCGATG GAAAACAAGG
101 GTTTGAACAT CTTTAAACACC AAGTTTCGTCC TTGCCGACAG CCGCACC GCC
151 ACCGATACCG ATTTCAAGAG CATCGAATCC GTGGTCGGAC ACGAGTATTT
201 CCACAACCTG ACGGGCAACC GCGTAACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGCTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 CGCGCCAGCC GCGCGTGC GCGCATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAGACG CAGGCCCCGAC CGCCCATCCG GTGCGCCCCG
401 CCAGCTATGA GGAGATGAAC AATTTCTACA CCATGACCGT TTATGAAAAA
451 GCGCGCGAAG TAGTGCAGAT GTATCACACC CTGCTCGGCG AAGAGGGCTT
501 CCAGAAAGGC ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCGGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGCGG ACGCGAACGG CATCAATCTC
601 GACCAGTTCG CTTGTGGTA CAGCCAGGCG GGCACGCCCG TTTTGGAAAGC
651 GGAAGGTCGT CTGAAAAACA ATATTTTCGA GTTGACCGTC AAACAAACCG
701 TGCCGCCAC GCGGATATG ACGGATAAAC AGCCGATGAT GATTCCCGTC
751 AAGGTCGGGC TGCTGAACCG CAACGGCGAA GCGGTGGCAT TCGACTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CCTTCCTGCT CGAAGCGGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGTGCA TCTGAACAT CCGTACAGCG ACGACGACCT
951 CTGCTCCTG CTCGCCATG ACAGCGACG CTTACGCGC TGGGAAGCCG
1001 CCAAACGCT CTACCGCCGC GCCGTCGCG CCAACCTTGC CACGCTTTCA
1051 GACGGCGTTG AGCTGCCGAA ACACGAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTC GACGACCTCT TAGACAACGC CTTCAAAGCC CTGCTTTTGG
1151 GCGTGCCATC CGAAGCCGAG CTGTGGGACG GCGCAGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATACGC TTGCCGTCCA
1251 CTTCTGCCG AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAATACAGC CCCGAAGCCG CCGGCTGGCG CACGCTGCGC

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```

13 51 AACGTCTGCC GCGCCTTTGT CCTGCGCGCC GACCCCGCGC ACATCGAAAC
14 01 CGTTGCCGAA AAATACGGCG AAATGGCGCA AACATGACC CACGAATGGG
14 51 GCATCCTGTC CGCGCTCAAC GGCAACGAAA GCGATACGCG CAACCGCCTG
15 01 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA
15 51 ATATTTTGCC CTCGTCGGCT CAAGCCGCGG CAGCGACACC CTGCAACAGG
16 01 TTCGAACCGC CTTGCAGCAT CCGAAATTCA GCCTCGAAAA CCCCAACAAA
16 51 GCCCGTTTCG TCATCGGCAG CTTAGCCGCG AACGTCCCGC ATTTCCACGC
17 01 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG
17 51 ACCGCTTCAA CCCGAGGTC GCCGCCGCT TAGTGCAGGC GTTCAACCTC
18 01 TGCAACAAGC TCGAGCGCA CCGCAAAAC TTGGTGAAAC AAGCATTGCA
18 51 GCGCATTCGG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG
19 01 GCAAAATTTT GGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2162; ORF 665>:

```

m665.pep
  1 MKWDETRFGL EYDLDFMVV AVGDFNMGM ENKGLNIFNT KFLVADSRTA
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD
101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPASYEEMN NFYTMTVYEK
151 GAEVVRMYHT LLGEEGFQKG MKLYFQRHDG QAVTCDDFRA AMADANGINL
201 DQFALWYSQA GTPVLEAAGR LKNNIFELTV KQTVPTPDM TDKQPMIIPV
251 KVGLLNRNGE AVAFDYQGR ATEAVLLTE AEQTFLLGV TEAVVPSLLR
301 GFSAPVHLNY PYSDDDL LLAHDSDAFTR WEAQAQTL YRR AVAANLATLS
351 DGVELPKHEK LLAIVEKVIS DDLLDNAFKA LLLGVPSEAE LWDGAENIDP
401 LRYHQAREAL LDTLAVHFLP KWHELNROQA KOENQSYEYS PEAAGWRTL R
451 NVCRAFLVLA DPAHIETVAE KYGEMAQNMT HEWGILSAVN GNESDTRNRL
501 LAQFADKFS DALVMDKYFA LVGSSRRSDT LQQVRTALQH PKFSLENPNK
551 ARSLIGSFSR NVPFHAEADG SGYRFIADKV IEIDRFNPQV AARLVQAFNL
601 CNKLEPHRKN LVKQALQRIR AQEGLSKDVG EIVGKILD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m665/g665 96.1% identity in 637 aa overlap

```

m665.pep      10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIES
|||||
g665          10      20      30      40      50      60
MKWDETRFGL EYDLDFMVVAVGDFNMGMENKGLNIFNTKFLVADSRTATDTDFEGIES

m665.pep      70      80      90      100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF
|||||
g665          70      80      90      100     110     120
VVGHEYFHNW TGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQNF

m665.pep     130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG
|||||
g665         130     140     150     160     170     180
PEDAGPTAHPVRPASYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHDG

m665.pep     190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM
|||||
g665         190     200     210     220     230     240
QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTVPTPDM

m665.pep     250     260     270     280     290     300
TDKQPMIIPVKVGLLNRNGEAVAFDYQGRATEAVLLTEAEQTFLLGVTEAVVPSLLR
:|||||
g665         250     260     270     280     290     300
ADKQPMIIPVKVGLLNRNGEAVAFDYQGRATEAVLLMTEAEQAFPLEGVTEAVVPSLLR

```

1060

	310	320	330	340	350	360
m665.pep	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTWEAAQTLRYRAVANLATLSDGVELPKHEK					
g665	GFSAPVYLNYPYSDDDLLLLLAHDSDAFTCWEAAQTLRYRAVANLAALSDGIGLPHKEK					
	310	320	330	340	350	360
	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNFAKALLLGVPEAEWDGAENIDPLRYHQAREALLDTLAVHFLP					
g665	LLAAVEKVISDDLLDNFAKALLLGVPEAEWDGTENIDPLRYHQAREALLDTLAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNQAAKQENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNM					
g665	KWHELDQAAKQENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNM					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQH					
g665	HEWGILSAVNGNESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFSRNVPHFHAEDGSGYRFIADKVIEIDRFNPQVAARLVQAFNL					
g665	PKFSLENPNKARSLIGSFSRNVPHFHAQDGSYRFIADKVIEIDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
g665	CNKLEPHRKNLVKQELQIRAQEGLSKDVGEIVGKILGX					
	610	620	630			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2163>:

```

a665.seq
1  ATGAAGTGGG ACGAAACGCG CTCGGTTTG GAATACGACT TGGATATTTT
51  CATGGTCGTC GCCGTGGGCG ATTCAATAT GGGTGCATG GAAAACAAGG
101 GTTTGAACAT CTTTAACACC AAGTTCGTCC TTGCCGACAG CCGTACCGCC
151 ACCGATACCG ATTTTGAAGG CATCGAATCC GTGGTCGGAC ACGAATATTT
201 CCACAACCTGG ACGGGCAACC GCGTGACCTG CCGCGACTGG TTCCAGCTTT
251 CGCTGAAGGA AGGGTTGACC GTGTTCCGCG ACCAAGAATT TTCCGGCGAC
301 GCGCCAGCC GCGCCGTGCG CCGTATCGAA AACATCCGCC TGCTGCGCCA
351 GCACCACTTC CCCGAAGACG CAGGTCCGAC CGCACATCCG GTGCGCCCGC
401 CCCGATATGA GGAGATGAAC AATTCTACA CCATGACCGT TTATGAAAAA
451 GGCGCGGAAG TGGTGGCGAT GTATCACACC TTGCTCGGCG AAGAGGGCTT
501 CCAAAAAGGT ATGAAGCTCT ATTTCCAACG CCACGACGGA CAGGCTGTTA
551 CCTGCGACGA TTTCCGCGCG GCGATGGTGG ACGCGAACGG CATCAACCTC
601 GACCAATTCG CTTGTGGTA CAGCCAAGCA GGTACGCCGG TTTTAGATGC
651 TCAAGGGCGT CTGAAAAACA ATGTGTTTCA GTTAACCATC AAACAAACCG
701 TGCCGCCAC GCGCGATATG GCGGACAAAC AGCCGATGAT GATTCCGTC
751 AAAATCGGGC TGCTGAACTG CAACGGCGAA GCGGTGGCAT TTGATTATCA
801 GGGCAAACGC GCGACCGAAG CCGTGTGCT GCTGACCGAA GCCGAACAGA
851 CTTTCAGTT CGAAAGCGTA ACCGAAGCCG TCGTTCCTC GCTGCTGCGC
901 GGGTTCAGCG CGCCGGTGCA TCTGAATAT CCGTACAGCG ACGACGACCT
951 GCTGCTTCTG CTCGCCCATG ACAGCGACGC CTTACGCGC TGGGAAGCCG
1001 CACAAACGCT CTACCGCCGT GCCGTGCGCG CCAACCTTG CGCGCTTTCA
1051 GACGGCGTCG AGTTGCCGAA ACACGAAAAA CTGCTTGCCG CCGTCGAAAA
1101 AGTCATTTC GACGACCTCT TAGACAACGC TTTCAAAGCC CTGCTTTTGG
1151 GTGTGCCGTC TGAAGCCGAG CTGTGGGACG GCGCGGAAAA CATCGACCCG
1201 CTGCGCTACC ATCAGGCGCG CGAAGCCTTG TTGGATATAC TTGCCGTCCG
1251 CTTTCTGCCG AAATGGCAGC AATTGAACCG TCAGGCGGCG AAGCAGGAAA
1301 ACCAAAGCTA CGAGTACAGC CCCGAAGCCG CCGGTTGGCG CACGCTGCGC
1351 AATGTCTGCC GCGCCTTCGT CTGCGCGCC GATCCGCGC ACATCGAAAC

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1401 CGTTGCCGAG AAATACGCCG AAATGGCGCA AAACATGACC CACGAATGGG  
 1451 GCATCCTGTC CGCGTCAAC GGCAACGAAA GCGATACCGG CAACCGCCTG  
 1501 CTGGCGCAGT TTGCCGACAA GTTTTCAGAC GACGCGCTGG TGATGGACAA  
 1551 ATATTTCGCC CTCGTCGGCT CAAGCCGCCG CAGCGACACC CTGCAACAGG  
 1601 TTCAAACCGC CTTGCAGCAT CCGAAGTTCA GCCTCGAAAA TCCCAACAAA  
 1651 GCCCGCTCGC TCATCGGCAG CTTACGCCGC AACGTCCCGC ATTTCCACGC  
 1701 AGAAGACGGC AGCGGCTACC GCTTCATCGC CGACAAAGTC ATCGAAATCG  
 1751 ACCGCTTTAA CCCGAGGTC GCCGCCGCCG TGGTGCAGGC GTTCAACCTC  
 1801 TGCAACAAGC TCGAGCCGCA CCGCAAAAC TGGTGAAAC AAGCATTGCA  
 1851 GCGCATTGCG GCGCAGGAAG GATTGTCGAA AGACGTGGGC GAAATCGTCG  
 1901 GCAAAATTTT GGATTGA

This corresponds to the amino acid sequence <SEQ ID 2164; ORF 665.a>:  
 a 665.pep

1 MKWDETRFGL EYDLDFMVV AVGDFNMGAM ENKGLNIFNT KFVLADSRTA  
 51 TDTDFEGIES VVGHEYFHNW TGNRVTCRDW FQLSLKEGLT VFRDQEFSGD  
 101 RASRAVRRIE NIRLLRQHOF PEDAGPTAHP VRPARYEEMN NFYTMTVYEK  
 151 GAEVVRMYHT LLGEEGFQKG MKLYFORHDG QAVTCDDFRA AMVDANGINL  
 201 DQFALWYSQA GTPVLDAQGR LKNNVFELTI KQTVPTPDM ADKQPMMPV  
 251 KIGLLNCNGE AVAFDYQGR ATEAVLLLE AEQTFQFESV TEAVVPSLLR  
 301 GFSAPVHLNY PYSDDDLLLL LAHDSDAFTR WEAQTLRYR AVAANLAALS  
 351 DGVELPKHEK LLAAVEKVIS DDLNDNAFKA LLLGVPSEAE LWDGAENIDP  
 401 LRYHQAREAL LDILAVRFLP KWHELNQAAA KOENQSYEYS PEAAGWRTLR  
 451 NVCRAFLVRA DPAHIETVAE KYAEMAQNMN HEWGILSAVN GNESDTRNRL  
 501 LAQFADKFSD DALVMDKYFA LVGSSRRSDT LQQVQTALQH PKFSLENPNK  
 551 ARSLIGSFSR NVPHFAEDG SGYRFIADKV IEIDRFNPQV AARLVQAFNL  
 601 CNKLEPHRKN LVKQALQIR AQEGLSKDVG EIVGKILD\*

m665/a665 97.3% identity in 638 aa overlap

m665.pep	10	20	30	40	50	60
a665	MKWDETRFGLEYDLDIFMVVAVGDFNMGAMENKGLNIFNTKFVLADSRATD					
m665.pep	70	80	90	100	110	120
a665	VVGHEYFHNWVTGNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHOF					
m665.pep	130	140	150	160	170	180
a665	PEDAGPTAHPVRPARYEEMN NFYTMTVYEKGAEVVRMYHTLLGEEGFQKG MKLYFORHDG					
m665.pep	190	200	210	220	230	240
a665	QAVTCDDFRAAMADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTVPTPDM					
m665.pep	250	260	270	280	290	300
a665	TDKQPMMPVVKVGLLRNGEAVAFDYQGRATEAVLLLTEAEQTFLEGVTEAVVPSLLR					
m665.pep	310	320	330	340	350	360
a665	GFSAPVHLNYPYSDDDLLLLLAHDSDAFTRWEAAQTLRYRAVANLATLSDGVELPKHEK					

	370	380	390	400	410	420
m665.pep	LLAAVEKVISDDLLDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDTLAVHFLP					
a665	LLAAVEKVISDDLLDNAFKALLLGVPSEAEIWDGAENIDPLRYHQAREALLDILAVRFLP					
	370	380	390	400	410	420
	430	440	450	460	470	480
m665.pep	KWHELNROAAKQENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEYKQEMAQNMT					
a665	KWHELNROAAKQENQSYEYSPEAGWRTLNRNVCRAFLRADPAHIETVAEYKQEMAQNMT					
	430	440	450	460	470	480
	490	500	510	520	530	540
m665.pep	HEWGILSAVNGNESDTRNRLAQFADKFSDDALVMDKYFALVGSSRRSDTLQOVRTALQH					
a665	HEWGILSAVNGNESDTRNRLAQFADKFSDDALVMDKYFALVGSSRRSDTLQOVQRTALQH					
	490	500	510	520	530	540
	550	560	570	580	590	600
m665.pep	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEDRFNPQVAARLVQAFNL					
a665	PKFSLENPNKARSLIGSFNRNVPFHAEADGSGYRFIADKVIEDRFNPQVAARLVQAFNL					
	550	560	570	580	590	600
	610	620	630	639		
m665.pep	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
a665	CNKLEPHRKNLVKQALQIRAQEGLSKDVGEIVGKILD					
	610	620	630			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2165>:

g665-1.seq

```

1  ATGAGCAAAA CCGTCCGTTA TCTGAAAGAT TACCAAAACG CTGCCTACCG
51  CATTCTTGAA ACCGAAGTGC ATTTCGACAT TGCCGAACCG CAAACCGTGC
101 TGAAGTCGCG TTTGACGCTC GAGCCGCGA GCGCGGGCGA GCCGCTGGTG
151 TTGGACGGTT CGGCAAAACCT CTTGTCCGTC AAAATCAACG GCGCGGGCGG
201 GGATTATGTG TTGGAAGGCG AGACGCTGAC GATTGCAGAC GTACCGTCCG
251 AACGCTTCAC CGTCGAAGTG GAAACCGAAA TCCTGCCGCG GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGCG AATCTGTTTA CCCAGTGGCA
351 GCCGGAGGGC TTCCGCAAAA TCACGTTCTA CATCGACCGT CCGGATGTGA
401 TGTCCAAGTT CACGACCACC ATCGTCGCGG ACACAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GCGGAGTTTT CAGACGGCGC
501 CCATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTCCG GGGCGATTTC GCGGTAACGG AAGACCGTTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAAC
651 CAAGGTCGCG TTTGCCGTGG AATCGTTGAA AAACGCGATG AAGTGGGACG
701 AAACGCGCTT CGGTTGGAA TATGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTAGGCGATT TCAATATGGG CGCGATGGAA AACAAGGGTT TGAACATTTT
801 TAACACCAAG TTCGTCTCTG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT TGAATCCGTG GTCGGACACG AATATTTCCT CAACCTGGACG
901 GGCAACCGCG TAACCTGCCG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAGTTTTC CCGCGACCGC GCCGGCCGCG
1001 CCGTGCGCCG CATCGAGAAC ATCCGCGCTG TGCGCCAGAA CCAAGTTCCC
1051 GAAGACGCAG GCCCGACCGC CCATCCGGTG CGCCCCGTCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAGGAGG CCGGAAGTGG
1151 TGCGGATGTA TCATACCCCTG CTCGGCGAAG AGGGCTTCCA AAAAGGCATG
1201 AAGCTATATT TCCAACGCCA CGACGGACAG GCAGTGACCT GCGACGATTT
1251 CCGCGCGGCG ATGGCGGATG CGAACGGCAT CAATCTCGAC CAGTTCGCTC
1301 TGTGGTACAG CCAGGCGGGC ACGCCCGTTT TGGAGCCGA AGGCCGCTCT
1351 AAAACAATG TTTTCGAGTT AACCATTAAA CAAACCGTGC CGCCACGCGC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA GTCGGGCTTC
1451 TGAACCGCAA CGCGGAAGCG GTGGCATTCT ATTATCAGGG CAAACGCGCA
1501 ACCGAAGCCG TGTGCTGAT GACCGAAGCC GAACAGGCCT TCCCGCTCGA
1551 AGGTGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CAGTGATCTT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCACGACA GCGACGCTTT CACGTGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGTCGCGCC GTCGCCGCA ACCTTGCCG GCTTTCAGAC GGATCGGGT

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1751 TGCCGAAACA CGAAAACTG CTTGCCGCCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTGG ACAACGCCCT CAAAGCCCTG CTTTGGGGCG TGCCGTCCGA
1851 AGCCGAACCTG TGGGACGGCA CGGAAACAT CGACCCGCTG CGCTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATACGCTT CCGTCCGCTT CCTGCCGAAA
1951 TGGCAGCAAT TGGACCGTCA GGCGGCGAAG CAGGAAAACC AAAGTTACGA
2001 ATACAGCCCC GAAACGCCCG ACTGGCGCAC GCTGCGCAAC GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAC CCCGCGCACA TCGAACTGT TGCCGAAAAA
2101 TACGGCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CTGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCTT
2251 ATCGGCTCAA GCCGCCGCGAG CGACACCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAATTCAGTC TCGAAAACCC CAACAAAGCC CGTTCGCTCA
2351 TCGGAGCTT CAGCCGCAAC GTCCCGCATT TTCACGCACA AGACGGCAGC
2401 GGCCTACCGT TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCAACC CAAAACTTG GTGAAACAAG AATTGCAGTG CATTCGGGCG
2551 CAGGAAGGAT TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AGATTTTGGG
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2166; ORF 665-1.ng>:

g665-1.pap

```

1 MSKTVRYLKD YQTPAYRILE TELHFDIAEP QTVVKSRLTV EPORAGEPLV
51 LDGSAKLLSV KINGAADYV LEGETLTIAD VPSEFTVEV ETEILPAENK
101 SLMGLYASGG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDBGHHV KWEDPFAKPS YLFALVAGDL AVTEDRETTM
201 SGRNVKIEFY TTEADKPKVG FAVESLRNAM KWDETRFGL EYLDIFMVVA
251 VGDFFNMGME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRWF QLSLKEGLTV FRDQEFSGDR AGRVVRRIEN IRLLRQNFPP
351 EDAGPTAHVP RPVSYEEMNN FYTMTVYKGG AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSOAG TPVLEAREGL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK VGLLNRNGEA VAFDYQKRA
501 TEAVLLMTEA EQAFPLEGVT EAVVPSLLRG FSAPVYLYNP YSDDDLLLLL
551 AHDSDAFTCW EAAQTLYRRA VAANLAALSD GIGLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSAEAL WDGTEINIDPL RYHQAREALL DTLAVRFLPK
651 WHELDROAAK QENQSYEYSP ETADWRTLRLN VCRAFLVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNCLL AQFADKFSDD ALVMDKYFAL
751 IGSRRSDTL QQVQALQHP KFSLENPNKA RSLIGSFSRN VPHFHAQDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQELQCIRA
851 QEGLSKDVG EIVGKILG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2167>:

m665-1.seq

```

1 ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51 TATTCTCAAA ACCGATTAC ATTTTGATAT TAATGAACCG CAAACCGTCG
101 TGAAGTCGCG TTTGACGGTT GAGCCGCGA GGGTAGGGGA GCCGCTGGTG
151 TTGGACGGTT CGGCGAAACT CTGTCCGTC AAAATCAACG GGGCGGCGGC
201 GGATTATGTG TTGGAAGGAG AGACGCTGAC GATTGCGGGC GTGCCGTCCG
251 AACCGCTTAC CGTCGAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301 TCGCTGATGG GGCTGTATGC TTCCGGCGGC AATTGTGTTA CCCAGTGCGA
351 GCCGGAGGGC TTCCGCAAAA TCACATTTTA CATCGACCGT CCGGATGTGA
401 TGTCCAAATT CACCACCACC ATCGTCGCGC AAAAAACG CTATCCCGTT
451 TTGCTTTCCA ACGGCAACAA AATCGACGGC GGCGAGTTT CAGACGGCCG
501 CCATTGGGTG AAATGGGAAG ACCCGTTTTC CAAACCGAGC TATCTGTTG
551 CTTTGGTTCG GGGCGATTG GCGGTAACGG AAGACTATT CACCACCATG
601 AGCGGCAGAA ACCTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAGGTCGGC TTTGCCGTGG AATCGTTGAA AAACGCGATG AAATGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTGCTCGCC
751 GTGGGCGATT TCAATATGGG CGCGATGGA AACAAGGTT TGAACATCTT
801 TAACACCAAG TTCGTCTTGG CCGACAGCCG CACCGCCACC GATACCGATT
851 TCGAAGGCAT CGAATCCGTG GTCGGACACG AGTATTTCCA CAACCTGGACG
901 GGCAACCGCG TAACCTGCGG CGACTGGTTC CAGCTTTCGC TGAAGGAAGG
951 GCTGACCGTG TTCCGCGACC AAGAATTTT CCGCGACCGC GCCAGCCGCG
1001 CCGTGCGCCG CATCGAAAAC ATCCGCTTGC TCGCCAGCA CCAAGTTCCC
1051 GAAGACGCGA GCCCGACCGC CCATCCGGTG CGCCCGCCA GCTATGAGGA
1101 GATGAACAAT TTCTACACCA TGACCGTTTA TGAAGAGGC GCGGAAGTAG
1151 TCGGATGTA TCACACCTG CTCGCGGAAG AGGGCTTCCA GAAGGCATG
1201 AAGCTCTATT TCCACGCCA CGACGGACAG GCCGTACCT GCGACGATT
1251 CCGCGCGGCG ATGCGGACG CGAACGGCAT CAATCTCGAC CAGTTCGCCT
1301 TGTGGTACAG CAGGCGGGC ACGCCGTTT TGAAGCGGA AGGTCGCTG
1351 AAAACAATA TTTTCGAGT GACCGTCAA CAAACCGTGC CGCCACGCC
1401 CGATATGACG GATAAACAGC CGATGATGAT TCCCGTCAAG GTCGGGCTGC
1451 TGAACCGCAA CGGCGAAGCG GTGGCATTG ACTATCAGG CAAACCGCGC

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1064

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1501 ACCGGAAGCCG TGTGCTGCT GACCGAAGCC GAACAGACCT TCCTGCTCGA
1551 AGGCCTAACC GAAGCCGTCG TTCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTCCTGCTC
1651 GCCCATGACA GCGACGCCTT CACGCGCTGG GAAGCCGCCC AAACGCTCTA
1701 CCGCCGCGCC GTGCGCGCCA ACCTTGCCAC GCTTTCAGAC GCGGTTGAGC
1751 TGGCGAAACA CGAAAACTG CTTGCCGCGC TCGAAAAAGT CATTTAGAC
1801 GACCTCTTAG ACAACGCCTT CAAAGCCCTG CTTTGGGCG TGCCATCCGA
1851 AGCCGAGCTG TGGGACGGCG CAGAAAAATC CGACCCGCTG CGCTACCATC
1901 AGGCCTGCGA AGCCTTGTG GATACGCTG CCGTCCACTT CCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGGCGAAG CAGGAAAAAC AAAGTACGA
2001 ATACAGCCCG GAAGCCGCGG GCTGCGCAC GCTGCGCAAC GTCTGCGCGC
2051 CCTTGTCTCT GCGCGCGCAC CCCGCGCACA TCGAAACCGT TGCCGAAAAA
2101 TACGCGGAAA TGGCGCAAAA CATGACCCAC GAATGGGCGA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGGTGA TGGACAAATA TTTGCCCCC
2251 GTCGGCTCAA GCCGCCGAG CGACACCCTG CAACAGGTTT GAACCGCCTT
2301 GCAGCATCCG AATTCAGCC TCGAAAAACC CAACAAAGCC CGTTCGCTCA
2351 TCGGCAGCTT CAGCCGCAAC GTCCGCGATT TCCACGAGA AGACGGCAGC
2401 GGCTACCGTT TCATCGCGCA CAAAGTCATC GAAATCGACC GCTTCAACCC
2451 GCAGGTCGCC GCCCGCTTAG TGCAGGCGTT CAACCTCTGC AACAAAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTCGGGCG
2551 CAGGAAGGAT TGTGAAAGA CGTGGCGGAA ATCGTGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2168; ORF 665-1>:

m665-1.pep

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV
51 LDGSAKLLSV KINGAAADYV LEGETLTIAG VPSEKFTVEV ETEILPAENK
101 SLMGLYASGG NLFQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYDLDFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHQFP
351 EDAGPTAHFV RPASYEEMNN FYTMTVYERK AEVVRMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MADANGINLD QFALWYSQAG TPVLEAEGRL
451 KNNIFELTVK QTVPTPDMT DKQPMIPVK VGLNLRNGEA VAFDYQKRA
501 TEAVLLLETA EQTFLLLEGVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLATLSD GVLPKHEKL LAAVEKVISD
601 DLLDNFAFKL LLGVPSAEEL WDGAENIDPL RYHQAREALL DTLAVHFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTLRLN VCRFVLRAD PAHIETVAEK
701 YGEMAQNMTH EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSSRRSDTL QQVRTALQHP KFSLENPNKA RSLIGSFSRN VPHFHAEDGS
801 GYRFIADKVI EIDRFNPOVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

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m665-1/g665-1 96.1% identity in 866 aa overlap

	10	20	30	40	50	60
m665-1.pep	MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTVVKSRLTV EPQRVGEPLV LDGSAKLLSV					
g665-1	MSKTVRYLKD YQTPAYRI LTELHFDIAEP QTVVKSRLTV EPQRVGEPLV LDGSAKLLSV					
	70	80	90	100	110	120
m665-1.pep	KINGAAADYV LEGETLTIAG VPSEKFTVEV ETEILPAENK SLMGLYASGG NLFQCEPEG					
g665-1	KINGAAADYV LEGETLTIAD VPSEKFTVEV ETEILPAENK SLMGLYASGG NLFQCEPEG					
	130	140	150	160	170	180
m665-1.pep	FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFSDGRHWV KWEDPFSKPS					
g665-1	FRKITFYIDR PDVMSKFTTT IVADKKRYPV LLSNGNKIDG GEFSDGRHWV KWEDPFAKPS					
	190	200	210	220	230	240
m665-1.pep	YLFALVAGDL AVTEDYFTTM SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL E					
g665-1	YLFALVAGDL AVTEDRFTTM SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL E					
	250	260	270	280	290	300
m665-1.pep	YDLDFMVVA VGDFNMGAMENK GLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT					
g665-1	YDLDFMVVA VGDFNMGAMENK GLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT					

	250	260	270	280	290	300
m665-1.pep	310	320	330	340	350	360
	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRASRAVRRIENIRLLRQHQPEDAGPTAHPV					
g665-1	GNRVTCRDWFQLSLKEGLTVFRDQEFSGDRAGRAVRRIENIRLLRQHQPEDAGPTAHPV					
	310	320	330	340	350	360
m665-1.pep	370	380	390	400	410	420
	RPASYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGGQAVTCDDFRAA					
g665-1	RPVSYEEMNNFYTMTVYEKGAEVVRMYHTLLGEEGFQKGMKLYFQRHGGQAVTCDDFRAA					
	370	380	390	400	410	420
m665-1.pep	430	440	450	460	470	480
	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNIFELTVKQTPPTPDMDKQPMPIPVK					
g665-1	MADANGINLDQFALWYSQAGTPVLEAEGRLKNNVFELTIKQTPPTPDMDKQPMPIPVK					
	430	440	450	460	470	480
m665-1.pep	490	500	510	520	530	540
	VGLLNRNGEAVAFDYQGKRATEAVLLLTAEQTFLEGGVTEAVVPSLLRGFSAPVHLNYP					
g665-1	VGLLNRNGEAVAFDYQGKRATEAVLLMTAEQAFPLEGGVTEAVVPSLLRGFSAPVYLNYP					
	490	500	510	520	530	540
m665-1.pep	550	560	570	580	590	600
	YSDDDL LLLLAHDSDAFTTRWEAAQTL YRRAVANLATLSOGVELPKHEKLLAAVEKVISD					
g665-1	YSDDDL LLLLAHDSDAFTCWEEAAQTL YRRAVANLAALSOGIGLEPKHEKLLAAVEKVISD					
	550	560	570	580	590	600
m665-1.pep	610	620	630	640	650	660
	DLLDNAFAKALLGVPSAEELWDGAENIDPLRYHQAREALLDTLAVHFLPKWHELNROAAK					
g665-1	DLLDNAFAKALLGVPSAEELWDGTENIDPLRYHQAREALLDTLAVRFLPKWHELDROAAK					
	610	620	630	640	650	660
m665-1.pep	670	680	690	700	710	720
	QENQSYEYSPEAAGWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
g665-1	QENQSYEYSPETADWRTLNRNVCRAFLRADPAHIETVAEKYGEMAQNMTHEWGILSAVNG					
	670	680	690	700	710	720
m665-1.pep	730	740	750	760	770	780
	NESDTRNRLLAQFADKFSDDALVMDKYFALVGSSRRSDTLQQVRTALQHPKFSLENPNKA					
g665-1	NESDTRNCLLAQFADKFSDDALVMDKYFALIGSSRRSDTLQQVQTALQHPKFSLENPNKA					
	730	740	750	760	770	780
m665-1.pep	790	800	810	820	830	840
	RSLIGSFSRNVPFHAEADGSGYRFIADKVI EIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
g665-1	RSLIGSFSRNVPFHAEADGSGYRFIADKVI EIDRFNPQVAARLVQAFNLCNKLEPHRKNL					
	790	800	810	820	830	840
m665-1.pep	850	860				
	VKQALQIRAQEGLSKDVGEIVGKILD					
g665-1	VKQELQCIRAQEGLSKDVGEIVGKILGX					
	850	860				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2169>:

a665-1.seq

```

1  ATGAGCAAAA CCGTGCATTA TCTCAAAGAC TATCAAACGC CCGCCTACCA
51  TATTCTCAAA ACCGATTTAC ATTTTGATAT TAACGAACCG CAAACCATTG
101  TGAAGTCGCG TTTGACGGTC GAGCCGAAGA GGGTGGGAGA GCCGCTGGTG
151  TTGGACGGTT CGCGAAACT CTGTCCGTC AAAATCAACG GCGTGGCGGC
201  GGATTATGTG TTGAAGGCG AGACGCTGAC GATTGCGGAC GTGCCGTCCG
251  AAGCCTTCAC CGTCAAGTG GAAACCGAAA TCCTGCCGGC GGAAACAAA
301  TCGCTGATGG GGCTGTATGC GTCCGCCGGT AACCTGTTA CCCAGTGCGA
351  GCCGGAGGGC TTCCGCAAAA TCACGTCTA TATCGACCGT CCGGATGTCA
401  TGTCCAAGTT CACGACCACC ATCGTCGGG ACAAAAACG CTATCCCGTT
451  TTGCTCTCCA ACGCAACAA AATCGACGGC GGCGAGTATT CAGACGGCCG

```

```

501 CCAATTGGGTG AAATGGGAAG ACCCGTTTGC CAAACCGAGT TATCTGTTTG
551 CTTTGGTTCGC GGGCGATTTC GCGGTCACGG AAGACTATTT CACCACCATG
601 AGCGGCAGAA ACGTCAAAAT CGAGTTTAC ACCACCGAAG CGGACAAGCC
651 CAAAGGTCGGC TTTGCCGTGG AATCGCTGAA AAACGCAATG AAGTGGGACG
701 AAACGCGCTT CGGTTTGGAA TACGACTTGG ATATTTTCAT GGTCTGCGCC
751 GTGGGCGATT TCAATATGGG TGCATGGAA AACAAGGTTT TGAACATCTT
801 TAAACCAAG TTCGTCTTGG CCGACAGCCG TACCGCCACC GATACCGATT
851 TTGAAGGCAT CGAATCCGTG GTCGGACACG AATATTTCCA CAACTGGACG
901 GGC AACCGCG TGACCTGCCG CGACTGGTTC CAGCTTTTCG TGAAGGAAGG
951 GTTGACCGTG TTCGCGGACC AAGAATTTTC CGGCGACCGC GCCAGCCGCG
1001 CCGTGGCGCG TATCGAAAAC ATCCGCTGCG TCGCCAGCA CCAATTCCCC
1051 GAA GACGAG GTCCGACCGC ACATCCGGTG CGCCCCGCCG GATATGAGGA
1101 GAT GAACAAT TTCTACACCA TGACCGTTTA TGA AAAAGG CCGGAAAGTG
1151 TGC GGAATG TAACACCTTG CTCGGCGAAG AGGGCTTCCA AAAAGGTATG
1201 AAGCTCTATT TCCAACGCCA CGACGGACAG GCTGTACCT GCGACGATTT
1251 CCGCGCGCGC ATGGTGGACG CGAACGGCAT CAACCTCGAC CAATTCGCCT
1301 TGTGGTACAG CCAAGCAGGT ACGCCGGTTT TAGATGCTCA AGGGCGTCTG
1351 AAAAACAAATG TGTTTCGAGTT AACCATCAAA CAAACCGTGC CGCCACGCC
1401 CGATATGGCG GACAAACAGC CGATGATGAT TCCCGTCAAA ATCGGGCTGC
1451 TGA ACTGCAA CGGCGAAGCG GTGGCATTTC ATTATCAGGG CAAACGCGCG
1501 ACCGAAGCCG TGTTGCTGCT GACCGAAGCC GAACAGACCT TCCAGTTCGA
1551 AAGCGTAACC GAAGCCGTCG TTCCCTCGCT GCTGCGCGGG TTCAGCGCGC
1601 CGGTGCATCT GAACTATCCG TACAGCGACG ACGACCTGCT GCTTCTGCTC
1651 GCCCATGACA CGGACGCCCTT CACGCGCTGG GAAGCCGCAC AAACGCTCTA
1701 CCGCGGTGCC GTCGCCGCCA ACCTTGCCGC GCTTTCAGAC GCGCTCGAGT
1751 TGC CGAAACA CGAAAACTG CTGCGCGCG TCGAAAAAGT CATTTCAGAC
1801 GACCTCTTAG ACAACGCTTT CAAAGCCCTG CTTTGGGTG TGCCGTCTGA
1851 AGCCGAGCTG TGGGACGGCG CGGAAAACAT CGACCCGCTG CGTACCATC
1901 AGGCGCGCGA AGCCTTGTG GATATACTTG CCGTCCGCTT TCTGCCGAAA
1951 TGGCAGCAAT TGAACCGTCA GCGCGCGAAG CAGGAAAACC AAAGCTACGA
2001 GTACAGCCCC GAAGCCGCGG GTTGGCGCAC GCTGCGCAAT GTCTGCCGCG
2051 CCTTCGTCTT GCGCGCCGAT CCCGCGCACA TCGAAAACCG TGCCGAGAAA
2101 TACGCCGAAA TGGCGCAAAA CATGACCCAC GAATGGGGCA TCCTGTCCGC
2151 CGTCAACGGC AACGAAAGCG ATACGCGCAA CCGCCTGCTG GCGCAGTTTG
2201 CCGACAAGTT TTCAGACGAC GCGCTGCTGA TGGACAAATA TTTCGCCCTC
2251 GTCGGCTCAA GCCGCCGAG CGACACCCTG CAACAGGTTT AAACCGCCTT
2301 GCAGCATCCG AAGTTCAGCC TCGAAAATCC CAACAAAGCC CGCTCGCTCA
2351 TCGCGAGCTT CAGCCGCAAC GTCCCGCATT TCCACGCAGA AGACGGCAGC
2401 GGCTACCCTG TCATCGCCGA CAAAGTCATC GAAATCGACC GCTTTAACCC
2451 GCAGGTGCGC GCCCGCCTGG TGCAGGCGTT CAACCTCTGC AACAGCTCG
2501 AGCCGCACCG CAAAAACTTG GTGAAACAAG CATTGCAGCG CATTGGGGCG
2551 CAGGAAGATG TGTCGAAAGA CGTGGGCGAA ATCGTCGGCA AAATTTTGA
2601 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2170; ORF 665-1.a>:

a665-1.pap

```

1 MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV
51 LDGSAKLLSV KINGVAADYV LEGETLTIAD VPSEKFTVEV ETEILPAENK
101 SLIMGLYASAG NLFTQCEPEG FRKITFYIDR PDVMSKFTTT IVADKKRYPV
151 LLSNGNKIDG GEYSGRHWV KWEDPFAKPS YLFALVAGDL AVTEDYFTTM
201 SGRNVKIEFY TTEADKPKVG FAVESLKNAM KWDETRFGL EYLDIFMVVA
251 VGDFNMGAME NKGLNIFNTK FVLADSRAT DTFEGIESV VGHEYFHNWT
301 GNRVTCRDWF QLSLKEGLTV FRDQEFSGDR ASRAVRRIEN IRLRQHOFQ
351 EDAGPTAHVP RPARYEEMNN FYTMTVYK EGVVVMYHTL LGEEGFQKGM
401 KLYFQRHDGQ AVTCDDFRAA MVDANGINLD QFALWYSQAG TPVLDAQGRL
451 KNNVFELTIK QTVPTPDMA DKQPMMPVK IGLLNCNGEA VAFDYQKRA
501 TEAVLLLTEA EQTFQFESVT EAVVPSLLRG FSAPVHLNYP YSDDDLLLLL
551 AHDSDAFTRW EAAQTLYRRA VAANLAALSD GVLPKHEKL LAAVEKVISD
601 DLLDNAFKAL LLGVPSEAE LWDGAENIDPL RYHQAREALL DILAVRFLPK
651 WHELNROAAK QENQSYEYSP EAAGWRTLRL VCRAFLRAD PAHIETVAEK
701 YAEMAQNMTN EWGILSAVNG NESDTRNRL AQFADKFSDD ALVMDKYFAL
751 VGSRRSDTL QVQVTAHQH KFSLENPNKA RSLIGSFERN VPHFAEDGS
801 GYRFIADKVI EIDRFNPQVA ARLVQAFNLC NKLEPHRKNL VKQALQIRIA
851 QEGLSKDVGE IVGKILD*

```

a665-1/m665-1 97.2% identity in 867 aa overlap

```

          10      20      30      40      50      60
a665-1.pap MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          |||
m665-1      MSKTVHYLKD YQTPAYHILK TDLHFDINEP QTIVKSRLTV EPKRVGEPLV LDGSAKLLSV
          10      20      30      40      50      60

          70      80      90     100     110     120

```



1068

	790	800	810	820	830	840
	850	860				
a665-1.pep	VKQALQRI	RAQEGLSKDVGEIVGKILDX				
m665-1	VKQALQRI	RAQEGLSKDVGEIVGKILDX				
	850	860				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2171>:

```

g666.seq
1  ATGCTTTGTA TGAATTATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTAGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGGTA ATCTCCGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTAA TTCTGCTGTC
151 ATCGCAGGTG CAGACGCTCA CACGCCTGAA CATGTAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT AGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCGGTGGTG CATTGTGTT GTATTGGGAC AATACCGCCA
401 AAACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCAGAATTAT TTTTGGATAA AGATGGTTAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGCT CGGTAGGTAC GCCTGCTATC CCTAAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2172; ORF 666.ng>:

```

g666.pep
1  MLCMNYQSNS GEGVLVAKTY LLTALIMSMV ISGCQVIHAN QGKVNTNSAV
51  IAGADAHTPE HVTGLTEQKQ VIASDFIVAS ANPLATQAGY DILKQGGSA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGX PLKFMEAVVA RXVRLSLN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2173>:

```

m666.seq
1  ATGCCTTGTA TGAATCATCA ATCAAACCTCA GGCGAAGGAG TGCTTGTGGC
51  TAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGTG CAGACGCTCA CACGCCTGAA CATGCAACGG GACTGACCGA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GGTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGGTAG AGCCACAGTC
351 GTCAGGCTTG GGCGGTGGTG CATTGTGTT GTATTGGGAT AATACCGCCA
401 AAACATTGAC CACATTGAT GGGCGTGAGA CGGCACCGAT GCGTGCGACG
451 CCGGAATTAT TTTTGGATAA AGATGGTCAA CCATTGAAAT TTATGGAAGC
501 GGTGGTCGTG GTCGCTCGGT GGGTACGCTT GCTATCCCTA AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2174; ORF 666>:

```

m666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTNSAV
51  ITGADAHTPE HATGLTEQKQ VIASDFMVAS ANPLATQAGY DILKQGGSA
101 DAMVAVQTTL SLVEPQSSGL GGGAFVLYWD NTAKTLTTFD GREAPMRAT
151 PELFLDKDGQ PLKFMEAVVV VARWVRLSL N*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m666/g666 93.9% identity in 181 aa overlap

	10	20	30	40	50	60
m666.pep	MPCMNHQSNS	GEGVLVAKTY	LLTALIMSMT	ISGCQVIHAN	QGKVNTNSAV	ITGADAHTPE
		:				
g666	MLCMNYQSNS	GEGVLVAKTY	LLTALIMSMT	ISGCQVIHAN	QGKVNTNSAV	IAGADAHTPE
	10	20	30	40	50	60
	70	80	90	100	110	120
m666.pep	HATGLTEQKQ	VIASDFMVAS	ANPLATQAGY	DILKQGGSA	DAMVAVQTTL	SLVEPQSSGL

```

g666      HVTGLTEQKQVIASDFIVASANPLATQAGYDILKQGSSAADAMVAVQTTLSLVEPQSSGL
           70          80          90          100          110          120

           130          140          150          160          170          180
m666.pep  GGGAFVLYWDNTAKTTLTTFDGREAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
           |||
g666      GGGAFVLYWDNTAKTTLTTFDGREAPMRATPELFLDKDGXPLKFMEAVV--ARXVRLLSL
           130          140          150          160          170

m666.pep  NX
           ||
g666      NX
           180

```

```

a666.seq
1  ATGCCCTTGTA TGAATCATCA ATCAAACCTCA GCGGAAGGAG TGCTTGTGGC
51  TAAAAACATAT TTATTGACTG CATTGATAAT GTCTATGACA ATCTCTGGAT
101 GTCAAGTCAT CCATGCCAAT CAAGGCTAAGG TTAATACTCA TTCTGCTGTC
151 ATCACAGGCTG CAGACGCTCA CAGCGCTGAA CATGAAACCGG GACTGACCCA
201 ACAAAGCAG GTGATTGCAA GTGATTTTAT GTTAGCGTCA GCCAATCCAT
251 TAGCAACACA AGCTGGCTAT GATATCTTAA AGCAAGGCGG TAGCGCTGCA
301 GATGCGATGG TGGCGGTGCA GACGACACTA AGCTTGCTAG AGCCACAGTC
351 GTCAGGCTTG GCGCGTGGTG CATTTGTGTT GTATTGGGAT AATACGCCCA
401 AAACATTGAC CACATTGATG GGGCGTGAGA CGGCACCGAT CGGTGCGACG
451 CCGGAATTAT TTTTGTGATA AGATGGTCAA CATTGGAAGT TTAGGAAGC
501 GGTGGTCTGTG GTCGCTCGGT GGGTACGCCT GCTATCCCTA AACTGA

```

```

a666.pep
1  MPCMNHQSNS GEGVLVAKTY LLTALIMSMT ISGCQVIHAN QGKVNTHSAV
51 ITGADAHTPE  HATGLTEQKQ  VIASDFMVAS ANPLATQAGY DILKQGSAA
101 DAMVAVQTTL  SLVEPQSSGL  GGGAFVLYWD NTAKTLTTFD  GRETAPMRAT
151 PELFLDKDGQ  PLKFEAVVVV  VARWVRLLSL N*

```

```

10      20      30      40      50      60
m666.pep  MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a666      MPCMNHQSNSGEGVLVAKTYLLTALIMSMTISGCQVIHANQGKVNTHSAVITGADAHTPE
          10      20      30      40      50      60

70      80      90      100     110     120
m666.pep  HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a666      HATGLTEQKQVIASDFMVASANPLATQAGYDILKQGGSAADAMVAVQTTLSLVEPQSSGL
          70      80      90      100     110     120

130     140     150     160     170     180
m666.pep  GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
          |||||||||||||||||||||||||||||||||||||||||||||||||||
a666      GGGAFVLYWDNTAKTLTTFDGRETAPMRATPELFLDKDGQPLKFMEAVVVVARWVRLLSL
          130     140     150     160     170     180

m666.pep  NX
          ||
a666      NX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2177>:

```
g667.seq
1  atgcggtttg tcttctgttt gggcgGAGAG ATAGtttctg atccgtgtga
51  tttccAtttg gtattcgtcc gcgtcgaatc tgccgctgAc CAGAcagaaa
101 cgCAGataca tCaaatacgt attcacggca tcggttttcgc aatAAttgcg
151 GAtttccttc agcgtgcccg cgtgGAacgc ttcccacact ttgctgccgt
201 ccataCCCAg ctTGCCCGGA AAGCCGCACA GTTTCgcCat atcgtccagC
251 GGCACATTcg ccctcggctG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCActtg AAATCGCGGC
351 tgtcgccgAA ATCGccgTCG CCCGTATCCC AATAGCGCGC GGC GTTGTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGGTCTGA AACCGCGGCC
451 GTTCCAGCTG ACCAGTTGCG GCGTATGTTT TTCAACCAAT TCGAAAACT
501 TGGCAATCAC GACTTCTTCG CCATCGTCCA TCTCGCCGAT GGTGCCGACA
551 TGAACCTTGT CCTGCCCCCA GCGCATAACG CAGGAAACCG CCACAACCTG
601 ATGGAGGTGG TGCTGCATAA AATCGCCGCC GGTCTGTGCG CGGCGTTTCT
651 GCTGCGCGAA CAGCACCAC TCGTCATCCG GCAGGGAAGA CGGCAAGTCA
701 TACAACGTAC GGATACCCTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCGTA TTCATGGCag tACCTTGCAT tcaAAAACAG ACTTGCGCCT
801 ATTgTgtcaT TAA
```

This corresponds to the amino acid sequence <SEQ ID 2178; ORF 667.ng>:

```
g667.pep
1  MRFVFLGGE IVSDPCDFHL VFVRVESAAD QTETQIHQIR IHGIGFAIIA
51  DFLQARVER FPHFAAVHTQ LARKAAQFRH IVQRHIRPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVARIPIAR GVDVAVYQAV MQYGVETAA
151 VPADQLRRMF FNQFEKLGNH DFFAIVHLAD GADMLVLPP AHTAGNRHNL
201 MEVVLHKIAA GLCAAFLLRE QHHFVIRQGR RQVIQRTDTL HIGYGFNIEN
251 QNRHGSTLH SKTDLRLCH *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2179>:

```
m667.seq (PARTIAL)
1  ATGCGGCTTT TCCCCGCTT GTGCGGACAG GTAATTCCGC ATCCGTTTGA
51  TTTCCATTTT GTATTCGTCC GCATCCAGCC TGCCGCTGAC CAGACAGAAA
101 CGCAGGTACA TCAGATAAGT GTTTGCCGCG TCGGTTTCGC AATAATTGCG
151 GATTTCCTTC AGCCTGCCCG TATGGAATGC CTCCCAAACC TTGCTGCCGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAGC
251 GGCACGTTTG CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 GTGGCGTTGG TGATAACGGC TGATGTAGTT GTTCCACTTG AAATCGCGGC
351 TGTCGCCGAA ATCGCCGTCG CCCATATCCC AATAGCGCGC GGC GTTGTATG
401 CCGTATATCA GGGAGCGGTA ATGCAGTACG GGCAGATCTGA AACCGCGGCC
451 GTTCCAAC TG ACCAGTTGCG GCGTATGTTT TTCAATCAAT TCGAAAAATT
501 TGCATATGAC CACTTCTTCG CCGTCATCCA TCTCGCCGAT GGTGCCGACA
551 TGTACTTTAT CCTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACCTG
601 ATGAAGATGA TGCTGCATAA AATCGCCGCC CGTCTGAGCA CGGCGTTTGT
651 GCTGGGCAAT CAGCACCAC TG...
```

This corresponds to the amino acid sequence <SEQ ID 2180; ORF 667>:

```
m667.pep (partial)
1  MRLFPGLCGQ VIPHPDFHF VFVRIQPAAD QTETQVHQIS VCRVGFALIA
51  DFLQPARMEC LPNLAAVHTQ LARKTAQFRH IVQRHVCPRL VKREQIHQIA
101 VALVITADV VPLEIAAVAE IAVAHIPIAR GVDVAVYQAV MQYGVETAA
151 VPTDQLRRMF FNQFEKFSND HFLAVIHLAD GADMYFILPP THAARNRHL
201 MKMMLHKIAA RLSTAFVLGN QHHL...
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m667/g667 75.0% identity in 224 aa overlap

```

              10      20      30      40      50      60
m667.pep  MRLFPGLCGQVIPHPDFHFVFVRIQPAADQTETQVHQISVCRVGFALIAADFLQPARMEC
           ||:  | |::: | ||:||||: |||||:||||: : ||||| |||: ||:|
```

```

a667.seq
1  ATCGCGTTTG TCTTCTGTTT GGGCGGAGAG ATAGTTTCTG ATCCGCTTGA
51  TTTCATTTC GTATTTCGTT GCGTCGAATC TGCCGCTGAC CAGACAGAAA
101 CGCAGATACA TCAGATAGGT ATTTACCGCA TCGGTTTCGC AATAATTGCG
151 GATTTCTTTC AGCCTGCCCC GTTGAACGCG CCCCACACCC TTGTCGCGGT
201 CCATACCCAG CTTGCCCGGA AAACCGCACA GTTTCGCCAT ATCGTCCAAC
251 GGCACATTTC CCCTCGGCTG GTAAAGCGCG AGCAAATCCA TCAAATCGCA
301 ATGACGTTGG TGGTAGCGCG TGTATGTAGT GTTCCACTTG AAATCGCGGG
351 TGTGCGCGAA ATCGCCGTCG CCATATCCC AATGACGTCG GGCCTTGATG
401 CCGTGTAGCA GCGAACGGTA ATGCAGAAC GCGAGGTGCA AACCGCCGCC
451 GTTCCAAC TGACGTTGCG GCGTATGTTT TTCAATCAAC TCGAAAAATT
501 TGGCGATAAC CACTTCCTCG CCGTCATCCA TCTCGCCGAT TGTACCGACA
551 TGGACTTTAT CTTGCCCCCA ACGCATGCAG CACGAAATCG CCACAACTGT
601 ATGAAGATGA TGCTGCATAA AATCCCCACG CCTCTGAGCA CGGGCTTTTT
651 GCTGGGCAAA CAGCACCAC TCAATCGTCG GCAGCGAGGA CGGCAAGTCA
701 TACAGCGTAT GGATACACTG CACATCGGGT ACGGTTTCAA TATCGAAAGC
751 CAAAATCTGT GTCATGACAG CACCTTGTAT TAAAAA.CAG ACTTGCGCCT
801 ATTGTGTCAT TAA

```

a667.pap

1	MRFVFCVLGGE	IVSDPLDFHF	VFVCVESAAD	QTETQIQHIG	IYRIGFAIIA
51	DFLQPARVER	LPHLAAVHTQ	LARKTAQFRH	IVQRHIRPLR	VKREQIHQIA
101	MTLVVAADV	VPLEIAVAE	IAVAHIPIAR	GVDAV*QRTV	MQNRQVETAA
151	VPTDQLRRMF	FNQLEKFGDN	HFLAVIHLAD	CTDMDFILPP	THAARNRHLN
201	MKMLLHKIPT	RLSTAFLLGK	QHHFIVGQRG	RQVIQRTDTL	HIGYGFNISS
251	QNRGHDSTLY	LKXDRLILCH	*		

```

      10          20          30          40          50          60
m667.pep MRLFPGLCGQVIPHFFDFHFVFVR IQPAADQTETQVHQISVCRVGFAIIADFLQPAMEC
||: | |:| :|:: |:||||| :: |||||||:|:: |:|||||:|:|:|
a667 MR FVFC LGGEIVSDPLDFH FVFCVES AADQTETQIHQIGIYRIGFAIIADFLQPARVER
      10          20          30          40          50          60

      70          80          90         100         110         120
m667.pep LPNLAAVHTQLARKTAQFRHIVQRHVCPRLVKREQIHQIAVALVITADVVPLEIAAAVE
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a667 LPHLAAVHTQLARKTAQFRHIVQRHIRPRLVKREQIHQIAMTLVVAADVVPLEIAAAVE

```



	70	80	90	100	110	120
m667.pap	130	140	150	160	170	180
	IAVAHIPIARGVD	AVYQGAVM	QYGOIETA	AAVPTD	QLRRMFF	NQFEKFSNDHFLAVIHLAD
a667						
	IAVAHIPIARGVD	AVXQRTVM	QNRQVETA	AAVPTD	QLRRMFF	NQLEKFGDNHFLAVIHLAD
	130	140	150	160	170	180
m667.pap	190	200	210	220		
	GADMYFILP	PPTHAARN	RHNLKMM	MLHKIAAR	LSTAFVL	GNQHHL
a667	:				:	:
	CTDMDFILP	PPTHAARN	RHNLKMM	MLHKIPT	RLSTAF	LGKQHFFIVGQRGRQVIQRTDTL
	190	200	210	220	230	240
a667	HIGYGFN	IESQNR	GHDS	TYLKX	DLRL	LCHX
	250	260	270			

```
g669.seq
1  ATGCGCCGCA TCGTTAAAAA ACACGAGCCC GTAAACGCGC CACATATCGT
51  TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGA A ACGTCC CCATCATCAT GACCGCAGCC TTCGCGGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCCAA AGCGGCAGAC AGCCGGTTTG CACC A AACC G CCAAACACGG
251 CAGACCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACTGTA A
```

g669.pep  
1 MRRIVKKHQF VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRQHGFI  
51 EGMGDFDKQI FRHVQSSNRQ SGRQPVCTKP PNTASLQTAL SRPAVEGYNA  
101 DIKRIL\*

```
m669.seq
1  ATGCGCCGCA TCATAAAAA ACACGAGCCC ATAAACGCGC CACATATCGT
51  TTTGGA AATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAACGTC TC CATCATCAT GACAGCAGCC TTCGCGGGCA ACACGGGATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTCGG TTACAATGCC
301 GACATCAAAC GGATACGTGA A
```

```
m669.pep
  1  MRRRIKKHQF INAPHIVLEI RIMKLRHAFV FLGRKRPHHH DSSLRRQHGI
 51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQ TAL SRPAVFGYNA
101  DIKRIL*
```

**m669/g669 96.2% identity in 106 aa overlap**

	10	20	30	40	50	60
m669.pep	MRRRIKKHQPINAPHIVLEIRIMKLHRAVFVLGRKRPHHHDS	SSLRROHQHIEGMGDFKQI				
g669	MRRIVKKHQPVNAPHIVLEIRIMKLHRAVFVLGRKRPHHHDS	SLRRQHGIEGMGDFKQI				
	10	20	30	40	50	60
	70	80	90	100		

```

m669.pép    FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
g669        FRHVQSSNRQSGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2187>:

```

a669.seq
1   ATGCGCCGCA TCATTAAAA ACACCAGCCC GTAAACGCGC CACATATCGT
51  TTTGGAAATT CGGATAATGA AACTGCATCG CGCGTTTGTC TTCCTTGGGC
101 GGAAACGTCC CCATCATCAT GACCGCAGCC TTCGGCGGCA ACACGGAATC
151 GAAGGGATGG GTTTCGATTT CAAGCAGATT TTCAGACACG TTCAATCCTC
201 CAACAGGCAA AACGGCAGAC AGCCGGTTTG CACCAAACCG CCAAACACGG
251 CAAGCCTTCA AACAGCATTA TCACGCCCTG CCGTTTTTCG TTACAATGCC
301 GACATCAAAC GGATACTGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2188; ORF 669.a>:

```

a669.pép
1   MRRIKKHQP VNAPHIVLEI RIMKLHRAFV FLGRKRPHHH DRSLRRQHGI
51  EGMGFDFKQI FRHVQSSNRQ NGRQPVCTKP PNTASLQTAL SRPAVFGYNA
101 DIKRIL*

```

m669/a669 98.1% identity in 106 aa overlap

```

m669.pép    10      20      30      40      50      60
             MRRIKKHQPINAPHIVLEIRIMKLHRAFVFLGRKRPHHHDSLRRQHGIEMGFDFKQI
             |||||:|||||
a669        10      20      30      40      50      60
             MRRIKKHQPVNAPHIVLEIRIMKLHRAFVFLGRKRPHHHDRSLRRQHGIEMGFDFKQI

m669.pép    70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX
             |||||:|||||
a669        70      80      90      100
             FRHVQSSNRQNGRQPVCTKPPNTASLQTALSRPAVFGYNADIKRILX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2189>:

```

g670.seq
1   ATGACTTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTTCG GGTGGTGAA
51  AAACGCTTCC GCGGTTTCGT CTTCAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAAGT CCGCTCGTCA AACAGCATCA
251 CGCGCGGCTC CATCGCCAGC CCGCGCGCAA TCGCCACGCG TTGCTGCTGG
301 CCGCCGGAAG GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAAGTCCGAC
351 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
401 CCTTAACCTT CATCGGTGCG AGGGTGATGT TGTCCAACAC GGTCAGGTGC
451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2190; ORF 670.ng>:

```

g670.pép
1   MTCCRNLAR SCFGLVKNAS GVSSSRICPL STKITSATS RANPISWVTH
51  IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NSITRGSIAS PRAIATRCW
101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMLSNTVRC
151 G*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2191>:

```

m670.seq
1   ATGACCTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTTCG GGTGGTGAAA
51  AAACGCTTCC GCGGTTTCGT CTTCGAGGAT TTGCCCTTTA TCGACGAAAA
101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTACGCAC
151 ATCATCGTCA TGCCGCTTTC TGCCAAGTCT TTCATCACTT TCAACACTTC
201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CCGTTCGTCA AACAAACATTA

```

1074

```

2 51 CCGCGCGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
3 01 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
3 51 GCGTTCCAAA AGCTCCATTG CCTTTTCTC CGCCTGTTCC GCATTTTGCC
4 01 CCTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
4 51 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2192; ORF 670>:

```

m670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
  51 IIVMPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
 101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AFCPLTFIGA RVMFSNTVRC
 151 G*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m670/g670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep    MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
g670         MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              10      20      30      40      50      60

              70      80      90     100     110     120
m670.pep    FITFNTSPTISGSSAEVGSSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK
              |||||
g670         FITFNTSPTISGSSAEVGSSNSITRGSIASPRAIATRCWPPEWEGKASFLCASPTRSK
              70      80      90     100     110     120

              130     140     150
m670.pep    SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              |||||
g670         SSIAFFSACS AFCPLTFIGARVMSNTVRCGX
              130     140     150

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2193>:

```

a670.seq
  1 ATGACCTGTT GCAGGAACGT CTTGGCGCGT TCGTGTTTCG GGTGCGTAAA
  51 AAACGCTTCC GGCGTTTCGT CTTGAGGAT TTGCCCTTTA TCGACGAAAA
 101 TCACGCGGTC GGCAACTTCG CGGGCAAACC CCATTTCGTG GGTTACGCAC
 151 ATCATGGTCA TACCGCTTTC CGCCAAGTCT TTCATCACTT TCAACACTTC
 201 GCCGACCATT TCGGGGTCGA GTGCGGAGGT CGGTTCGTCA AACAACTTA
 251 CCGCGCGTTC CATCGCCAAA CCGCGTGCAA TCGCCACGCG TTGCTGCTGG
 301 CCGCCGGAAA GTTGGGAAGG GAAGGCGTCT TTTTGTGTG CCAGTCCGAC
 351 GCGTTCCAAA AGTTCCATCG CTTTTTCTC TGCCTGTTCC GCATTTTGAC
 401 CTTTAACCTT CATCGGTGCG AGGTAATGT TTTCCAACAC GGTGAGGTGC
 451 GGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2194; ORF 670.a>:

```

a670.pep
  1 MTCCRNCLAR SCFGLVKNAS GVSSSRICPL STKITRSATS RANPISWVTH
  51 IMVIPLSAKS FITFNTSPTI SGSSAEVGSS NNITRGSIAK PRAIATRCW
 101 PPESWEGKAS FLCASPTRSK SSIAFFSACS AF*PLTFIGA RVMFSNTVRC
 151 G*

```

m670/a670 98.0% identity in 151 aa overlap

```

              10      20      30      40      50      60
m670.pep    MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIIVMPLSAKS
              |||||
a670         MTCCRNCLARSCFGLVKNASGVSSSRICPLSTKITRSATS RANPISWVTHIMVIPLSAKS
              10      20      30      40      50      60

```

1075

	70	80	90	100	110	120
m670.p ep	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
a670	FITFNTSPTISGSSAEVGSNNITRGSIAKPRAIATRCWPPEWEGKASFLCASPTRSK					
	70	80	90	100	110	120
	130	140	150			
m670.p ep	SSIAFFSACS AFCPLTTFIGARVMFSNTVRCGX					
a670	SSIAFFSACS AFXPLTTFIGARVMFSNTVRCGX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2195>:

g671.s eq

1	ATGATCAGCA	GGGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACACC
51	GCCCAAAATG	CGGTTGGCAA	AGCCAGACC	GACCGCCGAA	ACTGCGCCGG
1 01	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
1 51	GAAATGAATG	ACAGagccaa	TGCAAACAgg	cggggTTGGA	ACGaggCAAA
2 01	GGCGAGGTcg	gcgaaggGTG	CGGCaaAGAG	TTTggcaaAA	AAGAaggAAA
2 51	ccaccCATGC	cACCATCgaa	ccTGCTCCG	CAATCAGCC	GCGCATCGTG
3 01	GAAATGACGA	TGCAGGCGGC	GATGACGGcg	gAGGCGAGGA	GGTCGGCAAT
3 51	GGGGAGGCTA	TTCATTTCGT	ACCTGGCCGG	CGATGCCGTG	CACGCGCAGT
4 01	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2196; ORF 671.ng>:

g671.p ep

1	MISRVTIKTP	FNAPNTPPKM	RLAKPRPTAE	TAPVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKGAAKSLAK	KKETTHATIE	PASAITPRIV
1 01	EMTMQAAMTA	EARRSAMGRL	FIRYLAGDAV	HAQFVQIAFG	IPCVFIVA*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2197>:

m671.s eq

1	ATGACCAGCA	GGGTAACAAT	CAAAACGCCT	TTCAATGCAC	CGAATACGCC
51	GCCCAAAATG	CGGTTGGCAA	AGCCCAAACC	GACCGCCGAA	ACTGCGCTGG
1 01	TCAGCAGCGA	ACGAGGCATT	TTCTGGATCA	GACAGGCAAT	GACGAACAGG
1 51	GAAATGAACG	ACAGAGCCAA	TGCAAACAGG	CGGGGTTGGA	ACGAGGCCAAA
2 01	GGCGAGGTG	GCGAAGGAGG	CGGCAAAGAG	TTTGGCGAAA	AAGAAGGAAA
2 51	CCACCCATGC	CGCCATTGAG	CCTGCCTCCG	CAATCAGCC	GCGCATCGCG
3 01	GATAGCACGA	TGCAGGCGGC	GATGACGGCG	GAGACGAGGA	GGTCGGCAAT
3 51	GGGGAGGCTA	TTCATTTCGT	ACCTGACCGG	CGATACCGTG	TACGCGCAAT
4 01	TTGTTCAAAT	CGCGTTCGGC	ATCCCTTGCG	TTTTTATAGT	TGCTTGA

This corresponds to the amino acid sequence <SEQ ID 2198; ORF 671>:

m671.p ep

1	MTSRVTIKTP	FNAPNTPPKM	RLAKPKPTAE	TALVSSERSI	FWIRQAMTNR
51	EMNDRANANR	RGWNEAKARS	AKEAAKSLAK	KKETTHAAIE	PASAITPRIA
1 01	DSTMQAAMTA	ETRRSAMGRL	FIRYLTGDTV	YAQFVQIAFG	IPCVFIVA*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m671/g671 91.9% identity in 148 aa overlap

	10	20	30	40	50	60
m671.p ep	MTSRVTIKTPFNAPNTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR					
g671	MISRVTIKTPFNAPNTPPKMRLAKPRPTAETAPVSSERSIFWIRQAMTNREMNDANANR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m671.p ep	RGWNEAKARSAKEAAKSLAKKKETTHAAIEPASAITPRIADSTMQAAMTAETRRSAMGRL					

1076

```

|||||
g671      RGWNEAKARSAKGAAKSLAKKETHATIEPASAITPRIVEMTMQAAMTAEARRSAMGRL
              70      80      90      100      110      120

              130      140      149
m671.pep   FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              |||||:|||||:|||||:|||||
g671      FIRYLAGDAVHAQFVQIAFGIPCVFIVAX
              130      140

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2199>:

```

a671.seq
1  ATGACCAGCA GGGTAATAAT CAAAATGCCT TTCAATGCAC CGAATACGCC
51  GCCCAAAATG CCGTTGGCAA AGCCCAAACC GACCGCCGAA ACTGCCCCGG
101 TCAGCAGCGA GCGGAGTATT TTCTGGATCA GACAGGCAAT GACGAATAGG
151 GAAATGAACG ACAGAGCCAA TGCAAACAGG CGGGGTTGGA ACGATGCAAA
201 GCGCATGTCT GCGAAGGGTG CCGCAAAGAG TTTGGCGAAA AAAAAGGCAA
251 CCACCCATGC CGCCATTGAG CCAGCCTCCG CAATCACGCC GCGCATCGCG
301 GATAGCACGA TGCAGGCGGC GATGATGGCG GAGACGAGGA GGTGCGCAAC
351 GGGGAGGTTA TTCATTCTGTT ACCTGACCGG CGATACCGTG TACGCGCAAT
401 TTGTTCAAAT CGCGTTCGGC ATCCCTTGCG TTTTATAGT TGCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2200; ORF 671.a>:

```

a671.pep
1  MTSRVIKMP FNAPNTPPKM RLAKPKPTAE TAPVSSERSI FWIRQAMTNR
51  EMNDRANANR RGWNAKAMS AKGAAKSLAK KKATTHAAIE PASAITPRIA
101 DSTMQAAMMA ETRRSATGRL FIRYLTGDTV YAQFVQIAFG IPCVFIVA*

```

m671/a671 93.9% identity in 148 aa overlap

```

              10      20      30      40      50      60
m671.pep     MTSRVTIKTPFNAENTPPKMRLAKPKPTAETALVSSERSIFWIRQAMTNREMNDANANR
              |||||
a671         MTSRVIKMPFNAENTPPKMRLAKPKPTAETAPVSSERSIFWIRQAMTNREMNDANANR
              10      20      30      40      50      60

              70      80      90      100      110      120
m671.pep     RGWNEAKARSAKEAAKSLAKKETHAAIEPASAITPRIADSTMQAAMTAEETRRSAMGRL
              |||||:|||||
a671         RGWNAKAMSAGAAKSLAKKATTHAAIEPASAITPRIADSTMQAAMMAETRRSATGRL
              70      80      90      100      110      120

              130      140      149
m671.pep     FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              |||||:|||||:|||||
a671         FIRYLTGDTVYAQFVQIAFGIPCVFIVAX
              130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2201>:

```

g672.seq
1  ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51  ACTGTATGCC GCCCAGCCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
101 CCCAAAGCCC CCGCGTATC GACATCATT AAGCACAAA AATCGCCGCC
151 GCACTGCCGC CGTTTGTCTGCGTGTCTGCC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGGCGA CGAAGACGAT GCATTCTGCC GGCAGTTCGA CCGCCCCTAT
301 ATTAAAGCCA TTCGTGTCTA GACGGCATCA GACATCCGAA ACGCCGCCAC
351 GCGCTTCCCC AACGCTCAGG CACTGCTGTT CGATGCCTAT CACCCTTCGG
401 AATACGGCGG CACCGGACAC CGCTTCGact GGacgctgtt ggcggAATAT
451 TCGGGCAAGC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCCGTC CGCATCACCG GAGCGGAAGC GGTGACGTA TCCGGCGGCG
551 TGAAGCGTC TAAAGGCAAA AAAGACCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2202; ORF 672.ng>:

```

g672.pep
  1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAI DIIKAQKIAA
 51 ALPPFVSVVA LEVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFDRPY
101 IKAIRVQTAS DIRNAATREF NAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAEAVDV SGGVEASKGK KDKPAKVAEFI
201 ATANRLSR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2203>:

```

m672.seq
  1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
 51 AGCTGCCGCC GCAGCGGCAG GTGCGGATGC CGTCGGGCTG GTCTTTTTC
101 AAGGCAGCAG CCGGGCCGTC GATATTGCCC GCGCCAAAAA AATCACCGCC
151 GCACTGCCGC CGTTTGTCTAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
201 GCAAAACATC CGCCGCATCC TTGCCGAAGT GCCGATACAC ATCATCCAAT
251 TCCACGCGCA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCTAT
301 ATCAAAGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCGCCAC
351 GCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
401 AATACGGCGG CACCGGAAAC CGCTTCGACT GGACGCTGCT GCGGGAATAT
451 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTCGG
501 CGAAGCGGTC CGCATCACCG GAGCGGAATC GGTTCGATGA TCCGGCGGTG
551 TGAAGCGGTC TAAAGGCAAA AAAGATGCCG CCAAAGTCGC CGCCTTTATC
601 GCAACCGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2204; ORF 672>:

```

m672.pep
  1 MRKIRTKICG ITTPEDAAAA AAAGADAVGL VFFQSSRAV DIARAKKITA
 51 ALPPFVSVVA LEVNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAATREF DAQALLFDAY HPSEYGGTGN RFDWTLAEY
151 SGKPWVLAGG LTPENVGEAV RITGAESVDV SGGVEASKGK KDAKVAEFI
201 ATANRLSR*

```

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m672/g672 91.3% identity in 208 aa overlap

```

          10      20      30      40      50      60
m672.pep  MRKIRTKICGITTPEDAAAAAAGADAVGLVFFQSSRAVDIARAKKITAALPPFVSVVA
          |||||
g672      MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAIDIKAQKIAAALPPFVSVVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m672.pep  LEVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATREF
          |||||
g672      LEVNESAQNIRRLAEVPIHIIQFHGDEDDAFCRQFDRPYIKAIRVQTASDIRNAATREF
          70      80      90      100     110     120

          130     140     150     160     170     180
m672.pep  DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV
          :|||
g672      NAQALLFDAYHPSEYGGTGHFRFDWTLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV
          130     140     150     160     170     180

          190     200     209
m672.pep  SGGVEASKGKKDAKVAEFIATANRLSRX
          |||||
g672      SGGVEASKGKKDKPAKVAEFIATANRLSRX
          190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2205>:

a672.seq

1078

```

1 ATGAGGAAAA TCCGCACCAA AATCTGCGGC ATCACCACAC CGGAAGACGC
51 ACTGTATGCC GCCACGCCG GCGCAGACGC ATTGGGACTG GTTTTTTACC
1 01 CCCAAAGCCC CCGCGTGTG GACATCATTA AAGCACAAAA AATCACCGCC
1 51 GCACTGCCGC CGTTTGTGAG CGTTGTGCGC CTTTTCGTCA ACGAAAGCGC
2 01 GCAAAACATC CGCCGCATCC TTGCCGAAGT ACCGATACAC ATCATCCAAT
2 51 TCCACGGCGA CGAAGACGAC GCATTCTGCC GCCAGTTCCA CCGCCCCTAT
3 01 ATCAAGGCCA TTCGTGTTCA GACGGCATCA GACATCCGAA ACGCCGCCGA
3 51 CCGCTTCCCC GACGCTCAGG CACTGCTGTT CGATGCCTAC CATCCTTCGG
4 01 AATACGGCGG CACCGGACAC CGCTTCGACT GGACGCTGTT GCGCGAATAT
4 51 TCGGGCAAAC CGTGGGTGCT TGCCGGCGGG CTGACCCCTG AAAACGTGCA
5 01 CGAAGCCATC CGCATCACCG GAGCGGAAGC GGTGATGTA TCCGGCGGCG
5 51 TGGAAGCGTC TAAAGGCAAA AAAGACCCAG CCAAAGTGC CGCCTTTATC
6 01 GCAACGCCA ACCGCCTATC CCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2206; ORF 672.a>:

```

a672.pep
1 MRKIRTKICG ITTPEDALYA AHAGADALGL VFYQSPRAV DIKAQKITA
51 ALPPFVSVVA LFNESAQNI RRILAEVPIH IIQFHGDEDD AFCRQFHRPY
101 IKAIRVQTAS DIRNAADRFP DAQALLFDAY HPSEYGGTGH RFDWTLAEY
151 SGKPWVLAGG LTPENVDEAI RITGAEAVDV SGGVEASKGK KDPKVAAFI
201 ATANRLSR*

```

m672/a672 91.8% identity in 208 aa overlap

```

10 20 30 40 50 60
m672.pep MRKIRTKICGITTPEDAAGADAVGLVFFQSSRAVDIARAKKITAALPPFVSVVA
|||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||:
a672 MRKIRTKICGITTPEDALYAAHAGADALGLVFYQSPRAVDIIKAQKITAALPPFVSVVA
10 20 30 40 50 60

70 80 90 100 110 120
m672.pep LFNESAQNIRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAATRF
|||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||:
a672 LFNESAQNIRILAEVPIHIIQFHGDEDDAFCRQFHRPYIKAIRVQTASDIRNAADRFP
70 80 90 100 110 120

130 140 150 160 170 180
m672.pep DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVGEAVRITGAESVDV
|||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||:
a672 DAQALLFDAYHPSEYGGTGNRFDWTLAEYSGKPWVLAGGLTPENVDEAIRITGAEAVDV
130 140 150 160 170 180

190 200 209
m672.pep SGGVEASKGKKDAKVAAFIATANRLSRX
|||||:|||||: |||||:|||||: |||||:|||||: |||||:|||||:
a672 SGGVEASKGKKDPAKVAAFIATANRLSRX
190 200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2207>:

```

g673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTGGCGATTG TCGGTCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCG
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTCGTGTTT GTCGATACGC CGGGCTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CGGTGTGGAT
301 GTGGTGGTTT TCGTCGTGGA GCGGATGCGC CTTACCGATG CCGACCGCGT
351 CGTGTGTTAAA CAACTGCCCA AGCACACGCC GGTCATTTTA GTGATCAACA
401 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGTT
451 GCCCAAGTGC GCGCCGAATT TGAATTGCG GCGGCGGAGG CGGTGAGTGC
501 GAAACACGGT TTGCGGATTG CCAACCTGTT GGAGCTGCTC AAGCCGTATC
551 TGCCCGAAAG CGTACCGATG TATCCCGAAG ACATGGTTAC GGACAAATCG
601 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAACTCT TCCGCTATTT

```

```

6 51 GGGCGAGGAG CTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
7 01 AGGGAGACGG TTTGAACCGC ATCTACatcg cCGTTTTGGT CGACAAAGAA
7 51 AGCCAAAAGG CGATTTTGTAT CGGTAAAGGC GGGGAGCGTT TGAATAAAAT
8 01 TTCCACCGAA GCGCGGCTGG ATATGGAAAA ACTGTTTGTAT AACAAAGTAT
8 51 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCAGA CGACATTCGC
9 01 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2208; ORF 673.ng>:

```

g673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
1 01 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VINKIDKDKA KDRYALEAFV
1 51 AQVRAEFEDA AAEAVSAKHG LRIANLLELL KPYPESVPM YPEDMVTDKS
2 01 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEGDGLNR IYIAVLVDKE
2 51 SQKAILIGKG GERLKKISTE ARLDMEKLFD NKVFLKVWVK VKSGWADDIR
3 01 FLRELGL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2209>:

```

m673.seq
1 ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG GCGGATACCG
51 TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
1 01 TGATGAACCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAGGCCG
1 51 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
2 01 GTTCGTGTTT GTCGATACGC CCGGCTTTCA AACCGACCAC CGCAACGCGC
2 51 TCAACGACAG GCTGAATCAA AATGTTACCG AGGCGCTCGG CCGCGTGGAT
3 01 GTGGTGGTTT TCGTCGTGGA GGCGATGCGC TTTACCGATG CCGACCGCGT
3 51 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
4 01 AAATCGACAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTGTT
4 51 GCCCAAGTGC GCGCCGAATT TGAATTTGCG GCGCGGAGG CCGTCAGCGC
5 01 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
5 51 TGCCCGAAAG CGTGCCGATG TATCCGAAG ATATGGTTAC GGACAAATCG
6 01 GCGCGTTTTT TGGCGATGGA AATCGTGCCT GAAAAATTGT TCCGCTATTT
6 51 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
7 01 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTTGGT CGATAAGGAA
7 51 AGCCAAAAGG CAATTTAAT CGGTAAAGGC GGAGAACGTT TGAAGAAAAT
8 01 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTTGTAT ACCAAAGTAT
8 51 TTTTGAAGGT CTGGGTCAAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
9 01 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2210; ORF 673>:

```

m673.pep
1 MDIETFLAGE RAAGGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51 QTTRNRVTGI YDDTAQFVF VDTPGFQTDH RNALNDRLNQ NVTEALGGVD
1 01 VVVFVVEAMR LTDADRVVLK QLPKHTPVIL VNKIDKDKA KDRYALEAFV
1 51 AQVRAEFEDA AAEAVSAKHG LRIANLLELI KPYPESVPM YPEDMVTDKS
2 01 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
2 51 SQKAILIGKG GERLKKISTE ARLDMEKLFD TKVFLKVWVK VKSGWADDIR
3 01 FLRELGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m673/g673 98.4% identity in 307 aa overlap

```

m673.pep      10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
|||||
g673          10      20      30      40      50      60
MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
|||||

m673.pep      70      80      90     100     110     120
YDDTAQFVFVDTPGFQTDHNRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK
|||||

```



1080

```

g673      YTDDTAQFVFVDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVEAMRLTDADRVVLK
           70      80      90      100     110     120

           130     140     150     160     170     180
m673.pep  QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      QLPKHTPVILVINKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELL
           130     140     150     160     170     180

           190     200     210     220     230     240
m673.pep  KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      KPYPLESVPMYPEDMVTDKSARFLAMEIVREKLFYRLGEELPYAMNVEVEQFEEEDGLNR
           190     200     210     220     230     240

           250     260     270     280     290     300
m673.pep  IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVKS GWADDIR
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g673      IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDNKVFLKVWVKVKS GWADDIR
           250     260     270     280     290     300

m673.pep  FLRELGLX
           |||||
g673      FLRELGLX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2211>:

```

a673.seq
1  ATGGATATTG AAACCTTCCT TGCAGGGGAA CGCGCCGCCG ACGGATACCG
51  TTGCGGCTTC GTAGCGATTG TCGGCCGTCC GAACGTGGGC AAATCAACGC
101 TGATGAATCA TCTCATCGGT CAGAAAATCA GTATTACCAG CAAAAAGCGC
151 CAGACGACGC GCAACCGCGT AACGGGGATT TATACCGACG ATACCGCGCA
201 GTTTGTGTTT GTCGATACGC CCGGTTTTCA AACCGACCAC CGCAACGCGC
251 TCAACGACCG TTTGAATCAA AACGTTACCG AGGCACTCGG CGGCGTGGAT
301 GTGGTGTTT TCGTCGTGGA AGCGATGCGT TTTACCGATG CCGACCGCGT
351 CGTGTGAAA CAACTGCCCA AGCACACGCC GGTCAATTTA GTGGTCAACA
401 AAATCGATAA GGACAAGGCG AAAGACCGTT ACGCGCTGGA GCGGTTTGT
451 GCCCAGGTGC GCGCCGAATT TGAATTTGCG GCGGCGGAGG CGGTCAAGCG
501 GAAACACGGA TTGCGGATTG CCAACCTGTT GGAGCTGATT AAGCCGTATC
551 TGCCCGAAAG CGTGCCGATG TATCCCGAAG ATATGGTTAC GGACAAATCG
601 GCGCGTTTTT TAGCGATGGA AATCGTGCGT GAAAAATTGT TCCGCTATTT
651 GGGCGAGGAA TTGCCTTATG CGATGAACGT CGAAGTGGAG CAGTTTGAAG
701 AGGAAGACGG TTTGAACCGC ATCTATATCG CCGTTTGGT CGATAAGGAA
751 AGCCAAAAGG CGATTTTAAT CGGCAAAGGC GGGGAGCGTT TGAAGAAAT
801 TTCCACCGAA GCGCGGTTGG ATATGGAAAA ACTGTTGAT ACCAAAGTAT
851 TTTTGAAGGT CTGGGTCAA GTCAAATCCG GTTGGGCGGA CGACATCCGC
901 TTCCTGCGCG AGCTGGGTTT GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2212; ORF 673.a>:

```

a673.pep
1  MDIETFLAGE RAADGYRCGF VAIVGRPNVG KSTLMNHLIG QKISITSKKA
51  QTTRNRVTGI YTDDTAQFVF VDTPEGFQDH RNALNDRLNQ NVTEALGGVD
101 VVVVFVEAMR FTDADRVVLK QLPKHTPVIL VVNKIDKDKA KDRYALEAFV
151 AQVRAEFefa AAEAVSAKHG LRIANLLELI KPYPLESVPM YPEDMVTDKS
201 ARFLAMEIVR EKLFYRLGEE LPYAMNVEVE QFEEEDGLNR IYIAVLVDKE
251 SQKAILIGKG GERLKKISTE ARLDMEKLFDT KVFVKVWVK VKSGWADDIR
301 FLRELGL*

```

m673/a673 99.7% identity in 307 aa overlap

```

           10      20      30      40      50      60
m673.pep  MDIETFLAGERAAGGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a673      MDIETFLAGERAADGYRCGFVAIVGRPNVGKSTLMNHLIGQKISITSKKAQTTRNRVTGI
           10      20      30      40      50      60

```

	70	80	90	100	110	120
m673.pep	YTDDTAQFVFDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
a673	YTDDTAQFVFDTPGFQTDHRNALNDRLNQNVTEALGGVDVVVFVVEAMRFTDADRVVLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m673.pep	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
a673	QLPKHTPVILVVNKIDKDKAKDRYALEAFVAQVRAEFEEFAAAEAVSAKHGLRIANLLELI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m673.pep	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFRYLGEELPYAMNVEVEQFEEDGLNR					
a673	KPYLPESVPMYPEDMVTDKSARFLAMEIVREKLFRYLGEELPYAMNVEVEQFEEDGLNR					
	190	200	210	220	230	240
	250	260	270	280	290	300
m673.pep	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
a673	IYIAVLVDKESQKAILIGKGERLKKISTEARLDMEKLFDTKVFLKVWVKVSGWADDIR					
	250	260	270	280	290	300
m673.pep	FLRELGLX					
a673	FLRELGLX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2213>:

```

g674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAAGCGGACG AAGAATTGTT CAACAACTC
151 TTCTTCGGCA CACAAACCAA TGCAGCGGAC TACATCCAAA AAATCCGCCC
201 GCTGCTCGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTTTCCGCTA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCAGACGA GCCCAAACGC CGTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2214; ORF 674.ng>:

```

g674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
51  FFGTQTNAAD YIQKIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP
101 VIINEAIEVT KTFGGTDGKH FVNGILDKLA AQIRPDEPKR R*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2215>:

```

m674.seq
1  ATGAAAACAG CCCGCCGCGG TTCCCGCGAG CTTGCCGTAC AAGCCGTTTA
51  CCAATCCCTT ATCAACCGCA CCGCCGCGCC CGAAATTGCT AAAACATCC
101 GCGAAATGTC CGACTTTGCC AAGGCAGACG AAGAATTGTT CAACAACTT
151 TTCTTCGGCA CGCAAACCAA TGCAGCGGAC TATATCCGAC AAATCCGCCC
201 GCTACTTGAC AGGGACGAAA AAGACCTCAA CCCCATCGAA CGCGCCGTTT
251 TGCTGACCGC CTGCCACGAG CTGTCCGCCA TGCCCGAAAC GCCCTACCCC
301 GTCATTATCA ACGAAGCCAT CGAAGTTACC AAAACCTTCG GCGGCACGGA
351 CGGGCACAAA TTCGTCAACG GCATCCTCGA CAAACTCGCC GCCCAAATCC
401 GCCCGACGA GCCCAAACGC CGTTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 2216; ORF 674>:

```

m674.pep
1  MKTARRRSRE LAVQAVYQSL INRTAAPEIA KNIREMSDFA KADEELFNKL
  
```

1082

51 FFGTQTNAAE YIRQIRPLLD RDEKDLNPIE RAVLLTACHE LSAMPETPYP  
 101 VIINEAIEVT KTFGGTDGHK FVNGILDKLA AQIRPDEPKR R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m674/g674 97.9% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
g674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLD RDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	::					
g674	YIQIRPLLD RDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
g674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2217>:

a674.seq

1	ATGAAAACAG	CCCGCCGCCG	TTCCCGCGAG	CTTGCCGTAC	AAGCCGTTTA
51	CCAATCCCTT	ATCAACCGCA	CCGCCGCGCC	CGAGATTGCT	AAAAACATCC
101	GCGAAATGCC	CGACTTTGCC	AAGGCAGACG	AAGAATTGTT	CAACAACTT
151	TTCTTCGGCA	CGCAAACCAA	TGCGGCAGAG	TACATCCGAC	AAATCCGCCC
201	CCTGCTCGAC	CGCGACGAAA	AAGACCTCAA	CCCCATCGAA	CGCGCCGTCC
251	TGCTGACCGC	CTGCCACGAG	CTGTCCGCCA	TGCCCCGAAAC	GCCCTACCCC
301	GTATCATCA	ACGAAGCCAT	CGAAGTAACC	AAAACCTTCG	GCGGCACGGA
351	CGGGCACAAA	TTCGTCAACG	GCATCCTCGA	CAAACCTCGC	GCCCAAATCC
401	GTCCCGACGA	GCCCAAACGC	CGTTGA		

This corresponds to the amino acid sequence <SEQ ID 2218; ORF 674.a>:

a674.pep

1	MKTARRRSRE	LAVQAVYQSL	INRTAAPEIA	KNIREMPDFA	KADEELFNKL
51	FFGTQTNAAE	YIRQIRPLLD	RDEKDLNPIE	RAVLLTACHE	LSAMPETPYP
101	VIINEAIEVT	KTFGGTDGHK	FVNGILDKLA	AQIRPDEPKR	R*

m674/a674 99.3% identity in 141 aa overlap

	10	20	30	40	50	60
m674.pep	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMSDFAKADEELFNKLFFGTQTNAAE					
a674	MKTARRRSRELAVQAVYQSLINRTAAPEIAKNIREMPDFAKADEELFNKLFFGTQTNAAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m674.pep	YIRQIRPLLD RDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
a674	YIRQIRPLLD RDEKDLNPIERAVLLTACHELSAMPETPYPVIINEAIEVTKTFGGTDGHK					
	70	80	90	100	110	120
	130	140				
m674.pep	FVNGILDKLAAQIRPDEPKRRX					
a674	FVNGILDKLAAQIRPDEPKRRX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2219>:

g675.seq

```
1 ATGAACACCA TCGCCCCaa cctcgacgGC AAACACCTCC GCATCGGCAT
51 CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCCAAATG CTCAAAGTCT
1 01 GCTGCCGCAC CCTCCAAGAA TTGGGCGTAG CAGACGAAAa catcaccgtc
1 51 gCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAAC TTGC
2 01 CTCTTCGAA AAATTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
2 51 GCGAAACCTA CCATTTCGAG CTGGTTGCCA ACGAATCCGG CGCAGGGATC
3 01 GGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAACG CCGTCCTGAC
3 51 CACCGAAAAC GACGCGCAGG CAATTGAACG GATTGGAGAA AAAGCCTCGG
4 01 ATGCCGCCAA AGTCGCCGTA GAATGCGCCA ACCTCGTCAA CCTTCTGCTC
4 51 GAAGAACAGT TTGAAGACGA AGAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2220; ORF 675.ng>:

1084

g675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSQM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVANESGAGI
101 GRVALDYNIP IANAVLTEN DAQAIERIGE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2221>:

m675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCCGAA AAGTTTGACG CACTGATTGC CATCGGCGTC GTCATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGCGTC
301 AGCCGCGTCG CACTCGACTA CAATATCCCG ATTGCCAATG CCGTCCTAAC
351 CACCGAAAAC GACGCGCAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTC GAATGCGCCA ACCTCGTCAA CCGTCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2222; ORF 675>:

m675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV
101 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL
151 EEQFEDEE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m675/g675 96.8% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCCTRLQELGVADENITVATVPGALEIP					
g675	MNTIAPNLDGKHLRIGIVQARFTNEIGSQMLKVCCTRLQELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFE LVSNEGAGVSRVALDYNIPIANAVLTEN					
g675	IALMNFASSEKFDALIAIGVVIRGETYHFE LVANESGAGIGRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130 140 150 159					
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEX					
g675	DAQAIERIGEKASDAAKVAVECANLVNLLLEEQFEDEX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2223>:

a675.seq

```

1  ATGAACACCA TCGCCCCCAA CCTCGACGGC AAACACCTCC GCATCGGCAT
51  CGTACAGGCA CGCTTCACCA ACGAAATCGG CAGCGAAATG CTCAAAGTCT
101 GCTGCCGCAC CCTCCAAGAA TTGGGCGTGG CAGACGAAAA CATTACCGTC
151 GCCACCGTAC CCGGCGCGCT TGAAATCCCC ATCGCGCTGA TGAACTTTGC
201 CTCTTCTGAA AAATTGACG CACTGATTGC CATCGGCGTC GTTATCCGTG
251 GCGAAACCTA CCATTTGAG CTGGTTTCCA ACGAATCCGG AGCAGGGGTC
301 AGCCGCGTCG CACTCGACTA CAACATCCCG ATTGCCAATG CCGTCCTGAC
351 CACGGAACAA GACGCACAGG CAATCGAACG GATTGAAGAA AAAGCCTCGG
401 ATGCCGCCAA AGTCGCGGTA GAATGCGCCA ACCTCGTCAA CCTCCTGCTC
451 GAAGAACAGT TTGAAGACGA AGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2224; ORF 675.a>:

a675.pep

```

1  MNTIAPNLDG KHLRIGIVQA RFTNEIGSEM LKVCCTRLQE LGVADENITV
51  ATVPGALEIP IALMNFASSE KFDALIAIGV VIRGETYHFE LVSNEGAGV

```

1085

1 01 SRVALDYNIP IANAVLTEN DAQAIERIEE KASDAAKVAV ECANLVNLLL  
1 51 EEQFEDEE\*

m675/a 675 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m675.pep	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLOELGVADENITVATVPGALEIP					
a675	MNTIAPNLDGKHLRIGIVQARFTNEIGSEMLKVCRTLOELGVADENITVATVPGALEIP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m675.pep	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
a675	IALMNFASSEKFDALIAIGVVIRGETYHFELVSNESGAGVSRVALDYNIPIANAVLTEN					
	70	80	90	100	110	120
	130	140	150	159		
m675.pep	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
a675	DAQAIERIEEKASDAAKVAVECANLVNLLLEEQFEDEEX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2225>:

g677.seq  
1 ATGCCGAGA TTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTg  
51 ggAAACGGTG CGCTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGGC CTTCGGCGGT  
151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGG CAACGCGCCA  
201 ACGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGACG  
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGCCGCGCA ACAGACCGAC  
301 GGTGCGCGCG AAAAATACTT GGTGCGTTCG TCGCGCAAT TCGGGATCGA  
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG  
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG  
451 GTCGCGGTTG CTGCGCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2226; ORF 677.ng>:

g677.pep  
1 MPQILVRIFL IRYFSIWETV RLCRFRHSR SVDFDVDRK DFNFLTAFFR  
51 VQNHVAFAR FNQATRQRN PRNFVLRIGD FIDADDFDGL LAPVAAQQT  
101 GRAEKYLVR FAQFGIDDDG SLQTFGOETD AAVDFAHTAF AVKIVAVFAA  
151 VAVACRPVDD LDDEGAFFID QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2227>:

m677.seq  
1 ATGCCGAGA TTTGGTGCG GATTTTCCTC ATTCGGTATT CCTTTATTG  
51 GGAAACGGCG CGCTTTTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
101 TTGATGTATT CGACAGAAAG GATTTCAATT TCCTCACGCC CTTCGGCGGT  
151 GTTCAAAACC ACTTCGTGCG CTTCGCGCGC TTTAATCAGA CAACGAGCCA  
201 GCGGCGAAAT CCAAGAAATT TTGTTTTGCG CGGTATCGAT TTCATCGATG  
251 CCGACGATTT TGACGGTTTG CTCGCGCCCG TCGTCGCGCA ACAGTCCGAC  
301 CGTCGCGCGG AAAAACAATT GGTGCGTTCG TCGCGCAAT TCGGGATCGA  
351 CGACGACGGC AGCCTCCAAA CGTTTGGTCA GGAAACGGAT GCGGCGGTG  
401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGA TAGTCGCGT TTTGCTGCG  
451 GTCGCGGTTG CTGCGCGCCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
501 CTTTATTGAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGGCG  
551 GCGTAATGT AGTTTTTGGT TTCGGTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2228; ORF 677>:

m677.pep  
1 MPQILVRIFL IRYFSIWETA RLCRFRHSR SVDFDVDRK DFNFLTPFRR

1086

51 VQNHFAFAR FNQTSQRRN PRNFVLRGID FIDADDFDGL LAPVVAQQSD  
 1 01 RRAEKHLVGR FAQFGIDDDG SLQTFGQETD AAVDFAHTAF AVKIVAVFAA  
 1 51 VAVACRPVDD LDDEGAFFVD QLIKLVFQCL PSGGRNVVFG FGTHIVCG\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

m677/g677 94.9% identity in 198 aa overlap

m677.pep	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
g677	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETVRLCRFRHRSVDFDVFDRKDFNLTAFRRVQNHFAFAR					
m677.pep	70	80	90	100	110	120
	FNQTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRRAEKHLVGRFAQFGIDDDG					
g677	70	80	90	100	110	120
	FNQATRQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGDAEKYLVGRFAQFGIDDDG					
m677.pep	130	140	150	160	170	180
	SLQTFGQETDAAVDFAHTAFVAVFAAFAVACRPVDDLDDFGAFFVDQLIKLVFQCL					
g677	130	140	150	160	170	180
	SLQTFGQETDAAVDFAHTAFVAVFAAFAVACRPVDDLDDFGAFFIDQLIKLVFQCL					
m677.pep	190	199				
	PSGGRNVVFGFGTHIVCGX					
g677	190					
	PSGGRNVVFGFGTHIVCGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2229>:

a677.seq  
 1 ATGCCGCGA TTTTGGTGCG GATTTCCTC ATTCCGTATT CCTTTATTG  
 51 GGAAACGGCG CGTTTGTGCC GTTTCAGACG GCATTCCCGA TCAGTCGATT  
 101 TTGATGTATT CGACAGAAAG GATTCAATT TCCTCAGGCC CTTCCGGCGT  
 151 GTTTAAACCC ACTTCGTCGC CTTACGCGC TTTAATCAGA CAACGAGCCA  
 201 GCGGCGAAAT CCAAGAAATT TTGTTTTCG CCGTATCGAT TTCATCGATG  
 251 CCGACGATT TGACGGTTG CTCGCGCCG TCGCGCGCA ACAGACCGAC  
 301 GGTGCGCGCG AAAAACACTT GGTGCGTCG TTCGCGCAAT TCGGGATCAA  
 351 CGACGACGGC GGCTTCCAAA CGCTGGTCA GGAAACGGAT GCGGCGGTGCG  
 401 ATTTGCGGCA TACGGCGTTT GCCGTAAAGG TAGTCGCGGT TTTCGCTGCG  
 451 GTCGCGGTTG CCGCGCGCC AGTTGACGAT TTGGACGATT TCGGGGCGTT  
 501 CTTTATTAAC CAGTTGATAA AGCTCGTCTT TCAATGCCTG CCATCCGCGC  
 551 GCGTAATGT AGTTTGGT TTCGCTACTC ATATTGTGTG CGGATGA

This corresponds to the amino acid sequence <SEQ ID 2230; ORF 677.a>:

a677.pep  
 1 MPQILVRIFL IRYFSIWETA RLCRFRHRS SVDFDVFDRK DFNFLT

m677/a677 93.4% identity in 198 aa overlap

m677.pep	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARFCRFRHRSVDFDVFDRKDFNFLT	PFRRVQNHFAFAR				
a677	10	20	30	40	50	60
	MPQILVRIFLIRYSFIWETARLCRFRHRSVDFDVFDRKDFNFLT	PFRRVXNHFAFAR				
	70	80	90	100	110	120

1087

```

m677.Pep  FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVVAQQSDRAEKHLVGRFAQFGIDDDG
|||||
a677      FNQTTSQRRNPRNFVLRGIDFIDADDFDGLLAPVAAQQTGAEKHLVGRFAQFGINDDG
              70      80      90      100     110     120

              130     140     150     160     170     180
m677.Pep  SLQTFGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFVDQLIKLVFQCL
:|:|:|
a677      GFQTLGQETDAAVDFAHTAFVAVKIVAVFAAVAVACRPVDDLDFFGAFFINQLIKLVFQCL
              130     140     150     160     170     180

              190     199
m677.Pep  PSGGRNVVFGFGTHIVCGX
|||||
a677      PSGGRNVVFGFGTHIVCGX
              190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2231>:

```

g678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GCCTccgCCG TCATCGCCGC
51  CTGCATCGTC ATTCCACGA TCGCGGCGT GATTGCGGAA GCAGgttcGA
1 01 TGGTgGCATG ggtggTTTcc tTCTTTTttg ccAAACTCTt tGCCGCACcc
1 51 ttcgcccACC TCGCCTTTGc ctCGTTCCAA ccccgccTGT TTGCAttggc
2 01 tCTGTcATTC ATTTCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
2 51 TCCGTTcGCT GCTGACCGGC GCAGTTTCGG CGGTcGGTCT GGGCTTTGCC
3 01 AACCGcATTT TGGGCGGTGT ATTcGGTGCA TTGAAAGGCG TTTTGATTGT
3 51 TACCCTGCTG ATCATGCTTG CTTCAAAAAC CGACCTGCC GATACCGAAG
4 01 AATGGCAACA GTCCTATACC GTACCGTTT TCGTATCGCT TTCCGAAGCG
4 51 GTGTTAAACC atacggaCAA CGCaccgaa tCCctcgacg acgactaa

```

This corresponds to the amino acid sequence <SEQ ID 2232; ORF 678.ng>:

```

g678.pep
1   MNSLPIADLL ASAVIAACIV ISTMrgVIAE AGSMVAWVVS FFFAKLFAAP
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLLTG AVSAVGLGFA
1 01 NRILGGVFGA LKGVLIvTLL IMLASKTDLP DTEEWQSYT VPFFVSLSEA
1 51 VLNHTDNAPE SLDDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2233>:

```

m678.seq
1   ATGAATAGCC TCCCCATTGC CGACCTCCTC GTCTCCGCCG TCATCGCCGC
51  CTGCATCGTG CTATCCGCGA TCGCGGCGT GATTGCGGAG GCAGGCTCAA
1 01 TGGCGGCATG GGTGGTTTCC TTCTTTTTCG CCAAACCTTT TGCCGCCTCC
1 51 TTCGCCGACC TCGCCTTTGC CTCGTTCCAA CCCCgcCTGT TTGCATTGGC
2 01 TCTGTcGTTc ATTTCCTGT TCGTCATTGC CTGTCTGATC CAGAAAATGC
2 51 TCCGTTcGCT GCTGACCAGC GCAGTTTCGG CGGTcGGTTT GGGCTTTGCC
3 01 AACCGcATTT TGGGCGGCGT ATTcGGTGCA TTGAAAGGCG TTTTGATTGT
3 51 TACCCTGCTG GTCATGCTTG CTTCAAAAAC CGACCTGCC GATACCGAAG
4 01 AATGGCGGCA ATCTTACACA CTGCCGTTT TCGTATCGCT TTCCGAAGCC
4 51 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2234; ORF 678>:

```

m678.pep
1   MNSLPIADLL VSAVIAACIV LSAMrgVIAE AGSMAWVVS FFFAKLFAAS
51  FADLAFASFQ PRLFALALSF ISLFVIACLI QKMLRSLTTS AVSAVGLGFA
1 01 NRILGGVFGA LKGVLIvTLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
1 51 VLNHSGGTAE TPEDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m678/g678 89.7% identity in 165 aa overlap



1088

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	:     :     :     :     :					
g678	MNSLPIADLLASAVIAACIVISTMRGVIAEAGSMVAWVVSFFFAKLFAAPFADLAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	:     :     :     :     :					
g678	PRLFALALSFISLFVIACLIQKMLRSLTGAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	:     :     :     :     :     :					
g678	IMLASKTDLPDTEEWQSYTVPFFVSLSEAVLNHTDNAPESLDDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2235>:

```

a678.seq
1  ATGAATAACC TCCCCGTTGC CGACCTCCTC GTCTCCGCCA TCATCGCCGC
51 CTGCATCGTG CTATCCGCGA TGCGCGGCGT GATTGCGGAG GCTGGCTCAA
101 TGGCGGCATG GGTGGTTGCC TTTTTCCTCG CCAAACCTTT TGCCGCACCC
151 TTCGCCGACA TCGCCTTTGC ATCGTCCAA CCCCAGCTGT TTGCATTGGC
201 TCTGTCGTC ATTCCCTAT TCGTCATTGC CTGTCTGATC CAGAAAATAC
251 TCCGCTCGCT GCTGACCGGG GCAGTTTCGG CGGTCGGTTT GGGCTTTGCC
301 AACCGCATTT TGGCGGCGT ATTCGGTGCA TTGAAAGGCA TTTTGATTAT
351 TACCCTGCTG GTCATGCTCG CTTCAAAAAC CGACCTGCCC GATACCGAAG
401 AATGGCGGCA ATCTTACACA CTGCCGTTTT TCGTATCGCT TTCCGAAGCC
451 GTGTTGAACC ATAGCGGCGG CACGGCGGAA ACTCCGAAG ACGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2236; ORF 678.a>:

```

a678.pep
1  MNNLPVADLL VSAIIAACIV LSAMRGVIAE AGSMAAWVVA FFFAKLFAAP
51  FADIAFASFQ PRLFALALSF ISLFVIACLI QKILRSLTGA AVSAVGLGFA
101 NRILGGVFGA LKGILIIITLL VMLASKTDLP DTEEWQSYT LPFFVSLSEA
151 VLNHSGGTAE TPEDD*

```

m678/a678 93.9% identity in 165 aa overlap

	10	20	30	40	50	60
m678.pep	MNSLPIADLLVSAVIAACIVLSAMRGVIAEAGSMAAWVVSFFFAKLFAASFADLAFASFQ					
	:     :     :     :     :					
a678	MNNLPVADLLVSAIIAACIVLSAMRGVIAEAGSMAAWVVAFFFAKLFAAPFADIAFASFQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m678.pep	PRLFALALSFISLFVIACLIQKMLRSLTSAVSAVGLGFANRILGGVFGALKGVLIIVTLL					
	:     :     :     :     :					
a678	PRLFALALSFISLFVIACLIQKILRSLTGAVSAVGLGFANRILGGVFGALKGILIIITLL					
	70	80	90	100	110	120
	130	140	150	160		
m678.pep	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	:     :     :     :     :					
a678	VMLASKTDLPDTEEWQSYTLPFFVSLSEAVLNHSGGTAETPEDDX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2237>:

```

g680.seq
1  ATGACGAAGG GCAGTTCGGC GATGTCCAGC CCACGCGCGG CGATATCGGT
51  GCGGACGAGG ACGGCGAGGC TGCCGTCTTT GAAGGCGTTG AGTGTTCGA
101 GCCTGCTTTC TTGGGAACGG TCGCCGTGTA TCGCTGTGC GGACAGGTTG

```

```

151 CGGCGCACCA GTTCGCGCGT TACGCGGTG ACGCTTTGTT TGGTtttgCA
201 AAAGACGATA ACTTGGTTCA TATGCAGATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCTT TTGGAAGGTA TCGACGGCGA TGATGTgttg ttcGACGTTG
301 GCGTTGGTGG TGTTTTGGGC GGCAACCTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGTGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAACC CCATATCCAA CATGCGGTCT GCTTCGTCCA GAACGACGAT
501 TTCGGCTTGT TTTAACTGA TGTTTTCTG TTTACATGG TCGAGCAGCC
551 GTCCGACGGT GGCACGACT ATTTCCGAGC CGGCACGCAG GTCGGCGGTT
601 TGTTTGTCCA TGTTGACACC GCCGAAGAGG ACGGTATGCC GCAGCGGCAG
651 GTTTTTAATg tag

```

This corresponds to the amino acid sequence <SEQ ID 2238; ORF 680.ng>:

```

g680.pep
1 MTKGSSAMSS PRAAISVATR TRRLPSLKAL SVSSLLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQKTI TWFICRSTIS RSSRLRFWKV STAMMCCSTL
101 ALVVFWAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SINPISNMRS ASSRTTISAL FKLMEFCFTW SSSRPTVATT ISQPARRSAV
201 CLSMLTPPKR TVCRSGRFLM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2239>:

```

m680.seq
1 ATGACGAAGG GCAGTTCGGC AATGTCCAGC CCGCGCGCGG CGATGTCGGT
51 GGCAGCAGAG ACGCGCAGGT TGCCGTCTTT GAAGGCGTGT AGTGTTCGCA
101 GCCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTG ACGCTTTGTT TGGTTTTCGA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCGCT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGTTTTGGCG GGCGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTTG GCGTTGGCGG GGCAGCATCT GCATGATTTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATAAGGTG GCTTCGTCCA AAACGACGAT
501 TTCGACTTTG TTCAAATGGA TGTTTTCTG TTTACGTTG TCGAGCAGCC
551 GTCCGACGGT GGCACGAGC ATTTCCGAGC CGGCACGCAG GTCGGCGGTC
601 TGTTTGTCCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTGTATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2240; ORF 680>:

```

m680.pep
1 MTKGSSAMSS PRAAMSVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51 RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVECAATS TVSGAFMKSC ASLRIGAELV AEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMEFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m680/g680 90.9% identity in 220 aa overlap

```

          10      20      30      40      50      60
m680.pep MTKGSSAMSSPRAAMSVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      MTKGSSAMSSPRAAISVATRTRRLPSLKALSVSSLLCWERSPCACADRLRRTSSRVTRS
          10      20      30      40      50      60

          70      80      90     100     110     120
m680.pep TLCLVLQNTMTWFICKSTISRSSRLRFKXVMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g680      TLCLVLQKTIITWFICRSTISRSSRLRFWKVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
          70      80      90     100     110     120

          130     140     150     160     170     180
m680.pep ASLRIGAELVAEKSRVWRWRGSICMILRMSSIKPISSIRSASSKTTISTLFKWMEFCFTW

```

1090

```

|||||
g680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSINPISNMRSASSRTTISALEFKLMFFCFTW
           130      140      150      160      170      180

           190      200      210      220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
           |||||
g680      SSSRPTVATTISQPARRSAVCLSM LTPPKRTVCRSGRFLMX
           190      200      210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2241>:

```

a680.seq
1  ATGACGAAGG GCAGTTCGGC AATATCCAGC CCCC GCGCGG CGATATCGGT
51  GGCGACGAGG ACGCGCAGGT TGCCGCTCTT GAAGGCGTTG AGTGTTCGCA
101 GCGGCTTTG TTGGGAACGG TCGCCGTGTA TCGCCTGTGC GGACAGGTTG
151 CGGCGCACCA GTTCGCGCGT TACGCGGTCG ACGCTTGTG TGGTTTTGCA
201 GAACACGATG ACCTGGTTCA TATGCAAATC GACAATCAGC CGTTCGAGCA
251 GGTTCGCTT CTGAATGGTA TCGACGGCGA TGATGTGCTG CTCGACGTTG
301 GCGTTGGTGG TGCTTGCGC GCGGACTTCG ACGGTTTCGG GCGCGTTCAT
351 GAAGTCTTGC GCCAGTTTGC GTATCGGGGC GGAGAAGGTG GCGGAAAAGA
401 GCAGGGTTG GCGTTGGCGG GGCAGCATCT GCATGATTT GCGGATGTCG
451 TCGATAAAAC CCATATCCAG CATA CGGTGCG GCTTCGTCCA AAACGACGAT
501 TTCGACTTGG TTCAAATGGA TGTTTTCTG TTTCACGTGG TCGAGCAGCC
551 GTCCGACGGT GCGCAGCAGC ATTCGCGAG CCGCAGCAG GTCGGCGGTC
601 TGTTTGTTCA TATTCATACC GCCGAACAAG ACGGTGTGGC GCAGCGGCAG
651 GTTTTTGATG TAG

```

This corresponds to the amino acid sequence <SEQ ID 2242; ORF 680.a>:

```

a680.pep
1  MTKGSSAISS PRAAISVATR TRRLPSLKAL SVSSRLCWER SPCACADRL
51  RRTSSRVTRS TLCLVLQNTM TWFICKSTIS RSSRLRF*MV STAMMCCSTL
101 ALVVSCAATS TVSGAFMKSC ASLRIGA EKVAEKSRVWRWR GSICMILRMS
151 SIKPISSIRS ASSKTTISTL FKWMFFCFTW SSSRPTVATT ISQPARRSAV
201 CLSIFIPPNK TVWRSGRFLM *

```

m680/a680 98.6% identity in 220 aa overlap

```

           10      20      30      40      50      60
m680.pep  MTKGSSAMSSPRAAMS VATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
           |||||:|||||:|||||:|||||:|||||:|||||
a680      MTKGSSAISSPRAAISVATRTRRLPSLKALSVSSRLCWERSPCACADRLRRTSSRVTRS
           10      20      30      40      50      60

           70      80      90      100     110     120
m680.pep  TLCLVLQNTMTW FICKSTISRSSRLRF XMVSTAMMCCSTLALVVFCAATSTVSGAFMKSC
           |||||:|||||:|||||:|||||:|||||:|||||
a680      TLCLVLQNTMTW FICKSTISRSSRLRF XMVSTAMMCCSTLALVVS CAATSTVSGAFMKSC
           70      80      90      100     110     120

           130     140     150     160     170     180
m680.pep  ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTL FKWMFFCFTW
           |||||:|||||:|||||:|||||:|||||:|||||
a680      ASLRIGA EKVAEKSRVWRWRG SICMILRMSSIKPISSIRSASSKTTISTL FKWMFFCFTW
           130     140     150     160     170     180

           190     200     210     220
m680.pep  SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
           |||||:|||||:|||||:|||||:|||||:|||||
a680      SSSRPTVATTISQPARRSAVCLSIFIPPNKTVWRSGRFLMX
           190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2243>:

```

g681.seq
1  ATGACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCGG AAGAGGCAAA
51  GTTCATCAGC GCGATGGGGA TTCAAGCGC GCCGGGTACG GTGGcgacgg

```

```

101 t gatgtTTTC GTCTGCTACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 T TGAGCATTT GGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTCGCGT cgaggttgGG GGCGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGGGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCAACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ACGCGCTGCC TTCGGGTTGG GAAAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGTGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCTCGGT
451 GTATTCGTCG GTTTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAAAGGAAGC CGACGGGCCG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT GCACGGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTTG GGGGGGGGGA AACTTGCGGA
651 TTTTACCACG ATTCGGCGT TGTCCGCGA CGGCGCGGT TTGGTGGTAC
701 AATGTGCGCC GTTTCAGCC TTAAGGTGT TCTGTATTT TGGAGTATGG
751 AAACGCATTC GGGCTGTTTT TTGCGGAAGA CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2244; ORF 681>:

**g681.pep**

```

1 MTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51 LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVNGLECA AVFGKLPRAA FGLGKQCGGF RVFGDVGGEA DDAEVVGVVG
151 VFVGFVAEE TPAAVVFKNG GFAVKEADGP VLFGDVGVDG AAVECRGKCL
201 CKCVHCGNTL GGGKLAFTT IPALSADGGG LVVQCAPFAA LRCFCIFGVW
251 KRIRAVFCGR R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2245>:

**m681.seq**

```

1 ATGACGACGC CGATGGCAAT CAGTGCCTCA AACTTTTCGG AAGAGGCAAA
51 GTTCATCAGC GCGATGGGGA TTTCAGCGC GCCGGGTACG GTGGCGACGG
101 TAATGTTTTT GTCTGCCACG CCCAATTCTT GGAGGGTGCG GCAGCAGACT
151 TTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTCGCGT CGAGGTTGGG GGCGATGGTG TTCATTGGGT
251 GTCCTTTGGT ATTCGGAGTT TCGGAATGCC GTCTGAAGGT TTCAGTCTTG
301 CGGCTGCCAG TCGGCGACGG TTTGGAATGT GCCGTCTTCG GCAAGCTCCC
351 ATGCGCTGCC TTCGGGTTGG GAGAGCAGTG CGGCGGTTTC AGGGTTGGTT
401 TTGGCGATGT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GATCGTCCGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGG TAGAGGAAGC CGACGGGCCG GTTTTGTGTTG
551 GCGACGGTGT TGGTGGCGAT ACAGCGGTCG AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTACGG GAATACGTTG GGGG.AAAAC TTACGGATTT
651 TACCACGATT CGTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCGGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGA
751 CGCATTCCGG CTGTTTTTTG CGGAAGACGG TAA

```

This corresponds to the amino acid sequence <SEQ ID 2246; ORF 681>:

**m681.pep**

```

1 MTTPMAISAS NFSEEAKFIS AMGISSAPGT VATVMFSSAT PNSWRVRQQT
51 LSIWLPISLV KRACTMPMRR CLPSRLGAMV FIGCPLVFGV SECRLKVSVL
101 RLPVGDGLECA AVFGKLPCAA FGLGEQCGGF RVFGDVGGEA DDAEVVRIVG
151 VFVGLVAEE TPAAVVFKNG GFAVEEADGP VLFGDVGVDG TAVECRGKCL
201 CKCVHYGNTL GXKLTDFTT RALSADGGGL VVQCAPFAAL RCFCIFGVWK
251 RIRAVFCGR *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* menA with menB

ORF 681 shows 94.6% identity over a 261 aa overlap with a predicted ORF (ORF681.a) from *N. gonorrhoeae*:

**m681/g681**

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPISLV					
g681	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSIWLPISLV					
	10	20	30	40	50	60

```
a681.seq
1   ATAACGACGC CGATGGCAAT CAGTGCCTCA AATTTTTCAG AAGAGGCCAA
51  GTTCATCAGC GCGATGGGGA TTTCAAGCGC GCCGGGTACG GTGGCGCAGG
101 TAATGTTTTG GTCTGCGACG CCCAATTCTT GCGAGGTTGC GTCCAGACAT
151 TTTGAGCATTT CGCTGCCGAT TTCGTTGGTG AAGCGTGCCT GTACGATGCC
201 GATGCGGAGG TGTTTGCCGT CGAGGTTGGG GCGCATGGTG TTCATTGAGT
251 GTCCTTTGGT ATTCGGAGGT TTCGGAATGC CGCTGAAGG GTCACTCTTT
301 AGGTTGCCAG TCGCGGACGG TATGGAATGT CCGCTCTTCT GCCAATTCCT
351 ACGCGCTGCC TTCAGGTTGG GAGAGCAGTG CGCGGGTTTC AGGGTTGGTT
401 TTGGTGATAT CGGCGAGGCT GACGATGCTG AAGTTGTCCG GGTCGTCGGT
451 GTATTCGTCG GTCTCGTCGC CGCTGAAGAA ACGCCAGCCG CTGTCGTTTT
501 CAAAAACGGG GGCTTCGCGC TAGAGGAAGC CGACGGGCTG GTTTTGTGTT
551 GCGACGGTGT TGGTGCCGAT GCAGCGGTCT AGTGCCGAGG AAAGTGCTTG
601 TGCAAATGCG TTCATTGCGG GAATACGTT. GGGGGA AAC TTGCGGATTT
651 TACCACGATT CTTGCGTTGT CGGCAGACGG CGGCGGTTTG GTGGTACAAT
701 GTGCGCCGTT TGCAGCCTTA AGGTGTTTCT GTATTTTGG AGTATGGAAA
751 CGCATCTCGG CTGTTTTTTC CGGAAGACGG TAA
```

```

a681.pep
  1  ITPMAISAS  NFSEEAKFIS  AMGISSAPGT  VATVMFSSAT  FNSWRVRQQT
  51  LSISLPISLV  KRACTMPMRR  CLPSRLGAMV  FIECPLVFVG  FGMPSEGSVL
101  RLPVGDGLEC  AVFCQFPRAA  FRLGEQCGGF  RVFGPDIGEA  DDAEVRVVG
151  VEVGLVAAEE  TPAAVVFKNG  GFAVEEADGL  VLFGDGVGGD  AAVECRGKCL
201  KCVVHCNGTX  GGKLDFTTI  LALSADGGGL  VVQCPFAAL  RCFCIFGVWK
251  RIRAVFCGRR  *

```

	10	20	30	40	50	60
m681.pep	MTTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPSISLV					
	:					
a681	ITTPMAISASNFSEEAKFISAMGISSAPGTVATVMFSSATPNSWRVRQQTLSISLPSISLV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m681.pep	KRACTMPMRCLPSRLGAMVFIGCPLVFGVSECRCLKVSVLRLPVGDLGECVFGKLPCAA					
a681	KRACTMPMRCLPSRLGAMVFIETCPLVFGGFGMPSEGSVRLRLPVGDLGECVFCQFPRAA					
	70	80	90	100	110	120

	130	140	150	160	170	180
m681.pép	FGLGEQCGGFRVGF	GDVGEADDAEVVR	IVGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGP	
a681	FRLGEQCGGFRVGF	DIGEADDAEVVR	VGVFVGLVAAEET	PAAVVFKNGGFAVEE	ADGL	
	130	140	150	160	170	180
	190	200	210	220	230	240
m681.pép	VLFGDVGVD	TAVECRGKCLCK	CVHYGNTLGXKLT	DFTTIRALSADGGGL	VVQCAPFAAL	
a681	VLFGDVGVD	DAVECRGKCLCK	CVHCGNTXGKGLAD	FTTILALSADGGGL	VVQCAPFAAL	
	190	200	210	220	230	240
	250	260				
m681.pép	RCFCIFGVWKRIR	AVFCGRRX				
a681	RCFCIFGVWKRIR	AVFCGRRX				
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2249>:

## g682.seq

```

1  ATGCGCGATT TCGCCGTATG GGTGCCTTAC GGGGAACGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCC CGCACCTTAT TCGCCTGAGC CCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTATATTTGT GTGAATGATG AAATAAAAT GCGTCTGAA CCCGATTGGA
251 TTCAGACGGC ATTTTGTATG GCAGGATTTA TTCGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2250; ORF 682>:

## g682.pép

```

1  MRDFAVWVPY GERRKNWDIR YCLPHLIRLS PTRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDYIC VNDEIKMPSE PDWIQTAFCM AGFIREFTDR
101 PILTRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2251>:

## m682.seq

```

1  ATGCGTGATT TCACCGTATG GGTGTCTTAC GGGAAATGCG GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACCTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 CTAT..... GAAA TGGCAATGCC GTCTGAACCC GATTGGATTG
251 AGACGGCATT TTGTATGGCG TACGGATTTA TTCGGTTTCC AACTGACCGA
301 CCATTTCGGA CAAGGCAGTC AGGCGTTGTT CGGATTTCGC CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 2252; ORF 682>:

## m682.pép

```

1  MRDFTVWVSF GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
51  ITPDLTMHYC PILILIDY... EMAMPSEP DWIQTAFCA YGFIREFTDR
101 PIITRQSGVV RISPTGFRY PTRSLPKSKK AYG*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 682 shows 88.1% identity over a 134 aa overlap with a predicted ORF (ORF682.a) from *N. gonorrhoeae*:

m682/g682

```

a682.seq
1  ATGCGCGATT TTACCGTATG GGTGCTTAC GGGAAATGGC GGAAAAATTG
51  GGACATAAGG TATTGCCTCT TGCACTTAT TCACCTGAGC TCAACCCGAT
101 TGAGAAAGTG TGGGCGAATA TTAAGCGGTA TCTGCGAACC GTTTTGTCTG
151 ATTACGCCCG ATTTGACGAT GCACTACTGT CCTATTTTGA TTTTAATTGA
201 ATAT.....
251 .....TATA TTCGGTTTCC AACTGACCGA
301 CCCATTCTGA CAAGGCCGAC AGCGGTTGTT CGGATTTTCG CACGAACGGG
351 TTTTCGGTAT CCCACGCGTA GCCTGCCAAA ATCGAAGAAA GCATACGGCT
401 GA

```

```
a682.pap
  1 MRDFTVWVSY GKWRKNWDIR YCLLHLIHLs STRLRKCGRI LSGICEPFCL
 51 ITPDLTMHYC PILILIEY.. ..... ..YIRFPTDR
101 PILRPTGVV RISPRTGFRY PTRSLPKSKK AYG*
```

```

      10      20      30      40      50      60
m682.pep MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFLITPDLTMHYC
|||||
a682 MRDFTVWVSYGKWRKNWDIRYCLLHLIHLSSSTRLRKCGRILSGICEPFLITPDLTMHYC
      10      20      30      40      50      60

      70      80      90     100     110     120
m682.pep PILILIDYEMAMPSEPDIQTAFCMAYGFIREFPTDRPIRTQSGVVRISPERTGFRYPTRS
|||||:|
a682 PILILIEY-----YIRFPTDRPILTRPTGVVRISPERTGFRYPTRS
                               70      80      90     100

      130
m682.pep LPKSKKAYGX
|||||||
a682 LPKSKKAYGX
      110

```

```
g683.seq
1  ATGATTAAGG AAACCCATAAT GCGCCCAATC TTCTATCTT TCGTTTTACT
51  CCTATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATTAATAAA
151 GACAGTGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATTAATAAAT
201 TGTTACCAAT CTGAACAACG AACGTTTTCG CAACACCCCC GCATACAAGA
251 CTGCCATTGC CGAGTGGGAA ATCCATGCGA ACAACAAAAC ATACCGCTTA
301 AGTTCGCTAC AGTTATTTGA TACAAAAAAC ACGGAATTTT CCACACAAA
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCTTGTC CCAGACATTA
```

401 CTGAAAAACA ATATGAAACC GTATGCGGGA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2256; ORF 683>:

g683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK  
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL  
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2257>:

m683.seq..

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT  
51 CCC TATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG  
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA  
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCAAG ATAAAAAAGT  
201 TGT TACCAAT CTAACAACAG AACGTTTTCG CAACACCCCC GCATACAAGA  
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA  
301 AGT TCGCTAC AGTTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA  
351 CTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA  
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2258; ORF 683>:

m683.pep..

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK  
51 DSVRKNGNLM IFQDKKVVVN LKQERFANTP AYKTAIAEWE IHCNNKTYRL  
101 SSLQLFDTKN TEISTQNYTA SSLRPMSILS GTLTEKQYET VCGKKL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 683 shows 99.3% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. gonorrhoeae*:

m683/g683 99.3% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
g683	MIKETLMRPIFLSFVLLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
g683	IFQDKKVVVNLKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMSILSGTLTEKQYETVCGKKLX					
g683	SSLRPMSILSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2259>

a683.seq

1 ATGATTAAGG AAACCCTAAT GCGCCCAATC TTCCTATCTT TCGTTTATT  
51 CCC TATTTTG ATAACCGCCT GCAGCACACC GGACAAGTCT GCCCGATGGG  
101 AAAATATCGG CACAATCTCA AACGGCAATA TTCATACATA TATCAATAAA  
151 GACAGCGTGA GAAAAACGG AAATCTGATG ATTTTCCNAG ATAAAAAAGT  
201 TGT TACCAAT CTAACAACAG AACGTTTTCG CNACACCCCC GCATACAAGA  
251 CTGCCATTGC CGAGTGGGAA ATCCACTGCA ACAACAAAAC ATACCGCTTA  
301 AGT TCGCTAC AATTGTTTGA TACAAAAAAC ACGGAAATTT CCACACAAAA  
351 NTACACAGCC TCTTCCCTCC GCCCGATGAG CATCCTGTCC GGGACATTAA  
401 CCGAAAAACA ATATGAAACC GTATGCGGAA AAAAAGCTCTG A

This corresponds to the amino acid sequence <SEQ ID 2260; ORF 683.a>:

a683.pep

1 MIKETLMRPI FLSFVLLPIL ITACSTPDKS ARWENIGTIS NGNIHTYINK  
51 DSVRKNGNLM IFXDKKVVVN LKQERFAXTP AYKTAIAEWE IHCNNKTYRL



101 SSLQLFDTKN TEISTQXYTA SSLRPMISLS GTLTEKQYET VCGKKL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 683 shows 97.9% identity over a 146 aa overlap with a predicted ORF (ORF 683) from *N. meningitidis*:

m683/a683 97.9% identity in 146 aa overlap

	10	20	30	40	50	60
m683.pep	MIKETLMRPILFSLVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
a683	MIKETLMRPILFSLVLPILITACSTPDKSARWENIGTISNGNIHTYINKDSVRKNGNLM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m683.pep	IFQDKKVVTNLQKQERFANTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQNYTA					
a683	IFXDKKVVTNLQKQERFAXTPAYKTAIAEWEIHCNNKTYRLSSLQLFDTKNTEISTQXYTA					
	70	80	90	100	110	120
	130	140				
m683.pep	SSLRPMISLSGTLTEKQYETVCGKKLX					
a683	SSLRPMISLSGTLTEKQYETVCGKKLX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2261>

g684.seq

1	ATGCGCCTTT	TCCCCATCGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACCGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCATCAACAC
201	CGCACAAAAC	CATGTTTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAC	CTTTGTTCTT
301	GCCTCAGGCA	GCGGCAGTAC	CGACAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2262; ORF 684>:

g684.pep

1	MRLFPAAAL	TLAACGTQVS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGVLVYT	DPYRINTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRTFVP
101	ASRSGSTDKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAAL	QGLKQAAQCM	VE*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2263>:

m684.seq

1	ATGCGCCTTT	TCCCGATTGC	CGCCGCCCTG	TCGCTTGCCG	CCTGCGGTAC
51	TGTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CACGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTGAGCAA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTCTT
301	GCCTCAGGCA	GCGGCAGTAC	CGAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TTCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CGATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCGAGTAA			

This corresponds to the amino acid sequence <SEQ ID 2264; ORF 684>:

m684.pep

1	MRLFPAAAL	SLAACGTQVS	TQYFVLPDSR	YIRPATQGGG	TAVEVRLAEP
51	LKRGGVLVYT	DPYRLNTAQN	HVWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTEKW	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD

151 GYAAMTAALE QGLKQAAQOM VE\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 684 shows 97.7% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. gonorrhoeae*:

m684/g684 97.7% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
g684	MRLFPPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVIYIDAFQGS					
g684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVIYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	
m684.pep	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
g684	YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2265>

a684.seq

1	ATGCGCCTCT	TCCCGATTGC	CGCCGCCCTG	ACGCTTGCCG	CCTGCGGTAC
51	TGTTGCAAAGC	ACACAATATT	TCGTGTTGCC	CGACAGCCGC	TACATCCGTC
101	CTGCAACGCA	AGGCGGCGAA	ACTGCCGTCG	AAGTCCGTCT	TGCCGAACCG
151	CTCAAACGCG	GCGGACTGGT	CTATCAAACC	GACCCCTACC	GCCTCAACAC
201	CGCACAAAAC	CAGTCTGGG	CAGACACCTT	GGACGATATG	CTCGAAGCGG
251	CGTTTGAGCA	TGCATTCAAC	CGTTTGGACA	GCACACGCAT	CTTTGTTTCT
301	GCCTCACGCA	GCGGCAGTAC	CGAAAAATGG	ACGGTCTATA	TCGACGCATT
351	CCAAGGCAGC	TACACGGGCA	AAACCCCTCAT	CAGCGGCTAC	GCCGTCCTAC
401	CCGACGGTAC	GAACAGACCC	TCCCATATCG	AAACCGAACA	GCAGGGTGAC
451	GGCTACGCCG	CCATGACCGC	CGCACTCGAA	CAGGGACTGA	AACAGGCGGC
501	GCAACAGATG	GTCAGATA			

This corresponds to the amino acid sequence <SEQ ID 2266; ORF 684.a>:

a684.pep

1	MRLFPPIAAAL	TLAACGTVQS	TQYFVLPDSR	YIRPATQGG	TAVEVRLAEP
51	LKRGGLVYQT	DPYRLNTAQN	HWADTLDDM	LEAALSNAFN	RLDSTRIFVP
101	ASRSGSTKWT	TVYIDAFQGS	YTGKTLISGY	AVLPDGTNRP	FHIETEQQGD
151	GYAAMTAALE	QGLKQAAQOM	VE*		

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 684 shows 99.4% identity over a 172 aa overlap with a predicted ORF (ORF 684) from *N. meningitidis*

m684/a684 99.4% identity in 172 aa overlap

	10	20	30	40	50	60
m684.pep	MRLFPPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
a684	MRLFPPIAAALSLAACGTVQSTQYFVLPDSRYIRPATQGGETAVEVRLAEPLKRGGLVYQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m684.pep	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVIYIDAFQGS					
a684	DPYRLNTAQNHWADTLDDMLEAALSNAFNRLDSTRIFVPASRSGSTKWTVIYIDAFQGS					
	70	80	90	100	110	120
	130	140	150	160	170	

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```

m684.pep      YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
              |||||||
a684          YTGKTLISGYAVLPDGTNRPFHIETEQQGDGYAAMTAALEQGLKQAAQOMVEX
              130      140      150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2267>

```

g685.seq
1  TTGTTTGGCC GTATCGGGAA TTTGCGTTT TCGCGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGcct GCGCGTCCTT GCCGGCCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAAct GTATccgCCG CATCCCAAGC
201 CGCAATCCACA CCTGTGCCCA CGGTGACCGT GCCGACCGCG CGGGGCGATG
251 CCGTTGTGCC GAAGAATCCC GAACgcgctcg ccgtgtAcga CtggCGGGCG
301 TtggaTACGC TGACCGAGCC GGGCGTGAAT GTGGGCGCAA CCACCGCGCC
351 GGTGCGCGTG GACTATTTCG AGCCTGCATT TGACAAGCGG GCAACGGTGG
401 GGACGCTGTT TGAGCCCGAT TCGGAATCCC TGCACCGCCA CAATCCGCAG
451 TTTGTCATTA CCGCGGGGCC GGGTGCAGAA GCGTATGAAC AGTTGGCGAA
501 AAACGCGACC ACCATAGATT TGACGGTGGG CAACGGCAAT ATCCGCACCA
551 GCGGCGAGAA GCAGATGGAG ACCCTGTCGC GGATTTCGG TAAGGAAGCG
601 CGCGTGCCGG AATTGAATGC GCAGATTGAC GCGCTGTTCG CCCAAAAGCG
651 CGAAGCCGCC AAAGGCAAAG GACGCGGGCT GGTGCTGTCT GTTACAGGCA
701 ACAAAGGTGC CGCCTTCGGC ACGCAATCGC GGTGGCAAG TTGATACAC
751 GCGGACATCG GCCTGCCGCC CGTGGACGAA TCTTTACGCA ACGAAGGGCA
801 CGGCGAGCCC GTTTCCTTCG AATACATCAA AGAGAAAAAC CCCGGCTGGA
851 TTTTCATCAT CGACCGCACC GCCGCCATCG GGCAGGAAGG GCCGGCTGCC
901 GTGGAGTGT TGGATAACGC GCTGGTATGC GGCACGAACG CTGGAAGCG
951 CAAGCAAATC ATCGTCATGC CTGCCCGGAA CTACATTGTC GCGGGCGGCG
1001 CGCGGCAGTT GATACAGGCG GCGGAACAGT TGAAGCGGCG GTTTGAAAAA
1051 GCAGAACCCG TTGCGGCGCA GTAG

```

This corresponds to the amino acid sequence <SEQ ID 2268; ORF 685>:

```

g685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLPAA
51  CSPEPAAEKT VSAASQAAS T PVATLTVP TA RGDVAVPKNP ERVAVYDWAA
101 LDTLTPEPGV N VSATTAPVRV DYLPAPFKA ATVGTLFEPD CESLHRHNPO
151 FVITCGPGAE AYEQLAKNAT TIDLTVDN GN IRTSGEKOME TLSRIFKKEA
201 RVAELNAQID ALFAQKREAA KGKGRGLVLS VTGNKVSAFG TQSRSLASWIH
251 GDIGLPPVDE SLRNEGHGQP VSFYIKEKN PGWIFIIDRT AATGQEGPAA
301 VEVLNALVC GTNAWKRKQI IVMPAANYIV AGGARQLIQ A EQLKA AF EK
351 AEPVAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2269>:

```

n685.seq
1  TTGTTTGGCC GTATCGGGAA TTTGCGTTT TCGCGCGTGG TTTCTGCAGG
51  TTGTTTGGCTT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTTAT TGGGCAGCCT GCGCGTCCTT GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAAct GTATCCGCCG CATCCGCATC
201 TGCCGCCACG CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GCGTGAATGT GGGCGCAACC ACCGCGCCGG TCGCGGTGGA
351 TTATTGTCAG CCTGCATTG ACAAGGCGGC AACGGTGGGG ACGCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGTACA ATCCTCAGCT TGTCATTACC
451 GCGGGGCCGG GCGCGGAAGC GTATGAACAG TTAGCGAAAA ACGCGACCAC
501 CATAGATCTG ACGGTGGACA ACGCAATAT CCGCACCAGC GCGGAAAAGC
551 AGATGGAGAC CTTGGCCCGG ATTTTCGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCCGC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGA CGCGGGCTGG TGCTGTCGGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG
851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAAct ACATTGTCGC GGGCGGCGCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGCGGCGT TAAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAAAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2270; ORF 685>:

n685.pep

```

1  LFC RIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSP EPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLO PAFDKAATVG TLFEPTYEAL HRYNPQLVIT
151 GGP GAEAYEQ LAKNATTIDL TVDNGNIRTS GEKOMETLAR IFGKEARAAE
201 LKA QIDALFA QTREAAKKGK RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPP VDES LRN EGHGQPVSE YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNA LVRGTNA WKRKQIIVMP AANYIVAGGA RQLIQAAEQ KAAFKKAEPV
351 AAGKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 685 shows 94.4% identity over a 356 aa overlap with a predicted ORF (ORF 685) from *N. gonorrhoeae*:

m685/g685 94.4% identity in 356 aa overlap

```

m685.pep      10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPEPAAEKT
|||||:|||||:|||||:|||||:|||||:|||||:
g685          10      20      30      40      50      60
LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLPAACSPEPAAEKT

m685.pep      70      80      90     100     110
VSAASASA----ATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRV
|||||:|||||:|||||:|||||:|||||:|||||:
g685          70      80      90     100     110     120
VSAASQAASTPVATLTVPTARGDAVVPKNPERVAVYDWAALDTLTEPGVNVGATTAPVRV

m685.pep     120     130     140     150     160     170
DYLPQAFDKAATVGTLFEPDYEALHRYNPQLVITGGPGAEAYEQLAKNATTIDLTVDNGN
|||||:|||||:|||||:|||||:|||||:|||||:
g685         120     130     140     150     160     170     180
DYLPQAFDKAATVGTLFEPDCESLHRHNPQFVITGGPGAEAYEQLAKNATTIDLTVDNGN

m685.pep     180     190     200     210     220     230
IRTSGEKOMETLARIFGKEARAAELKAQIDALFAQTREAAKKGKRGVLVSVTGNKVSAGF
|||||:|||||:|||||:|||||:|||||:|||||:
g685         180     190     200     210     220     230     240
IRTSGEKOMETLSRIFGKEARVAELNAQIDALFAQKREAAKKGKRGVLVSVTGNKVSAGF

m685.pep     240     250     260     270     280     290
TQSRLASWIHGDIGLPPVDES LRNEGHGQPVSEFYI KEKNPDWIFIIDRTAAIGQEGPAA
|||||:|||||:|||||:|||||:|||||:|||||:
g685         240     250     260     270     280     290     300
TQSRLASWIHGDIGLPPVDES LRNEGHGQPVSEFYI KEKNPDWIFIIDRTAAIGQEGPAA

m685.pep     300     310     320     330     340     350
VEVLDNA LVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEPVAAAGKKX
|||||:|||||:|||||:|||||:|||||:|||||:
g685         300     310     320     330     340     350
VEVLDNA LVCGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFEKAEPVAAQX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2271>

```

a685.seq
1  TTGTTTGGCC GTATCGGGAA TTTGCGTGT TCGGCGGTGG TTTCTGCAGG
51  TTGTTTGCCT AATAATAAAC ATTCTTATTC GTATGCAAAG GAACCGCACA
101 CCGTGAAACC GCGTTTTAT TGGGCAGCCT GCGCCGTCTC GCTGACCGCC
151 TGTTCGCCCG AACCTGCCGC CGAAAAAACT GTATCCGCCG CATCCGCATC
201 TGCCGCCACA CTGACCGTGC CGACCGCGCG GGGCGATGCC GTTGTGCCGA
251 AGAATCCCGA ACGCGTCGCC GTGTACGACT GGGCGGCGTT GGATACGCTG
301 ACCGAATTGG GTGTGAATGT GGGCGCAACC ACCGCGCCGG TGCGCGTGGA
351 TTATTTGCAG CCTGCATTG ACAAGCGCGC AACGGTGGG ACCTGTTCG
401 AGCCCGATTA CGAAGCCCTG CACCGCTACA ATCCTCAGCT TGTCAATACC
451 GGCGGGCCGG GCGCGGAAGC GTATGAACAG TTGGCGAAA ACAGGACCAC
501 CATAGATCTG ACGGTGGACA ACGGCAATAT CCGCACCAGC GGCGAAAAGC
551 AGATGAGAGC CTTGGCGCGG ATTTTCGGCA AGGAAGCGCG CGCGGCGGAA
601 TTGAAGGCGC AGATTGACGC GCTGTTCGCC CAAACGCGCG AAGCCGCCAA
651 AGGCAAGGA CGCGGGCTGG TGCTGTCCGT TACGGGCAAC AAGGTGTCCG
701 CCTTCGGCAC GCAGTCGCGG TTGGCAAGTT GGATACACGG CGACATCGGC
751 CTACCGCCTG TAGACGAATC TTTACGCAAC GAGGGGCACG GGCAGCCTGT
801 TTCCTTCGAA TACATCAAAG AGAAAAACCC CGATTGGATT TTCATCATCG

```

1100

```

851 ACCGTACCGC CGCCATCGGG CAGGAAGGGC CGGCGGCTGT CGAAGTATTG
901 GATAACGCGC TGGTACGCGG CACGAACGCT TGAAGCGCA AGCAAATCAT
951 CGTCATGCCT GCCGCGAAT ACATTGTCGC GGGCGGCTCG CGGCAGTTGA
1001 TTCAGGCGGC GGAGCAGTTG AAGGAGGCGT TTGAAAAGGC AGAACCCGTT
1051 GCGGCGGGGA AAGAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2272; ORF 685.a>:

```

a685.pep
1  LFCRIGNFAF CGVVSAGCLL NNKHSYSYAK EPHTVKPRFY WAACAVLLTA
51  CSPEPAAEKT VSAASASAAT LTVPTARGDA VVPKNPERVA VYDWAALDTL
101 TELGVNVGAT TAPVRVDYLQ PAFDKAATVG TLFEPDYEAL HRYNPQLVIT
151 GGPGEAEYEQ LAKNATTIDL TVDNGNIRTS GEKQMETLAR IFGKEARAAE
201 LKAQIDALFA QTREAARKGK RGLVLSVTGN KVSAGTQSR LASWIHGDIG
251 LPPVDESLRN EGHGQPVSEF YIKEKNPDWI FIIDRTAAIG QEGPAAVEVL
301 DNALVRGTNA WKRKQIIVMP AANYIVAGGS RQLIQAAEQ KEAFEKAEPV
351 AAGKE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 685 shows 98.9% identity over a 355 aa overlap with a predicted ORF (ORF 685) from *N. meningitidis*:

```

m685/a685    98.9% identity in 355 aa overlap

              10      20      30      40      50      60
m685.pep     LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
a685          LFCRIGNFAFCGVVSAGCLLNNKHSYSYAKEPHTVKPRFYWAACAVLLTACSPPEAAEKT
              10      20      30      40      50      60

              70      80      90     100     110     120
m685.pep     VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
a685          VSAASASAATLTVPTARGDAVVPKNPERVAVYDWAALDTLTELGVNVGATTAPVRVDYLQ
              70      80      90     100     110     120

              130     140     150     160     170     180
m685.pep     PAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAEEYEQAKNATTIDLTVDNGNIRTS
a685          PAFDKAATVGTLEFPDYEALHRYNPQLVITGGPGAEEYEQAKNATTIDLTVDNGNIRTS
              130     140     150     160     170     180

              190     200     210     220     230     240
m685.pep     GEKQMETLARIFGKEARAAELKAQIDALFAQTREAARKGKRGVLVSVGNKVSAGTQSR
a685          GEKQMETLARIFGKEARAAELKAQIDALFAQTREAARKGKRGVLVSVGNKVSAGTQSR
              190     200     210     220     230     240

              250     260     270     280     290     300
m685.pep     LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
a685          LASWIHGDIGLPPVDESLRNEGHGQPVSEFYIKEKNPDWIFIIDRTAAIGQEGPAAVEVL
              250     260     270     280     290     300

              310     320     330     340     350
m685.pep     DNALVRGTNAWKRKQIIVMPAANYIVAGGARQLIQAAEQKAAFKKAEFVAAGKKX
a685          DNALVRGTNAWKRKQIIVMPAANYIVAGGSRQLIQAAEQKAEFEKAEPVAAGKEX
              310     320     330     340     350

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2273>

```

g686.seq (partial)
1  ..AATTTCCTCT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAGGCTTC ggcgGCATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TGCCTCAGCA TAGCGCCGGC
151 ATTGTGGAAA CGGTCGGCAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAGGC
351 TGAATCCGTC AACGGGACTA CCGGCTTCGT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2274; ORF 686 >:

g686.pep (partial)

```

1  ..NFSCRADDVF DDICSAVEGF GGIARSVQLG AVSGGAFESV AYSLRQHSAG
51  IVETVGKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVGGMVFVSV PMDAVKAESV NGTTGFVRIG M*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2275>:

m686.seq..

```

1  ATGATGTTGA AAAAATTCGT ACTCGCGCGT ATTGCCGCAT TGGTTTTGGC
51  GGCCTGCGGC GGTTCGGAAG GCGGCAGCGG AGCGNNNNNN NNNNNNAATT
101 TCCTCTGCAG CGCCGATGAT GTTTTAAACG ATATCTGCAG TGCCGTTGAA
151 GGCTTCGGCG GCATTGCCCG ATCTGTCCAG CTCGGGGCTG TATCGGGTGG
201 CGCGTTTGAA TCCGTCGCCT ACTCCTTGCG TCAGCATACT ACCGGCATTG
251 TGGAAACGGT CGGCAAGCCG TTGTCCGGTG CTGCGGTTGT CGGTCAGGTT
301 GAGGCGGATA TTTTGGGCAA CGCCTTTTAT GTCGTAGCTG TATATATCCC
351 TCGCGCCTTT GGGAGCGGGA TAGCCGCCGC CCTGTGGCCC GTCATAGCCG
401 TCGGCGGGAT GGTGTTGCTA TCCGTCCCAA TGGATGCGGT AAAGGCTAAA
451 TCCGTCAACG GGACTACCGG CTTTCATAGA ATCGGAATGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2276; ORF 686>:

m686.pep

```

1  MMLKKFVLGG IAAVLVLAACG GSEGGSGAXX XXNFSCSADD VFNDICSAVE
51  GFGGIARVQ LGAVSGGAFE SVAYSLRQHT TGIVETVGKP LSGAAVVGQV
101 EADILGNAFY VVAVYIPRAF GSGIAAALWP VIAVGMVFV SVPMDAVKAK
151 SVNGTTGFIR IGM*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 686 shows 95.4% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. gonorrhoeae*

g686/m686 95.4% identity in 131 aa overlap

g686.pep				10	20	30
				NFSCRADDVFDDICSAVEGFGGIARSVQLG		
m686	LKKFVLGGIAALVLAACG	GGSEGGSGAXX	XXNFSCSADDVFNDICSAVEGFGGIARSVQLG			
	10	20	30	40	50	60
g686.pep		40	50	60	70	80
		AVSGGAFESVAYSLRQHSAGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
m686		AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS				
		70	80	90	100	110
g686.pep		100	110	120	130	
		GIAAALWPVIAVGMVFVSVPMDAVKAESVNGTTGFVRIGMX				
m686		GIAAALWPVIAVGMVFVSVPMDAVKAESVNGTTGFVRIGMX				
		130	140	150	160	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2277>

a686.seq (partial)

```

1  ..AATTTCCTT GCCGCGCCGA TGATGTTTTT GACGATATCT GCAGTGCCGT
51  TGAAAGCTTC GCGGCGATTG CCCGATCTGT CCAGCTCGGG GCTGTATCGG
101 GTGGCGCGTT TGAATCCGTC GCCTACTCCT TCGCTCAGCA TACTACCGGT
151 ATTGTGGAAG CGGTCGACAA GCCGTTGTCC GGTGCTGCGG TTGTCGGTCA
201 GGTGAGGCGG GATATTTTGG GCAACGCCTT TTATGTCGTA GCTGTATATA
251 TCCCTCGCGC CTTTGGGAGC GGGATAGCCG CCGCCCTGTG GCCCGTCATA
301 GCCGTCGGCG GGATGGTGTT CGTATCCGTC CCAATGGATG CGGTAAGGCC
351 TGAATCCGTC AACGGGACTA CCGGCTTCAT CAGAATCGGA ATGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2278; ORF 686.a>:

a686.pep (partial)

1102

```

1  ..NFSCRADDVF DDICSAVESF GGIARSVQLG AVSGGAFESV AYSLRQHTTG
51  I VETVDKPLS GAAVVGQVEA DILGNAFYVV AVYIPRAFGS GIAAALWPVI
101 AVVGMVFVSV PMDAVKAESV NGTTGFIRIG M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 686 shows 96.2% identity over a 131 aa overlap with a predicted ORF (ORF 686) from *N. meningitidis*:

m686/a686 96.2% identity in 131 aa overlap

```

              10      20      30      40      50      60
m686.pep      LKKFVLGGIAALVLAACGGSEGGSGAXXXXNFSCSADDVFNDICSAVEGFGGIARSVQLG
a686              NFSCRADDVFDDICSAVESFSGGIARSVQLG
                      10      20      30

              70      80      90      100     110     120
m686.pep      AVSGGAFESVAYSLRQHTTGIVETVGKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
a686      AVSGGAFESVAYSLRQHTTGIVETVDKPLSGAAVVGQVEADILGNAFYVVAVYIPRAFGS
                      40      50      60      70      80      90

              130     140     150     160
m686.pep      GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
a686      GIAAALWPVIAVGGMVFSVPMDAVKAESVNGTTGFIRIGMX
                      100     110     120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2279>

```

g687.seq
1  ATGAAATCCA GACACCTCGC CCTCGCCCTC GCGGTGCGG CCCTGTTCGC
51  CCTTGCCGCG TCGCAGACGA AGTCCAAAC CAGCGTCCCC GCCGACAGCG
101 CGCCTGCCGC TTCGGCAGCC GCCGCCCGG CAGGACTGGT CGAAGGGCAA
151 AACTACACCG TCCTTGCCAA CCGGATTCCC CAACAGCAGG CAGGCAAGGT
201 TGAAGTGCTT GAGTTTTCG GCTATTTTG TCCGCACTGC GCCCGCCTcg
251 AACCTGTTTT GAGCAAAAC GCCAAGTCTT TTAAGACGA TATGTACCTG
301 CGTACCGAAC ACGTCGTCTG GCAGAAAGAA ATGCTGCCCG TGCCACGcct
351 cGCCGCCGCC GTCGATATGG CTGCCGCCGA AAGCAAAGAT GTGGCGAACA
401 GCCATATTTT CGATGCGATG GTCAACCAAA AAATCAAGCT GCAAGAGCCG
451 GAAGTCCTCA AAAAATGGCT GGGCGAACAa ACcgctTTG ACGGCAAAAA
501 AGTCCTTGCC GCCTACGAAT CCCCCGAAAG TCAGGCGCGC GCcggcAAAA
551 TGCAGGAGCT GACCGAAACC TTCCAAATCG ACGGTACGCC CACGGTTATC
601 GTCGGCGGCA AATATAAAGT CGAATTGGCC GACTGGGAGT CCGGTATGAA
651 CACCATCGAC CTTTGGCGG ACAAAGTACG TGAAGAACAA AAAGCCGCGC
701 AGTAG

```

This corresponds to the amino acid sequence <2280 ID 724; ORF 687>:

```

g687.pep
1  MKSRHLALAL GVAALFALAA CDSKVQTSVP ADSAPAASAA AAPAGLVEGO
51  NYTVLANPIP QQQAGKVEVL EFFGYFCPHC ARLEPVLSKH AKSFKDDMYL
101 RTEHVWQKE MLPLARLAAA VDMAAASKD VANSIFDAM VNQIKLQEP
151 EVLKKWLGEQ TAFDGGKVL AYESPESQAR AGKMQLTET FQIDGTPVI
201 VGGKYKVEFA DWESGMNTID LLADKVREEQ KAAQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2281>:

```

m687.seq
1  ATGAAATCCA GACACCTTGC CCTCGGCGTT GCCGCCCTGT TCGCCCTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAAGCGT CCCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCAAGG GCAAACTAT
151 ACCGTCTCTG CCAACCCGAT TCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CCTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTCGAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTG TCTGGCAGAA AGAAATGCTG ACGCTGGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAAA TCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAACCGCC TTTGACGGCA AAAAAGTCCT

```

```

501 TGC CGCCTAC GAGTCCCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGTAAATATA AAGTTGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2282; ORF 687>:

```

m687.pep
1  MKSRHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQNPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 687 shows 97.0% identity over a 234 aa overlap with a predicted ORF (ORF 687) from *N. gonorrhoeae*:

```

m687/g687      97.0% identity in 234 aa overlap

              10      20      30      40      50
m687.pep      MKSRHLAL--GVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              |||||
g687           MKSRHLALALGVAALFALAACDSKVQTSVPADSAPAASAAAAAPAGLVEGQNYTVLANPIP
              10      20      30      40      50      60

              60      70      80      90      100     110
m687.pep      QQQAGKVEVLEFFGYFCPHCAHLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLTTLARLAAA
              |||||
g687           QQQAGKVEVLEFFGYFCPHCARLEPVLSKHAKSFKDDMYLRTHEHVWQKEMLPLARLAAA
              70      80      90      100     110     120

              120     130     140     150     160     170
m687.pep      VDMAAADSKDVANSHIFDAMVNQKIKLQNPVLEVLKKWLGEQTA FDGKKVLAAYESPESQAR
              |||||
g687           VDMAAAESKDVANSHIFDAMVNQKIKLQEPVLEVLKKWLGEQTA FDGKKVLAAYESPESQAR
              130     140     150     160     170     180

              180     190     200     210     220     230
m687.pep      ADKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              |||||
g687           AGKMQELTETFQIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAQX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2283>

```

a687.seq
1  ATGAAATCCA AACACCTCGC CCTCGGCGTT GCCGCCCTGT TCGCACTTGC
51  CGCGTGCGAC AGCAAAGTCC AAACCAGCGT CCCGCCGAC AGCGCGCCTG
101 CCGCTTCGGC AGCCGCCGCC CCGGCAGGGC TGGTCGAAGG GCAAAATAT
151 ACTGTCCTTG CCAACCCGAT TCCCCAACAG CAGGCAGGCA AAGTCGAAGT
201 CTTTGAGTTT TTCGGCTATT TCTGTCCGCA CTGCGCCAC CTGCAACCTG
251 TTTTAAGCAA ACACGCCAAG TCTTTTAAAG ACGATATGTA CCTGCGTACC
301 GAACACGTCG TCTGGCAGAA AGAAATGCTG ACGCTCGCAC GCCTCGCCGC
351 CGCCGTCGAT ATGGCTGCCG CCGACAGCAA AGATGTGGCG AACAGCCATA
401 TTTTCGATGC GATGGTCAAC CAAAAATCA AGCTGCAAGA GCCGGAAGTC
451 CTCAAAAAAT GGCTGGGCGA ACAAACCGCC TTTGACGGCA AAAAAGTCCT
501 TGCCGCTTAC GAATCTCCCG AAAGCCAGGC GCGCGCCGAC AAAATGCAGG
551 AGCTGACCGA AACCTTCCAA ATCGACGGTA CGCCACGGT TATCGTCGGC
601 GGCAAAATATA AAGTCGAATT TGCCGACTGG GAGTCCGGTA TGAACACCAT
651 CGACCTTTTG GCGGACAAAG TACGCGAAGA ACAAAAAGCC GCGCACTAA

```

This corresponds to the amino acid sequence <SEQ ID 2284; ORF 687.a>:

```

a687.pep
1  MKSKHLALGV AALFALAACD SKVQTSVPAD SAPAASAAAA PAGLVEGQNY
51  TVLANPIPQQ QAGKVEVLEF FGYFCPHCAH LEPVLSKHAK SFKDDMYLRT
101 EHVWQKEML TLARLAAVD MAAADSKDVA NSHIFDAMVN QKIKLQEPV
151 LKKWLGEQTA FDGKKVLAAY ESPESQARAD KMQELTETFQ IDGTPTVIVG
201 GKYKVEFADW ESGMNTIDLL ADKVREEQKA AH*

```



Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 687 shows 98.7% identity over a 232 aa overlap with a predicted ORF (ORF 687) from *N meningitidis*:

m687/a687 98.7% identity in 232 aa overlap

	10	20	30	40	50	60
m687.pep	MKSRLHALGVAALFALAACDSKVQTSVPADSAPASAAAAAPAGLVEGQNYTVLANPIPQQ					
a687	MKSRLHALGVAALFALAACDSKVQTSVPADSAPASAAAAAPAGLVEGQNYTVLANPIPQQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m687.pep	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAJSFKDDMYLRTEHVWQKEMTLARLAAAVD					
a687	QAGKVEVLEFFGYFCPHCAHLEPVLSKHAJSFKDDMYLRTEHVWQKEMTLARLAAAVD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m687.pep	MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
a687	MAAADSKDVANSHIFDAMVNQIKLQNPVLKKWLGEQTAFDGKKVLAAYESPESQARAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m687.pep	KMQELTETFDIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAOX					
a687	KMQELTETFDIDGTPTVIVGGKYKVEFADWESGMNTIDLLADKVREEQKAAHX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2285>

g688.seq

1	GTGCTACACT	AGACATCCCG	ATTGACACAG	AAAGTTCTC	CCGTGAACAA
51	AACCTCTATC	CTGCCCTTT	CCGCCCTGTT	CAGCCTGACC	GCGTGCAGCG
101	TCGAACGCGT	CTGCTGTTT	CCCTCCTACA	AACTCAAAAT	CATCCAAGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTGCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAACCTGAC	CGTCTATTT	GAAACGCGC	TACTCGTCCG
351	CACCGAAGGC	GACGCCCTCC	AAAATGCCGC	CGAAGCCCTC	CGCGCGAAAC
401	AAAACGCAGA	CAACAATAA			

This corresponds to the amino acid sequence <SEQ ID 2286; ORF 688 >:

g688.pep

1	VLH*TSRFAQ	KGSPVNKTLI	LALSALFSLT	ACSVERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DALQNAEAL	RAKQNAKQ*	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2287>:

m688.seq

1	GTGTTACACT	ACCCATCCCG	ATTGACACAG	AAAGGCATT	CCGTGAACAA
51	AACCTCTATC	CTGCCCTTT	CCGCCCTCCT	CGGCCTTGCC	GCGTGCAGTG
101	CCGAACGCGT	TTCAGTGTTC	CCCTCGTACA	AACTCAAAAT	CATACAGGGC
151	AACGAACGCG	AACCGCGCGC	CGTTGCCGCC	CTCCGCCCCG	GCATGACCAA
201	AGACCAAGTC	CTGCTCCTGC	TCGGCAGCCC	CATACTGCGC	GACGCTTTCC
251	ATACCGACCG	CTGGGACTAT	ACCTTCAACA	CCTCCCGCAA	CGGCATCATC
301	AAAGAACGCA	GCAATCTGAC	CGTCTATTT	GAAACGCGC	TACTCGTCCG
351	CACCGAAGGC	GACGCTCCTGC	AAAACGCTGC	CGAAGCCCTC	AAAGACCGCC
401	AAAACACAGA	CAACCATAA			

This corresponds to the amino acid sequence <SEQ ID 2288; ORF 688>:

m688.pep

1	VLHYPSRFAQ	KGISVNKTLI	LALSALLGLA	ACSAERVSLF	PSYKLKIIQG
51	NELEPRAVAA	LRPGMTKDQV	LLLLGSPILR	DAFHTDRWDY	TFNTSRNGII
101	KERSNLTVYF	ENGVLVRTEG	DVLQNAEAL	KDRQNTDKP*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 688 shows 90.6% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. gonorrhoeae*:

```
m688/g688      90.6% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep      VLHYPSTRFAQKGISVNKTLILALSALLGLAACSARVSLFSPYKLIQNELEPRVAA
              ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688           VLHXTSRFAQKGSPVNKTLILALSALFSLTACSVVERVSLFSPYKLIQNELEPRVAA
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
              |:||||| |:|:|
g688           DALQNAAEALRAKQNAQKQX
              130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2289>

```
a688.seq
1  GTGTTACACT ACCCATCCCG ATTTGCACAG AAAGGCATT CCGTGAACAA
51 AACCTCATC CTGCCCTTT CCGCCCTCCT CGGCCTTGCC GCGTGCAGCG
101 TCGAACGCGT TTCCTGTTC CCCTCGTACA AACTCAAAAT CATACAGGGC
151 AACGAACTCG AACCTCGCGC CGTCGCCTCC CTCGCCCCG GTATGACCAA
201 AGACCAAGTC CTGCTCCTGC TCGGCAGCCC CATACTGCGC GACGCATTCC
251 ATACCGACCG CTGGGACTAT ACCTTCAACA CCTCCGCAA CGGCATCATC
301 AAAGACCGAA GCAATCTGAC CGTCTATTT GAAACGGCG TGCTCGTCCG
351 CACCGAAGGC AACGCCCTGC AAAATGCCGC CGAAGCCCTC CGCGTAAAC
401 AAAACGCAGA CAAACAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2290; ORF 688.a>:

```
a688.pep
1  VLHYPSTRFAQ KGISVNKTLI LALSALLGLA ACSVERVSLF PSYKLIQNE
51  LEPRVAVAS LRPGMTKDQV LLLGSPILR DAFHTDRWDY TFNTSRNGII
101 KDRSNLT VYF ENGVLVRTEG NALQNAAEAL RVKQNAQKQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 688 shows 93.5% identity over a 138 aa overlap with a predicted ORF (ORF 688) from *N. meningitidis*

```
m688/a688      93.5% identity in 138 aa overlap

              10      20      30      40      50      60
m688.pep      VLHYPSTRFAQKGISVNKTLILALSALLGLAACSARVSLFSPYKLIQNELEPRVAA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688           VLHYPSTRFAQKGISVNKTLILALSALLGLAACSARVSLFSPYKLIQNELEPRVAVAS
              10      20      30      40      50      60

              70      80      90      100     110     120
m688.pep      LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKERSNLT VYFENGVLVRTEG
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a688           LRPGMTKDQVLLLLGSPILRDAFHTDRWDYTFNTSRNGI IKDRSNLT VYFENGVLVRTEG
              70      80      90      100     110     120

              130     140
m688.pep      DVLQNAAEALKDRQNTDKPX
              |:||||| |:|:|
a688           NALQNAAEALRVKQNAQKQX
              130     140
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2291>

g689.seq (partial)

```

1  ...TCTCCGCCCC TTCCTCCGAT GAGCGGAAAA CTGATGGCGG TTTTGATGGC
51  GGTACTGGTC GCGCTGATGC CGTTTTCAT CGATGCCTAC CTGCCGCGA
101 T'TCCGAAAT GCGCGAGCCG CTGAACGCGG ATATCCACCG TATCGAATAG
151 AGTCTGAGTT TGT'TATGTT CCGCACGCGG TTCGGGCAAG TGGCCGGCGG
201 CCGCGTGTCC GACATCAAAG GCGCAAACC CGTCGCCCTG ACCGGTTTGA
251 T'TGTATATTG CTTTGGCGTT GCCGCCATCG TATTGCTTC GAGTACCGAA
301 CAGCTCCTTA ACCTGCGTGC GGTACAGGCG TTCGGCGCAG GCATGGCTGT
351 AGTCATCGTc ggtgcgatgg tgcgcgatTA TTATCCGGA CGCAAAGCCG
401 cgcAGATGTT TGCCCTTATC GGCATCATTC TGATGTTGT GCCGCTGGCC
451 GCACCCATGG TCGCGCATT GTTGCAGGGA TTGGGCGGAT GCGGGCGGAT
501 TTTCTTTTTTc ttggcGgcgt ATTGCGCCGT GCTGCCCGGT TTGGTACAGT
551 A'TTTCCTGCC CAATCCCGCC GTCGGCGGCA AAATCGGCAG GGATGTGTTc
601 GGGCTGGTGG CGGGGCGGTT CAAGCGCGTA TTGAAAACCC GTGCCGCGAT
651 GGGTtatCTG TTTTTTCAGG CATTGAGCTT CGGTCGATG TTCGCCTTTC
701 TGACCGAATC TTCCTTCGTG TACCGGCAGC TCTACCACGT TACGCCGCAC
751 CGGTACGCAT GGGTGT'TGC ACTCAACATC ATCAGCATGA TGT'TTTCAG
801 CCGCGTTACC GCGTGGCGGC TTA'AACCGG CGCGCATCCG CAAAGCATCC
851 TGCTCGGGG GATTGTCGTC CAATTGCGG CCAACCCGTC CCAACTCGCC
901 GCGGTGCTGT TTTTCGGGTT GCCCCCGTTT TGGCTGCCGG TCGCGTGCCT
951 GATGTTTTC GTCGGTACGC AGGGCCTGGT CGGTGCGGAC ACGCAGGCAT
1001 GCTTATATGTC TTATTTCAA GAAGAGGCGG GCAGCGCGAA CGCCGTGTCTG
1051 GGTGTATTCC GGTCTTAAT CCGCGCGGGC GTGGTCATGG CGGCAACCGT
1101 GATGGCGGCA ACCATGACCG CGTCCGCTC TTGCGGCATT GCGCTTTTGT
1151 GGCTCTGCTC GCACAAGGCG TGGAGGAAA ACGAAAAAA GCGAATACTT

```

This corresponds to the amino acid sequence <SEQ ID 2292; ORF 689>:

g689.pep (partial)

```

1  ...SPPLPMSGK LMAVLMAVLV ALMPFSIDAY LPAIPEMAQP LNADIHRIE*
51  SLSLFMFGTA FGQVAGGAVS DIKGRKPVAL TGLIVYCLAV AAIVFASSTE
101 QLLNLRAVQA FGAGMAVVIV GAMVRDYSYSG RKAACMFALI GIILMVVPLA
151 APMVGALLQG LGGWRAIFVF LAAYSPVLPG LVQYFLPNPA VGGKIGRDVF
201 GLVAGRFKRV LKTRAMGYL FFQAFSFGSM FAFLETSSFV YRQLYHVTPH
251 RYAWVFALNI ITMMFFSRVT AWRLKTGAHP QSILLRGIVV QFAANPSQLA
301 AVLFFGLPPF WLPVACVMFS VGTQGLVGAD TQACFMSYFK EEGGSANAVS
351 GVFRSLIGAG VVMAATVMAA TMTASASCGI ALLWLCSHKA WKENEKKRIL

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2293>:

m689.seq

```

1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCTT GTTGTGCGG GTGTGTTAAA ATTTCCGTT TCCGCGTATT
101 GTGTTTTCCT CCGCCGGGCG GTTGTGTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AACTGATGG CCGTTTGTAT
201 GGCGATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAA TCGCTGAACG CGGATGTTCA CCGCATCGAA
301 CAGAGTTTGA GTTTGTTTAT GTTCGGCAGC GCGTTCGGAC AGGTGGTCCG
351 CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCC CTGACCGGTT
401 TGATTGTATA TTGCCTTGCC GTTGCCGCCA TCGTATTGTT TTCGAGTGCC
451 GAACAGCTCC TCAACCTGCG CGTCGTGCAG GCATTCCGGT GCGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATTCC GGACGCAAAG
551 CCGCCAGATG GTTGGCCCTT ATCGGCATCA TTTTGATGGT TGTGCCGCTG
601 GTCGCACCCA TGGTCGGCGC ATTGTTGCAG GGCTTGGGTG GCTGGCAGGC
651 GATT'TTTGTT TTTCTGGCGG CGTATTGCGT GGTGCTGCTC GGT'TTGGTAC
701 AGTATTTTCT GCCCAAGCCC GCCGTCGGCG GCAAATCGG ACGGGACGTG
751 TTCGGGCTGG TGGCGGGGCG GTTCAAGCGC GTATTGAAA CCCGTGCTGC
801 GATGGGTTAT CTGTTT'TTC AGGCATTGAG CTTGCGTTTC ATGTTTCGCT
851 TTCTGACCGA ATCTTCCTTC GTGTACCAGC AGCTCTACCG TGT'TACGCTT
901 CATCAATACG CTTGGGCGTT TGCATCAAC ATCATCACGA TGATGTTTTT
951 CAACCGCGTT ACCGCGTGGC GGCTCAAAAC CGGCGTGATC CCGCAAAGCA
1001 TCCTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACTT GTCCCAACTC
1051 GCGCGCCGTC TGT'TTTCGG GTTGCCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGGCTT GGTGCGTGCA AACACGCAGG
1151 CGTGCTTTAT GTCTTATTTT AAAGAAGAGG CGCGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGCGGAC
1251 CTTCTTGACG GACGGTTCGG CAACCGTGAT GCGCGCAACG ATGACCGCGT
1301 CCACCTCTTG CGGCATTGCG CTTCTGTGTC TCTGCTCGCA TCGTCCGTGG

```

1351 AAGAAACG GCGAAGCGA ATACCTTAA

This corresponds to the amino acid sequence &lt;SEQ ID 2294; ORF 689&gt;:

m689.pep  
1 LLIHYIVPVR PVLPGLLLP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM  
51 PSAHYPEMSE KLMAVLMAML VTLMPFSDA YLPAIPEMAQ SLNADVHRIE  
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPA LTGLIVYCLA VAAIVFVSSA  
151 EQLNLNRVVQ AFGAGMTVVI VGAMVRDYS GRKAAQMFAL IGIILMVVPL  
201 VAPMVGALLQ GLGGWQAIQV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV  
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAFLTESSF VYQQLYRVTP  
301 HQYAWAFALN IITMMFFNRV TAWRLKTGVH PQSILLWGIV VQFAANLSQL  
351 AAVLFFGLPP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV  
401 LGVFQSLIGA GVGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW  
451 KENGQSEYL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 689 shows 88.0% identity over a 408 aa overlap with a predicted ORF (ORF 689) from *N. gonorrhoeae*:

m689/a689 88.0% identity in 408 aa overlap

m689.pep	30	40	50	60	70	80
	CAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSEKLMAVLMAMLVTLMPFSIDAY					
g689						
m689.pep	90	100	110	120	130	140
	LPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSVSDIKGRKPVALTGLIVYCLA					
g689						
m689.pep	150	160	170	180	190	200
	AAIVFVSSAEQLNLNRVVQAFGAGMTVVI VGAMVRDYSSGRKAAQMFALIGIILMVVPLV					
g689						
m689.pep	210	220	230	240	250	260
	APMVGALLQGLGGWQAIQVFLAAYSLVLLGLVQYFLPKPAVGGKIGRDVFGLVAGRFRKV					
g689						
m689.pep	270	280	290	300	310	320
	LKTRAAMGYLFFQAFSFGSMFAFLTESSFVYQQLYRVTPHQYAWAFALNIITMMFFNRVT					
g689						
m689.pep	330	340	350	360	370	380
	AWRLKTGVHPQSILLRGIVVQFAANLSQLAAVLFFGLPPFWLLVACVMFVSVGTQGLVGAN					
g689						
m689.pep	390	400	410	420	430	440
	TQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLHDGSATVMAATMTASTSCGIAL					
g689						
m689.pep	450	460				
	LWLCSHRAWKENGQSEYLX					
g689						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2295>

```
a689.seq
1  TTGTTAATCC ACTATATCGT TCCGGTTCGT CCGGTTTTCG CGGGGCTTTT
51  GTTGCCGCCT GTTTGTGCCG GTGTGTTAAA ATTTCCGTT TCCGCGTATT
101 GTGTTTTCGG CCGCCGGGCG GTTTGTTTGC GAATCGGACG AGAATTTATG
151 CCTTCTGCCC ATTATCCTGA AATGAGCGAA AAATGATGG CGGTTTGTAT
201 GGC GATGCTG GTTACGCTGA TGCCGTTTTC CATCGATGCC TACCTGCCCG
251 CGATTCCCGA AATGGCGCAG TCGCTGAACG CGGATGTCCA CCGCATCGAA
301 CAGAGCCTGA GTTTGTTTAT GTTCGGCAGC GCCTTCGGAC AGGTGGTCCG
351 CGGTTCGGTG TCCGACATCA AAGGGCGCAA ACCCGTCGCG CTGACCCGAC
401 TGGCCGCTCA CTGCCTTGCC GTTGCCGCCA TCGTATTGTC TTCGAGTGCC
451 GAA CAGCTCC TCAACCTGCG CGTCGTGCG GCATTCCGTG CGGGCATGAC
501 TGTGGTCATC GTCGGCGCAA TGGTGCAGCA TTATTATCC GGACGCAAG
551 CCGCCAGATG GTTGCCCTT ATCGGCATCA TTTGATGGT TGTGCGCTG
601 GTCGCACCCA TGGTGGGCGC ATTGTTGCG GGCTTGGGTG GCTGGCAGGC
651 GATTTTGTG TTTCTGGCGG CGTATTCGCT GGTGCTGCTC GGTTTGGTAC
701 AGTATTTCCT GCCCAAGCCC GCCGTCGGCG GCAAAATCGG CAGGGATGTG
751 TTCGGGCTGG TGGCTGGGCG GTTCAAACGC GTATTGAAA CCCGTGCCCG
801 GATGGGTAT CTGTTTTTC AGGCATTGAG CTTCGGTTCG ATGTTCCGCT
851 TTC TGACCGA ATCTTCTTC GTGTACCAGC AGCTCTACCA CGTTACGCCG
901 CAC CAGTACG CTTGGGCGTT TGCACCAAC ATCATCAGCA TGATGTTTT
951 CAACCGTATT ACCGCGTGGC GGCTCAAAAC CGGCGTGCAT CCGCAAAGCA
1001 TCTTGCTGTG GGGGATTGTC GTCCAGTTTG CCGCCAACCT GTCCCAACTC
1051 GCCGCCGTGC TGTTTTTTCG GTTGCCCCG TTTTGGCTGC TGGTCGCGTG
1101 CGTGATGTTT TCCGTCGGTA CGCAGGCGTT GGTGCGGTCA AACACGCAGG
1151 CGTGTTTTAT GTCCTATTTC AAAGAAGAGG GCGGCAGCGC AAACGCCGTA
1201 TTGGGTGTAT TCCAATCTTT AATCGGCGCG GGGGTGGGTA TGGCGGCGAC
1251 CTTCTTGAC GACGGTTCG CAACCGTGAT GCGGCAACC ATGACCGCGT
1301 CTACCTCTTG CGGCATTGCG CTTTGTGGC TCTGCTCGCA TCGTGCCTGG
1351 AAAGAAAACG GGCAAAGCGA ATACCTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2296; ORF 689.a>:

```
a689.pep
1  LLIHIVPVR PVLPGLLPP VCAGVLKFSV SAYCVFRRRA VCLRIGREFM
51  PSAHYPEMSE KLMAVLMAML VTLMPSIDA YLPAIPEMAQ SLNADVHRIE
101 QSLSLFMFGT AFGQVVGGSV SDIKGRKPVA LTGLAVYCLA VAAIVFASSA
151 EQLLNLRVVO AFGAGMTVVI VGAMVRDYYS GRKAAQMFAL IGIILMVVPL
201 VAPMVGALLQ GLGGWQAIFV FLAAYSLVLL GLVQYFLPKP AVGGKIGRDV
251 FGLVAGRFRK VLKTRAAMGY LFFQAFSFGS MFAELTESSV VYQQLYHVT
301 HOYAWAFALN IITMFFNRI TAWRLKTGVH PQSILLWGIV VQFAANLSQL
351 AAVLFFGLFP FWLLVACVMF SVGTQGLVGA NTQACFMSYF KEEGGSANAV
401 LGVEQSLIGA VGMAATFLH DGSATVMAAT MTASTSCGIA LLWLCSHRAW
451 KENGQSEYL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 689 shows 99.1% identity over a 459 aa overlap with a predicted ORF (ORF 689) from *N. meningitidis*:

m689/a689 99.1% identity in 459 aa overlap

	10	20	30	40	50	60
m689.pep	LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
a689	LLIHIVPVRPVLPGLLPPVCAGVLKFSVSAYCVFRRRAVCLRIGREFMPSAHYPEMSE					
	10	20	30	40	50	60
m689.pep	KLMAVLMAMLVTLMPSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
a689	KLMAVLMAMLVTLMPSIDAYLPAIPEMAQSLNADVHRIEQSLSLFMFGTAFGQVVGGSV					
	70	80	90	100	110	120
m689.pep	SDIKGRKPVALTGLIVYCLAVAAIVFSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS					
a689	SDIKGRKPVALTGLAVYCLAVAAIVFSSAEQLLNLRVVQAFGAGMTVVIVGAMVRDYYS					
	130	140	150	160	170	180
m689.pep	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP					
a689	GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAIFVFLAAYSLVLLGLVQYFLPKP					
	190	200	210	220	230	240
m689.pep						
a689						

```

a689      |||||
          GRKAAQMFALIGIILMVVPLVAPMVGALLQGLGGWQAFVFLAAYSLLVLLGLVQYFLPKP
          190      200      210      220      230      240

          250      260      270      280      290      300
m689.pep  AVGGKIGRDVFGVLVAGRFRKRVLKTAAANGYLFQAFSFGSMFAFLTESSFVYQQLYRVTP
          |||||
a689      AVGGKIGRDVFGVLVAGRFRKRVLKTAAANGYLFQAFSFGSMFAFLTESSFVYQQLYHVT
          250      260      270      280      290      300

          310      320      330      340      350      360
m689.pep  HQYAWAFALNIITMMFFNRVTAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFGLPP
          |||||
a689      HQYAWAFALNIITMMFFNRITAWRLKTGVHPQSILLWGI VVQFAANLSQLAAVLFGLPP
          310      320      330      340      350      360

          370      380      390      400      410      420
m689.pep  FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
          |||||
a689      FWLLVACVMF SVGTQGLVGANTQACFMSYFKEEGGSANAVLGVFQSLIGAGVGMAATFLH
          370      380      390      400      410      420

          430      440      450      460
m689.pep  DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEYLX
          |||||
a689      DGSATVMAATMTASTSCGIALLWLC SHRAWKENGQSEYLX
          430      440      450      460

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2297>

```

g690.seq (partial)
1  ATGAAAAACA AAACGTCATC ACTTCCCTTA TGGCTTGCCG CAATCATGCT
51  GGC CGCGCGT TCCCGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCGCGCTT GTCTTCCGCG TCATCGGCTT CTCCCAAAC CGATTGCAA
151 CCGCGCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCACT
201 GTGAAATTGC ACCGGCTGC ACCCGCCGC CGGCATTGGC GATCTCATAC
251 AGCAAAATCGC CGAACACATC GACTCGGACT GTCTGTTGC CCTTTCCCAT
301 AACGAACTGG AAACCGTTT CGGCTTACCC GCGCGCGCT ATGACAACAT
351 ACAGCGGctg CTgtttcccg ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT GCTGGCAATC GAAGACTTGC GTTACGGAAC GCGCACCATC
451 AGCcgGCAGG CACAAGATGC CATAATGGAA CAGGAACGCC gcctccGaGa
501 agCGACGCTG ATGCTGACAC AGGGCAGTCA AAAAACC CGC GGAACAAGGCG
551 AGGAACCGAA ACGGCACGT TATTTTGAAG TTTCGGCAAC ATctgCctat
601 TTgaaccggc ACRAcaacGG ACTTggcgGC AATTTC AAT ACATCGGCCA
651 ATTGCCCGGC TATCTGAAA TGCACGGAGA AATGCTTGAA AACCAATCAC
701 TCTTCCGCGT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTAGAC
751 ATCCATTTTG ACGAAAATGG CAAAATCAG CGTATTGTCG TTTACGAAA
801 AAATATCTAT...

```

This corresponds to the amino acid sequence <SEQ ID 2298; ORF 690>:

```

g690.pep (partial)
1  MKNKTSSLPL WLAAILAAR SPSKEDKKE NGASAASSSA SSASSQTDLQ
51  PAASAPDNVK QAESAPL*NC TGLHPAAGIG DLIQIAEHI DSDCLFALSH
101 NELETRFGLP GGYDNIQRL LFPDIRPEDP DYHQIMLAI EDLRYGTRTI
151 SRQAQDAIME QERRLREATL MLTQGSOKTR GQGEPEKRR YFEVSATSAY
201 LNRHNNGLGG NFQYIGQLPG YLKMHGEMLE NQSLFRLSNR ERNPDKPFLD
251 IHFDENGKIT RIVVYERNIY ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2299>:

```

m690.seq..
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTACCG CAATCATGCT
51  GACC CGCGTGT TCTCCGAGCA AAGACGATAA AACCAAAGAA GTCGGTGAT
101 CCGCTGCTTC GTCTCCGCG TCATCAGCTC CTCCCAAAC CGATTGCAA
151 CCGACCGCAT CCGCCCTGA TAACGTCAAG CAGGCAGAAA GCGCGCCGCC
201 GTCAAATTGC ACCAGCCTGC ACCCGCCAC CGGCATTGAC GATCTCATGC
251 AGCAAAATCGC CGAACACATT GACTCGGACT GTCTGTTGC CCTTTCCCAT
301 CACGAACTGG AAACCGTTT CGGCTTACCC GACGGTGGCT ATGACAACAT
351 ACAGCGGCTG CTGTTTCCCG ACATCCGCCC TGAAGATCCC GACTACCATC
401 AGAAAAATCAT ACTGGCAATT GAAGACTTGC GTTACGGAAC GCGCAGGATC
451 AGCCGGCAGG CACAAAATGC CTTGATGGAA CAGGAACGCC GCCTCCGAGA
501 AGCGACGCTG TTGCTGATAC AGGGCAGTCA AGAAACCCGC GGACAAGGCG

```

1110

```

551 AGGAGCCGAA ACGCACGCGT TATTTGAAG TTTCGGCAAC CCCTGCCTAT
601 TCGAGCCGGC ACAACAACGG ACTTGGCGGC AATTCCAAT ACATCAGCCA
651 ATTGCCCGGC TATCTGAAAA TACACGGAGA AATGCTTGAA AaccaATCAC
701 TCTTCCGGCT GTCCAACCGT GAACGCAATC CCGACAAACC GTTTTtagAC
751 ATCCATTTTG ACGAAATGG CAAATCACG CGTATTGTCG TTTACGAAAA
801 AAACATCTAC TTCAATCCAA ACACGGGGCG AATATAA

```

This corresponds to the amino acid sequence <SEQ ID 2300; ORF 690>:

```

m690.pep
1  MKNKTSLLLL WLTAIMLTAC SPSKDDKTKE VGASAASSSA SSAPSQTDLQ
51  PTASAPDNVK QAESAPPSNC TSLHPATGID DLMQIAEHI DSDCLFALSH
101 HELETRFGLP DGGYDNIQRL LFPDIRPEDP DYHQIILAI EDLRYGKRTI
151 SRQAQNALME QERRLREATL LLIQGSQETR GQGEPEKRTY YFEVSATPAY
201 SSRHNNGLGG NFQYISQLPG YLKHGEMLE NQSLFRLSNR ERNPDKPFEL
251 IHFDENGKIT RIVVYEKNIY FNPNTGRI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 690 shows 89.3% identity over a 408 aa overlap with a predicted ORF (ORF 690) from *N. gonorrhoeae*:

```

m690/g690      89.3% identity in 408 aa overlap

          10      20      30      40      50      60
m690.pep      MKNKTSLLLLWLTAIMLTACSPSKDDKTKEVGASAASSSAAPSQTDLOPTASAPDNVK
          |||||  |||:||||:|  |||:||||  |||||  |||||  |||||:|||||
g690           MKNKTSLLPLWLAAILAARSPSKEDKTENGASAASSSAAPSQTDLOPAASAPDNVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m690.pep      QAESAPPSNCTSLHPATGIDDLMQIAEHI DSDCLFALSHHELETRFGLPDGGYDNIQRL
          |||||  |||:||||:|  |||:||||  |||||  |||||  |||||:|||||
g690           QAESAPLXNCTGLHPAAGIGDLIQQIAEHI DSDCLFALSHNELETRFGLPGGGYDNIQRL
          70      80      90      100     110     120

          130     140     150     160     170     180
m690.pep      LFPDIRPEDPDYHQIILAI EDLRYGKRTISRQAQNALMEQERRLREATL LLIQGSQETR
          |||||  |||||  |||||  |||||  |||||  |||||:|||||
g690           LFPDIRPEDPDYHQIILAI EDLRYGTRTISRQAQDAIMEQERRLREATLMLTQGSQKTR
          130     140     150     160     170     180

          190     200     210     220     230     240
m690.pep      GQGEPEKRTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKHGEMLENQSLFRLSNR
          |||||  |||||  |||||  |||||  |||||  |||||:|||||
g690           GQGEPEKRTRYFEVSATPAYLNRRHNNGLGGNFQYIGQLPGYLMHGEMLENQSLFRLSNR
          190     200     210     220     230     240

          250     260     270     279
m690.pep      ERNPDKPFELDIHFDENGKITRIVVYEKNIYFNPNTGRIX
          |||||  |||||  |||||  |||||
g690           ERNPDKPFELDIHFDENGKITRIVVYEKNIY
          250     260     270

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2301>

```

a690.seq
1  ATGAAAAACA AAACCTCATC ACTTCTCTTA TGGCTTGCCG CAATGATGCT
51  GACCGCGTGT TCCCGGAGCA AAGAAGATAA AACGAAAGAA AACGGCGCAT
101 CCGCCGCGCTC GTCCACGGCA TCCGCGGCTT CGTCTTCGCG GCCCCAAACC
151 GATTTGCAAC CGGCGGCATC CGCCCTGAT AACGTCAAGC AGGCAGAAAG
201 CGTGCCGCGC TCAAATTGCA CCGACCTGCA CCGCGCCACC GGCATTGACG
251 ATCTCATGCA GCAATCGCC GAACACATTG ACTCGGACTG TCTGTTTGCC
301 CTTTCCCATC ACGAACTGGA AACCCGTTTC GGCTTACCCG GCGGCGGCTA
351 TGACAACATA CAGCGGCTGC TGTTTCCCGA CATCCGCCCT GAAGATCCCG
401 ACTACCATCA GAAATCATA CTGGCAATTG AAGACTTGC TACGGAAG
451 CGCACGATCA GCCGGCAGGC ACAAGATGCC TTGATGGAAC AGGAACGCCG
501 CCTCCGAGAA GCGACGCTGT TGCTGATACA GGCAGTCAA GAAACCCGCG
551 GACAAGCGCA GGAGCCGAAA CGCACGCGTT ATTTGAAGT TTCGGCAACC
601 CCGCTATT CGAGCCGGCA CAACAACGGA CTTGGCGGCA ATTTCCAATA
651 CATCGGCCAA TTGCCCGGCT ATCTGAAAT ACACGGAGAA ATGCTTGAAA

```

1111

701 ACCAATCACT CTTCGGCTG TCCAACCGTG AACGCAATCC CGACAAACCG  
 751 TTTTTAGACA TCCATTTGA CGAAATGGC AAAATCACGC GTATTGTCGT  
 801 TTACGAAAA AACATCTACT TCAATCCAAA CTGGGGCGA AGATAA

This corresponds to the amino acid sequence <SEQ ID 2302; ORF 690.a>:

a690.pep

1 MKNKTSLLL WLAAMLTAC SPSKEDTKE NGASAASSTA SAASSSAPQT  
 51 DLQPAASAPD NVKQAESVPP SNCTDLHPAT GIDDLMQQIA EHIDSDCLFA  
 101 LSHHELETRF GLPGGGYDNI QRLFPDIRP EDPDYHQKII LAIEDLRYGK  
 151 RTISRQAQDA LMEQERRLRE ATLLLIQGSQ ETRGQGEPEK RTRYFEVSAT  
 201 PAYSSRHNN LGGNFQYIGQ LPGYLKIHGE MLENQSLFRL SNRERNPDKP  
 251 FLDIHFDENG KITRIVVYEK NIYPNPNLGR R\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 690 shows 93.9% identity over a 280 aa overlap with a predicted ORF (ORF 690) from *N. meningitidis*:

m690/a690 93.9% identity in 280 aa overlap

	10	20	30	40	50
m690.pep	MKNKTSSLLLWLTAIMLTACSPSKDDRTKEVGASAASSSASSAPS---	QTDLOPTASAPD			
a690	MKNKTSSLLLWLAAMLTACSPSKEDKTKEVGASAASSTASAASSAPQTDLQPAASAPD				
	10	20	30	40	50
	60	70	80	90	100
m690.pep	NVKQAESAPPSNCTSLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
a690	NVKQAESVPPSNCTDLHPATGIDDLMQQIAEHIDSDCLFALSHHELETRFGLPDGGYDNI				
	70	80	90	100	110
	120	130	140	150	160
m690.pep	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQNALMEQERRLREATLLLIQGSQ				
a690	QRLFPDIRPEDPDYHQKII LAIEDLRYGKRTISRQAQDALMEQERRLREATLLLIQGSQ				
	130	140	150	160	170
	180	190	200	210	220
m690.pep	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYISQLPGYLKIHGEMLNQSFLRL				
a690	ETRGQGEPEKRTTRYFEVSATPAYSSRHNNGLGGNFQYIGQLPGYLKIHGEMLNQSFLRL				
	190	200	210	220	230
	240	250	260	270	279
m690.pep	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYPNPNLGR				
a690	SNRERNPDKPFLDIHFDENGKITRIVVYEKNIYPNPNLGR				
	250	260	270	280	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2303>

g691.seq

1 GTGCCGCTGC CTGCTCCCTG CCGTTTGGC AACCTGCCG CCTCTTTT  
 51 AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA  
 101 TCCCCCGGAA CGATTTTCAA CCGAAGTGGC ACATACGCCG GCTCGGGCTG  
 151 ACACAGGGTC AGCACAATGA GCTGCGTAAA ATCCGCGCCG CCTTCAAAAT  
 201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC  
 251 GCGGCTCTGT CGTCGAAATC ATTTCTTCGG ATGTTTTTAA TCGGAACGAG  
 301 GCGGCGGATT ATGTCGAAAG CCGCTACCAC TCCAGCATGG ATTTGCGGT  
 351 GGACGAATTG GAAATCCAAC ACCGCTTCTT CCATATTCTC ACACCGCAAC  
 401 AGCAGCAAAT GTGGCTTTCT TCCTGCCTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2304; ORF 691 >:

g691.pep

1 VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL  
 51 TOGQHNELRK IRAAFKMGD EARLKVHSE HSRRSVVEI ISSDVFNRE  
 101 ARDYVESRYH SSMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK\*



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2305>:

```
m691.seq
1  GTGCCACTGC CTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GTCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCC CCCC GAA CGATTTTCAA CCGAACTGCG ACATACGCCG ACTCGGGCTG
151 ACCCAAAGTC AGCACAATGA GTCGCGTAAA ATCCGCACCG CCTTCAAAT
201 GGC GGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GCCGGTCTGT CGTCGAAATC ATTTCTCTCG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGA CGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACGCCAAC
401 AGCAGCAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2306; ORF 691>:

```
m691.pep
1  VPLPAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPPNDFO PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 691 shows 97.2% identity over a 144 aa overlap with a predicted ORF (ORF 691) from *N. gonorrhoeae*:

```
m691/g691    97.2% identity in 144 aa overlap

          10      20      30      40      50      60
m691.pep    VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          |||||
g691         VPLPAPCRFAKPAASFLSMALLSCQLSHAATAYIPPNDFO PNCDIRRLGLTQSQHNELRK
          10      20      30      40      50      60

          70      80      90     100     110     120
m691.pep    IRTAFKMGDRARLKVHSEHSRRRSVVEI ISSDVFNRE ARDYVESRYLSGMDFAVDEL
          ||:|||||
g691         IRTAFKMGDRARLKVHSEHSRRRSVVEI ISSDVFNRE ARDYVESRYLSGMDFAVDEL
          70      80      90     100     110     120

          130     140
m691.pep    EIQRFFHILTPQQQMWLS SCLKX
          |||||
g691         EIQRFFHILTPQQQMWLS SCLKX
          130     140
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2307>

```
a691.seq
1  GTGCCACTGC NTGCTCCCTG CCGTTTGGCC AAACCTGCCG CCTCTTTTTT
51  AAGTATGGCT TTGCTTTCCT GCCAGCTTTC CCACGCCGCC ACGGCTTATA
101 TCC CCGTGAA CGATTTTCAA CCGAACTGCG ACATACGCCG GCTCGGACTG
151 ACACAGGGTC AGCACAATGA ACTGCGTAAA ATCCGCACCG CCTTCAAAT
201 GCGGGGCGAC AGGGCGCGTT TGAAGTTAT GCATTCCGAA CACAGCCGCC
251 GTCGGTCTGT CGTCGAAATC ATTTCTCTCG ATGTTTTTAA TCGGAACGAG
301 GCGCGCGATT ATGTCGAAAG CCGCTATTG TCCGGTATGG ATTTGCGGT
351 GGACGAATTG GAAATCCAAC ACCGGTTCTT CCATATCCTC ACACGCCAAC
401 AGCAGCAAT GTGGCTTCT TCCTGCCTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2308; ORF 691.a>:

```
a691.pep
1  VPLXAPCRFA KPAASFLSMA LLSCQLSHAA TAYIPLNDFQ PNCDIRRLGL
51  TQSQHNELRK IRTAFKMGD RARLKVHSE HSRRSVVEI ISSDVFNRE
101 ARDYVESRYL SGMDFAVDEL EIQRFFHIL TPQQQMWLS SCLK*
```

Computer analysis of this amino acid sequence gave the following results:

m691/a691 97.2% identity in 144 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEO ID 2309>

This corresponds to the amino acid sequence <SEO ID 2310; ORF 692>:

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 2311>:

```
m692.seq
  1  GTGTTGCACA  CGCTTTGTCG  CTGTTCCGGA  TCGATACGCC  GGATTCCGGC
51  GAATGGCAGG  GAATGGCCGA  TTAAGGACA  AAAATGCCGT  CTGAACACGG
101 ATACAGTTCA  GACGGCTCA  TTTTATACA  CTGCCATTAT  TGGCTGCGCC
151 TTCATTCCAT  GCGGCAGGG  ATTTGTAGCC  CTCGAAGCGT  TTGTGCGCGT
201 AGGCTTTGAA  CGCGTCGGAG  TTATAGGCCT  CGGTTACGTC  TTTAAGCCAT
251 TGGCTGTCTT  TGTCGGCGGT  TTTGACGGCA  GACCAGTTGA  CATAGGCAAA
301 GCTCGGTTCT  TGGAACAGG  CTTCCGTCAG  CTTCACTGCC  CTGCTTATGG
351 CGTAGTTGCC  GTTGACAGC  GCAAAATCCA  CGTCGGCGCG  CGTACGCGCG
```

1114

```

401 AGTTCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCGCGC
451 GATGTCGCT TCGATGCGG TCAACGGATT GATGCCGCTT TTGAGTTTGA
501 TCCAAACCCAG TTCGTCGAGC ATCACCAGA CGCGGGCGAA GTTGGACGGG
551 TCGTTGGGCG CGGATACGGT GCTGCCGCTT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGTACAGTC CCAAAGGCGC GGTGCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGGTTTG
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGTACATAG TCGGTAACT CGACCAGTTT GACGGTGTAG CCTTTTTTCT
801 CCACTCGGC TTGATTGT TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCCGA AGACGATTTC TTTTTCGCC GCGCCGTTGT CGGCGGCGCG
901 AGAAGCGGAT GCGCGGGCG CGCTGTCTT TTGACCGCCG CAGGCGGCGA
951 GGTGAGCGC GAGTGGGCG GCGGAAAGG TTTGAAGAA GGTTCATATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2312; ORF 692>:

```

m692.pep
1  VLHTLCRCSE SIRRIIRNGR EWRIKQKCR LNTDTVQTAS FYTTALFGCA
51  FIPCGRGFVA LEAFVRVGF EYGVIGLYV FKPLAVFVGG FDGRFPVDIGK
101 ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQVLG
151 DVREFGCGRI DAVFEFDPQ FVEHHQDAGE VGRVVGGRYG AAVDFDFQRF
201 QLARVQSQR GRHLEDFGDV QIVFFEVVK IGFVLEDVDV QLALSQCQIR
251 AYIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRRAVVG
301 RSGCGGRAV LTAAGGEDER ECGGKGFE GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 692 shows 91.1% identity over a 338 aa overlap with a predicted ORF (ORF 692) from *N. gonorrhoeae*:

```

m692/g692 91.1% identity in 338 aa overlap

          10      20      30      40      50      60
m692.pep  VLHTLCRCSESIRRIIRNGREWRIKQKCR LNTDTVQTASFYTTALFGCAFI PCGRGFVA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692       VSHTRCRCSESIRRIWRNGREWRIKQKCR LNTDAVQTASFYTTALFGCAFI PCGRVFVA
          10      20      30      40      50      60

          70      80      90      100     110     120
m692.pep  LEAFVRVGFERVGVIGLYVFKPLAVFVGFDGRFPVDIGKARFLEQGFQ LHAAYGVVA
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692       LEAFVRVGFERVGVIGLYVFKPLAVFVGFDGRFPVDIGKARLLEQGFQ LHAAYGVVA
          70      80      90      100     110     120

          130     140     150     160     170     180
m692.pep  VDDGKIHVGAATRQLRGFKLDDFVQVLGDVRFGCGQRIDAVFEFDPQ FVEHHQDAGE
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692       VDDGKIHVGAARQLCGFKLDDFVQVFRDVGFCGQRIDAVFEFDPQ FVQHHQGACE
          130     140     150     160     170     180

          190     200     210     220     230     240
m692.pep  VGRVVGGRYGAAVDFDFQRFQQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692       VGRVVGGRYGAAVDFDFQRFQFARIQSQRGRHLEGFQVQVFFFEIVKIGFVLEDVDV
          190     200     210     220     230     240

          250     260     270     280     290
m692.pep  QLALSQCQIRAYIVGKLDQFDGVAFFLQLGLDLFFDHIAEVADGRAEDDF FFRRAVVG--
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692       QLALRQCQIRAHIVGKFDQFDGVAFFLQLGLDLFFDHIAEVAGRAEDDF FFRRAVIGRR
          250     260     270     280     290     300

          300     310     320     330
m692.pep  GGRSGCGGRAVFLTAAGGEDERECGGGKGFE EGFHIFSX
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
g692       GGRGCGG-RAVFLTAAGCEDERECGGGKGFE EGFHIFSX
          310     320     330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2313>

```

m692.seq
1  GTGTTGCACA CGCTTTGTCG CTGTTGCGAA TCGATACGCC GGATTCGGCG

```

```

51  GAATGGCAGG GAATGGCAGG TTAAAGGACA AAAATGCCGT CTGAACACGG
101 ATACGGTTCA GACGGCATCA TTTTATACGA CTGCCTTATT TGGCTGCGCC
151 TTCAATCCAT GCGGCAGGGG ATTTGTAGCC CTCGAAGCGT TTGTGCGCGT
201 AGGCTTTGAA CGCGTCGGAG TTATAGGCCT CGGTTACGTC TTTAAGCCAT
251 TGCTGTCTT TGTGCGCGGT TTTGACGGCA GACCAGTTGA CATAGGCAAA
301 GCTCGGTCTT TGAACAGGG CTTGCGTCAG CTTTCATGCCG CTGCTTATGG
351 CGTAGTTGCC GTTGACGACG GCAAAATCCA CGTCGGCGCG GCTACGCGGC
401 AGTTGCGCGG CTTCAAGCTC GACGATTTTG ATGTTTTTCA GGTTCGCGC
451 AATGTCGCGT TTGGATGCGG TCAGCGGATT GATGCCGCTT TTGAGTTTGA
501 TCCAACCCAG TTCGTCGAGC ATCACCAGA CGCGGCGGAA GTTGACGCGG
551 TCCTTGGGCG CGGATACGGT GCTGCCGTCT TTGACTTCTT CCAGCGATT
601 CAGCTTGCCC GGTACAGTC CCAAAGGCGC GGTGCGCACT TGAAGACTT
651 CGGTGATGTC CAGATTGTGT TCTTTTTTGA AGTCGTCAAG ATAGGTTTGA
701 TGTGGAAGA CGTTGATGTC CAACTCGCCC TCAGCCAATG CCAGATTCGG
751 GCGCACATAG TCGGTAAACT CGACCAAGTT GACGGTGTAG CCTTTTTTCT
801 CCAGCTCGGG TTGGATTGTG TCTTTGACCA TATCGCCGAA GTCGCCGACG
851 GTCGTGCGGA AGACGATTTT TTTTTCGCC GCGCGGTGT CGGCGCGGCG
901 AGAAGCGGAT GCGCGGCGCG CGCTATCTTT TTGACGCGCG CAGGCGGCGA
951 GAGATGAGCG GAGTGCAGCG GCGGAAGGG TTTTGAAGAA GGTTCATATA
1001 TTTTCTCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2314; ORF 692.a>:

```

a692.pep
1:  VLHTLCRCSE SIRRIIRNGR EWRIGQKCR LNTDTVQTAS FYTTALFGCA
51:  FIPCGRGFVA LEAFVRVGFE RVGVIGLYV FKPLAVFVGG FDGRFVDIGK
101: ARFLEQGFQ LHAAYGVVA VDDGKIHVGA ATRQLRGFKL DDFDVQFVFG
151: NVRFQCGQRI DAVFEFDPQ FVEHHQDAGE VGRVVRGYG AAVFDFFORF
201: QLARVQSQR GRHLEDFGDV QIVFFFEVVK IGFVLEDVDV QLALSQCQIR
251: AHIVGKLDQF DGVAFFLQLG LDLFFDHIAE VADGRAEDDF FFRAVVGGG
301: RSGCGGRAIF LTAAGGEDER ECGGKGFEF GFHIFS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 692 shows 98.8% identity over a 336 aa overlap with a predicted ORF (ORF 692) from *N. meningitidis*:

```

m692/a692    98.8% identity in 336 aa overlap

          10      20      30      40      50      60
m692.pep    VLHTLCRCSESIRRIIRNGREWRIKQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
a692         VLHTLCRCSESIRRIIRNGREWRIKQKRLNTDTVQTASFYTTALFGCAFI PCGRGFVA
          10      20      30      40      50      60

          70      80      90     100     110     120
m692.pep    LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRFVDIGKARFLEQGFQ LHAAYGVVA
a692         LEAFVRVGFERVGVIGLYVFKPLAVFVGGFDGRFVDIGKARFLEQGFQ LHAAYGVVA
          70      80      90     100     110     120

          130     140     150     160     170     180
m692.pep    VDDGKIHVGAATRQLRGFKLDDFVQVLDVRFQCGQRI DAVFEFDPQ FVEHHQDAGE
a692         VDDGKIHVGAATRQLRGFKLDDFVQVFNVRFGCGQRI DAVFEFDPQ FVEHHQDAGE
          130     140     150     160     170     180

          190     200     210     220     230     240
m692.pep    VGRVVRGYGAAVDFDFQFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
a692         VGRVVRGYGAAVDFDFQFQLARVQSQRGRHLEDFGDVQIVFFFEVVKIGFVLEDVDV
          190     200     210     220     230     240

          250     260     270     280     290     300
m692.pep    QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRVAVGGG
a692         QLALSQCQIRAHIVGKLDQFDGVAFFLQLGLDLFFDHIAE VADGRAEDDF FFRVAVGGG
          250     260     270     280     290     300

          310     320     330
m692.pep    RSGCGGRAIFLTAAGGEDERECGGKGFEFEGFHIFSX
a692         RSGCGGRAIFLTAAGGEDERECGGKGFEFEGFHIFSX

```

310

320

330

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2315>:

```

g694.seq
1   TCGGCATTG TGTGCCCCA ACATCCGATG CCTGCGTTAA CGCCTGCGTC
51  AACGTTTGA CAAATCGGGT TTGGTTTCGC CCTCGCGGCG CAGCTCCTTG
101 GGCAGGACGA ACACGATGCT TTCTTCCGCG CCCCCCCTT CGCGCACGGT
151 TTCATGCCCC CATCCGCGTA TGGTTGCCAA TACTTCCCGC ACCAACACTT
201 CGGGCGCGGA CGCGCCTGCC GTTACGCCGA CTTTGCTTTT GCCTTCAAAC
251 CACGTGCGTT GCaggTAGGA CGCGTTGTCC ACCATATACG CATCGATTCC
301 GCGCGATGCC GCCACTTCGC GCAGGCGGTT GCTGTTGGAC GAATTGGGCG
351 AACCGACCAC AATCACGATG TCGCACTGTT CCGCCAGCTC TTTGACGGCG
401 GTTTGCCGGT TGGTCGTCGC ATAGCAGATG TCTTCTTGT GCGGATTGCG
451 GATATTGGGG AAACGCGCGT TCAGCGCGGC GATGATGTCT TTGGTTTCAT
501 GCACCGAGAG CGTGGTTTGG CTGACATAGG CGAGTTTGTC GGGGTTTCTG
551 ACTTCGAGTT TTGCCACATC TCCGACCGTT TCGACCAAAA GCATTTTGCC
601 CGGTGCAAGC TGCCCCATCG TGCCCTTCGAC CTCGCGGTGC CCCTTATGCC
651 CGATCATGAT GATTTCACAG TCTTGGGCAT CCAGTCGGGC GACTTCCTTA
701 TGCACTTTCG TCACCAGCGG GCAAGTCGCA TCAAATACCC GGAAACCGCG
751 CTCGCGCGCT TCCTGCTGCA CCGCCTTCGA TACGCGGTGT GCCGAATAAA
801 CCAGTGTCCG GCCCGGCGGC ACTTCCGCCA AGTCTTCGAT AAACACCGCG
851 CCTTTTTCGC GCAGGTTGTC CACGACGAAT TTGTTGTGGA CGACTTCGTG
901 GCGCACATAA ACCGGCGCGC CGAATCTTTC CAAAGCAGCT TCGACAATAC
951 TGATTGCCCC ATCCACACCG GCGCAGAAGC CGCGCGGATT GGCAAGGATG
1001 ATGGTTTTCG CGTTCATAAG TTTTGCAATC CGTGTTCAGA CGGCATTAC
1051 GTTTTTTTGC TNNATCTTTG CGATGGACGA TATTGTCAAG CACCGCCAAC
1101 ACCGCACCGA CGCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2316; ORF 694>:

```

g694.pap (partial)
1   SAFVLPKHPM PALTPASTFA QIGFGFALAA QLLGQDEHDA FFRAPPPFANG
51  FMPPPSAYGCG YFPQHFGFRG RACRYADFAF AFKPRALQVG RVVHHIRIDS
101 ARCRHFAQAV AVGRIGRTDH NHDVALFRQL FDGGLPVGRR IADVFLVRIA
151 DIGETRVRQG DDVFGFIDRE RGLADIGEFV GVSDFEFCHI SDRFDQKHFA
201 RCKLPHRAFD LGVPLMPDHD DFTVLGIQSG DFLMHRHQXR ASRIKYPETA
251 LRRFLLHRLR YAVCRINQCR ARRHFRQVFD KHRAFFAQVV HDEFVDDFV
301 AHINRRAEFF QSTFDNTDCP IHTGAEAAARI GKDDGFSVHK FCIPCSGDIH
351 VFLLXLCDDR YCQAPPTPHR RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2317>:

```

m694.seq
1   TTGGTTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGCAC
101 AAATCGGGTT TGGTTTCGCC CTCGCGGCGC AACTCTTTGG GCAGGACGAA
151 CACAATGCTT TCCTCCGCAC CCTCGCCTTC GCGTACGGTT TCGTGCCCCC
201 ATCCGCGTAT GGTGCCAGT ACTTCCCGCA CCAACACTTC GGGCGCGGAC
251 GCGCCTGCGG TTACGCCGAC TTTGTTTTTG CCCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACGC ATCGATTCCG CGCGATGCCG
351 CCACTTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCACGATGT CGCACTGTTC TGCCAACTCT TTGACGGCGG TTTGCCGGTT
451 GGTCGTCGCA TAGCAGATAT CTTCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGGT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAAG CATTTTGCCC GGCAGCAAGCT
651 GCCCATCGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG
701 ATTTACAGAT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CACGAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCGGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACTCTTCC AAAGCAGGTT CGACAATACT GATT GCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGACGAT GTTGTCACAC ACCGCCAACA CCGCACCAGC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2318; ORF 694>:

```

m694.pap
1   LVSASGTRQK CRLKPVOTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV

```

1117

```

151 GRRIADIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHISDRFDQK HFARRKLPHR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVNV DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 86.8% identity over a 372 aa overlap with a predicted ORF (ORF 694) from *N. gonorrhoeae*:

```

m694/g694      86.8% identity in 372 aa overlap

      10      20      30      40      50
m694.pep      LVASAGTRQKCR LKPQTAFVLPKHS----TPASTFAQIGFGFALAAQLFGQDEHNAFFR
g694           SAFVLPKHPMPALTPASTFAQIGFGFALAAQLLGQDEHDAFFR
              10      20      30      40

      60      70      80      90     100     110
m694.pep      TLAFAYGFVPPSAYGCQYFPHQHFGGRGRACRYADFV FALKPCALQVACIIHHIRIDSARC
g694           APPFAHGFMPSPAYGCQYFPHQHFGGRGRACRYADFAFAFKPRALQVGRVVHHIRIDSARC
              50      60      70      80      90     100

      120     130     140     150     160     170
m694.pep      RHFAQAVAVGRIGRTDHNHDVALFCQLFDGGLPVGRRRIADIFLVRIADIGETRVQRGDDV
g694           RHFAQAVAVGRIGRTDHNHDVALFRQLFDGGLPVGRRRIADVFLVRIADIGETRVQRGDDV
              110     120     130     140     150     160

      180     190     200     210     220     230
m694.pep      FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKH FARRKLPHRSFDLDVPLMPDHDDFT
g694           FGFIDRERGLADIGEFVGVSDFEFCHISDRFDQKH FARCKLPHRAFDLGVPLMPDHDDFT
              170     180     190     200     210     220

      240     250     260     270     280     290
m694.pep      VLGIQSGDFLMHFRHQASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHR
g694           VLGIQSGDFLMHFRHQASRIKYPETALRRFLHLRLRYAVCRINQCRARRHFRQVFDKHR
              230     240     250     260     270     280

      300     310     320     330     340     350
m694.pep      TFFTQVVHDEFVNVDFVAHINRRAELFQSTFDNTDCPIHTSAEAARIGKDDGFLVHKPGI
g694           AFFAQVVHDEFVNVDFVAHINRRAEFFQSTFDNTDCPIHTGAEAARIGKDDGFSVHKFCI
              290     300     310     320     330     340

      360     370     380
m694.pep      SFSDDGINIFLLGFYGGRCCTPTPTPHRRRX
g694           PCSDDGIHVFLXXLCDGRYCPPTPHRRRX
              350     360     370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2319>:

```

a694.seq
1   TTGGTTCCG CATCCGGCAC ACGGCAAAAA TGCCGTCTGA AGCCTGTTCA
51  GACGGCATTG GTGTTGCCCA AACATTCAAC GCCTGCGTCA ACGTTTGAC
101 AAATCGGGTT TGTTTCGCC CTCCGGCGC AACTCTTGG GCAGGACGAA
151 CACAATGCTT TCTTCGCAC CCTCGCCTC GCGTACGGT TCGTGCCCC
201 ATCCGCGTAT GGTGCCAGT ACTTCCGCA CCAACTTC GGGCGCGGAC
251 GCGCCTGCCG TTACGCGGAC TTTGTTTTG CCTCAAACC ATGCGCGTTG
301 CAGGTAGCCT GCATTATCCA CCATATACG ATCGATTCCG CGCGATGCCG
351 CCACCTCGCG CAAGCGGTTG CTGTTGGACG AATTGGGCGA ACCGACCACA
401 ATCAGGATGT CGCACTGTTT TGCCAACCTT TGACGGCGG TTTGCCGTTT
451 GGTCTGCGCA TAGCAGATAT CTCCTTGTG CGGATTGCGG ATATTGGGGA
501 AACGCGCGTT CAGCGCGGCG ATGATGTCTT TGGTTTCATC GACCGAGAGC
551 GTGGTTTGGC TGACATAGGC GAGTTTGTG GGGTTTCTGA CTTCGAGTTT
601 TGCCACATCT CCGACCGTTT CGACCAAAG CATTTTGCCG GCGCAAGCT
651 GCCCATCTGT TCCTTCGACC TCGACGTGCC CTTATGCCC GATCATGATG

```

1118

```

701 ATTTTCACAGT CTTGGGCATC CAGTCGGGCG ACTTCCTTAT GCACTTTCGT
751 CAC CAGCGGG CAAGTCGCAT CAAACACGCG GAAACCGCGC TCCGCCGCTT
801 CTTGCCGCAC CGCCTTCGAT ACGCCGTGTG CCGAATAAAC CAGTGTGCGG
851 CCCGGCGGCA CTTCCGCCAA GTCTTCAATA AACACCGCAC CTTTTTCACG
901 CAGGTTGTCC ACGACGAATT TGTGTGAAC GACTTCGTGG CGCACATAAA
951 TCGGCGCGCC GAACCTCTCC AAAGCACGTT CGACAATACT GATTGCCCGA
1001 TCCACACCAG CGCAGAAGCC GCGCGGATTG GCAAGGATGA TGGTTTTCTC
1051 GTTCATAAGC CCGGTATTTC GTTTCAGAC GGCATCAATA TTTTCTTCT
1101 TGGGTTTTAC GGTGGACGAT GTTGTCCAAC ACCGCCAACA CCGCACCAGC
1151 GCAGATAA

```

This corresponds to the amino acid sequence <SEQ ID 2320; ORF 694.a>:

```

a694.pep
1  LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFA LAAQLFGQDE
51  HNAFFRTLAF AYGFVPPSAY GCQYFPHQHF GRGRACRYAD FVFALKPCAL
101 QVACIIHHIR IDSARCRHFA QAVAVGRIGR TDHNDHVALF CQLFDGGLPV
151 GRRADIIFLV RIADIGETRV QRGDDVFGFI DRERGLADIG EFVGVSDFEF
201 CHI SDRFDQK HFARRKLPFR SFDLDVPLMP DHDDFTVLGI QSGDFLMHFR
251 HQRASRIKHA ETALRRFLPH RLRYAVCRIN QCRARRHFRQ VFNKHRTFFT
301 QVVHDEFVFN DFVAHINRRA ELFQSTFDNT DCPHTSAEA ARIGKDDGFL
351 VHKPGISFSD GINIFLLGFY GGRCCPTPPT PHRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 694 shows 100% identity over a 385 aa overlap with a predicted ORF (ORF 694) from *N. meningitidis*:

m694/a694 100.0% identity in 385 aa overlap

	10	20	30	40	50	60
m694.pep	LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
a694	LVSASGTRQK CRLKPVQTAF VLPKHSTPAS TFAQIGFGFALAAQLFGQDEHNAFFRTLAF					
	10	20	30	40	50	60
m694.pep	70	80	90	100	110	120
a694	70	80	90	100	110	120
	130	140	150	160	170	180
m694.pep	QAVAVGRIGR TDHNDHVALFCQLFDGGLPVGRRADIIFLVRIADIGETRVQRGDDVFGFI					
a694	QAVAVGRIGR TDHNDHVALFCQLFDGGLPVGRRADIIFLVRIADIGETRVQRGDDVFGFI					
	130	140	150	160	170	180
m694.pep	190	200	210	220	230	240
a694	190	200	210	220	230	240
	250	260	270	280	290	300
m694.pep	QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT					
a694	QSGDFLMHFRHQRASRIKHAETALRRFLPHRLRYAVCRINQCRARRHFRQVFNKHRTFFT					
	250	260	270	280	290	300
m694.pep	310	320	330	340	350	360
a694	310	320	330	340	350	360
	370	380				
m694.pep	GINIFLLGFY GGRCCPTPPT PHRRRX					
a694	GINIFLLGFY GGRCCPTPPT PHRRRX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2321>:

```

g695.seq
1   TTGCTCTCAA CTCGTCCGGC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGT TGAACGG AAGGGTGATG CGCGAAGCGG CTTTGTGATG GCCGCCCAGT
101 GTC AAAAATC TCAAAGATT CAATCAAAAC CTGCCGAACG ATACGCGGAT
151 TGT CCCCATC ACCCTGCCCG TCGGCGACGG TTTGACCTG CTTCTGAAAA
201 AAT AATGAAG ACCAAATTAC CGCTTTTAT CATTGGGCTG TCTGTGTCTG
251 CCT CCTGTGC TTCCGTTTTC CCCGTTCCGG AGGGCAGCGG AACCGAAATG
301 CCG ACACAGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCCACTCT
351 GCA AGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGGAACG
401 AAG TGGAAAT GTTAAACGGG AAAGTCAAAG CATTGGAGCA TACGAAAATA
451 CAC CCTTCCG GCAGGCATA CGTCCAAAAA CTCGACGACC GCAAATTGAA
501 AGA GCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACCGTCG
551 AAA CCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TCAAACGGGC
601 AGG TTTTCTG CCGCAGCCGC CTTGTTGAAG GGGGCGGACG GCGGAGACGG
651 CGG CAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTA TGGGGAA CTGTGAATCT GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGT TTCAAAG ACAGCCCAAC CGGCCCCGAA GTCATATTCA AAATCGGCGA
801 ATG CCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCC TGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG GCCTGCCGCA
901 CCC GTACGCA AACGATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2322; ORF 695>:

```

g695.pep
1   LPQTRPARRH HRHRQYFVER KGDARSGF*C AAQCONSQRF QSKPAERYAD
51  CPHPARRRR FDPASEKIMK TKLPLFIWL SVSASCASVL PVPEGSRTM
101 PTQENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVEMLNG KVKALEHTKI
151 HPSGRITYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYQNG
201 RFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE VIFKIGECQY RLQOKDIARA TWRSLIQTPY GSPAARKRAA
301 AVRKR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2323>:

```

m695.seq
1   TTGCTCTCAA CTCGTCCGTC AAGGCGGCAT CATCGCCATC GACAATATTT
51  TGCTGAACGG AAGGGTGATG CGCGAAGCGG CTTCCGATGC GCCGCCCAGC
101 GTCGGCATCC TCAAAGATT CAATCAAAAC CTGCCGAACG ACCCGCGCAT
151 CGT CCCCATC ACCCTGCCCG TCGGCGACGG CTTGACCTG CTTCTGAAAA
201 AATAATGAAG ATCAAATTAC CGCTTTTAT CATTGGGCTG TCTGTGTCCG
251 CCTCCTGTGC TTCCGTTTCA CCCGTTCCGG CAGGCAGCCA AACCGAAATG
301 TCGACACGGG AAAATGCTTC AGACGGCATT CCCTATCCCG TTCCGACCTT
351 GCAAGACCGT TTGGACTATC TGGAAAGCAA AATCGTCCGG CTGTGGAACG
401 AAGTGGAAAC CTTAAACGGC AAAGTCAAAG CACTGGAACA CGCAAAAACA
451 CATTCTTCCG GCAGGCATA CGTCCAAAAA CTCGACGACC GCAAGTTGAA
501 AGAGCATTAC CTCAATACCG AAGGCGGCAG CGCATCCGCA CATACTGTCTG
551 AAACCGCACA AAACCTCTAC AATCAGGCAC TCAAACACTA TAAAGCGGC
601 AAGTTTCTG CCGCTGCCTC CTTGTTGAAA GCGCGGACG GAGGCGACGG
651 CGG CAGCATC GCGCAACGCA GTATGTACCT GTTGCTGCAA AGCAGGGCGC
701 GTATGGGCAA CTGCAATCC GTCATCGAAA TCGGAGGGCG TTACGCCAAC
751 CGTTTCAAAG ACAGCCCAAC CGCGCCTGAA GCCATGTTCA AAATCGGCGA
801 ATG CCAATAC AGGCTTCAGC AAAAAGACAT TGCAAGGGCG ACTTGGCGCA
851 GCCTGATACA GACCTATCCC GGCAGCCCGG CGGCAAAACG GCCTGCCGCA
901 CCC GTGCGCA AACGATAG
  
```

This corresponds to the amino acid sequence <SEQ ID 2324; ORF 695>:

```

m695.pep
1   LPQTRPSRRH HRHRQYFAER KGDARSGFRC AAQRHPQRF QSKPAERPAH
51  RPHHPARRRR LDPASEKIMK IKLPLFIWL SVSASCASVS PVPAGSQTEM
101 STRENASDGI PYPVPTLQDR LDYLEGKIVR LSNEVETLNG KVKALEHART
151 HSSGRAYVQK LDDRKLKEHY LNTEGGSASA HTVETAQONLY NQALKHYKSG
201 KFSAAAALLK GADGGDGGSI AQRSMYLLLO SRARMGNCS VIEIGGRYAN
251 RFKDSPTAPE AMFKIGECQY RLQOKDIARA TWRSLIQTPY GSPAARKRAA
301 AVRKR*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 694 shows 90.8% identity over a 305 aa overlap with a predicted ORF (ORF 695) from *N. gonorrhoeae*:



m695/g695 90.8% identity in 305 aa overlap

m695.pep	10	20	30	40	50	60
	L.PQTRPSRRHRRHQYFAERKGDARSGFRCAAQRRHPQRFOSKPAERPAPHRPHHPARRRR					
	:           :           :           :           :					
g695	10	20	30	40	50	60
	L.PQTRPARRHRRHQYFVERKGDARSGFXCAAQCNQSRFOSKPAERYADCPHHPARRRR					
m695.pep	70	80	90	100	110	120
	L.DPASEKIMKIKLPLFIIWLSVSASCASVSPVPAGSQTEMSTRENASDGIPYPVPTLQDR					
	:					
g695	70	80	90	100	110	120
	F.DPASEKIMKTKLPLFIIWLSVSASCASVLPVPEGSRTemptQENASDGIPYPVPTLQDR					
m695.pep	130	140	150	160	170	180
	L.DYLEGKIVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDRLKLEHYLNTEGGSASA					
g695	130	140	150	160	170	180
	L.DYLEGKIVRLSNEVEMLNGKVKALEHTKIHPGRTYVQKLDRLKLEHYLNTEGGSASA					
m695.pep	190	200	210	220	230	240
	HTVETAQNLYNQALKHYKSGKFSAAAALLKGADGGDGGSIQSRSMYLLQLSRARMGNCS					
g695	190	200	210	220	230	240
	HTVETAQNLYNQALKHYQNGRFSAAAALLKGADGGDGGSIQSRSMYLLQLSRARMGNCS					
m695.pep	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAKRAAA					
g695	250	260	270	280	290	300
	VIEIGGRYANRFKDSPTAPEVIFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAKRAAA					
m695.pep	AVRKRKX					
g695	AVRKRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2325>:

a695.seq

```

1  TTGCTCAAG CTTGTCCGGC AAGGCGGCAT CATTGCCATC GACAATATTT
51  TGTGTAACGG AAGGGTGATG CGCGAAGCGG CTTCGGATGC GCCGCCGAGC
101  GTCGGCATCC TCAAAGATT TAAATCAAAC CTGCCGAACG ATACGCGGAT
151  TGTCCCCATC ACCCTGCCCC TCGGCGACGG TTTGACCTG CTCTGAAAA
201  AATAATGAAG ACCAAATTAC CGCTTTTAT CATTGGCTG TCCGTATCCG
251  CCGCCTGTTC TTCCCTGTG TCCCGCAATA TTCAGGATAT CGCGCTCGAA
301  CCGCAGGCAG AGGCAGGTAG TTCGGACGCT ATTCCCTATC CCGTTCCAC
351  TCTGCAAGAC CGTTGGATT ATCTGGAAGG CACACTCGTC CGCCTGTGCA
401  ACGAAGTGGA AACCTTAAAC GGCAAAGTCA AAGCACTGGA GCATGCGAAA
451  ACACACCCTT CCAGCAGGCG ATACGTCCAA AACTCGACG ACCGCAAGTT
501  GAAAGAGCAT TACCTCAATA CCGAAGGCGG CAGCGCATCC GCACATACCG
551  TCGAAACCGC ACAAACCTC TACAATCAGG CACTCAAACA CTATAAAAGC
601  GGCAGGTTT CTGCCGCTGC CTCCTGTG AAAGGCGCGG ACGGAGGCGA
651  CGGCGGCGAG ATCGCGCAAC GCAGTATGTA CTTGTTGCTG CAAAGCAGGG
701  CGCGTATGGG CAACTGCGAA TCCGTCATCG AAATCGGAGG GCGTTACGCC
751  AACC GTTCA AAGACAGCCC AACC GCGCCT GAAGCCATGT TCAAAATCGG
801  CGAATGCCAA TACAGGCTTC AGCAAAAAGA CATTGCAAGG GCGACTTGGC
851  CGAGCCTGAT ACAGACCTAT CCCGGCAGCC CGGCGGCAAA ACGCGCCGCC
901  GCAGCGGTGC GCAACGATA G

```

This corresponds to the amino acid sequence <SEQ ID 2326; ORF 695.a>:

a695.pep

```

1  LPQACPARRH HCHQYFVER KGDARSGFRC AAQRRHPQRF *SKPAERYAD
51  CPHHPARRRR FDPASEKIMK TKLPLFIIWL SVSAACSSPV SRNIQDMRLE
101  PQAEAGSSDA IPYPVPTLQD RLDYLEGLTV RLSNEVETLN GKVKALEHAK
151  THPSSRAYVQ KLDDRKLKEH YLNTEGGSAS AHTVETAQNL YNQALKHYKS
201  GRFSAAAALL KGADGGDGGG IAQRSMYLLL QSRARMGNCE SVIEIGGRYA
251  NRFKDSPTAP EAMFKIGECQ YRLQOKDIAR ATWRSLIQTY PGSPAAKRAA
301  AAVRKR*

```

Computer analysis of this amino acid sequence gave the following results:

m695/a695 88.3% identity in 308 aa overlap

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2329>:

1122

```

1  TTGGGTTGCC GGCAGGCGGC ATCCCATCAT TTTTGCCAAG GCAACAAATT
51  ATT'TGGCGGC ATCTTTCATT TTGTCTGCCG CTTCTGAGT CGCGTCGGCA
101 GCT'TTGTTC AAGTATCTTT AGCTGCTTCA GTTACAGCTT CTTTGGCTTC
151 AGT'TACAGCT TCCTCGGCAC TTGCCTTTCG ATCAGCCGCA GCATCTTTGA
201 CTT'GGTCTTT CGCTTCTTCG ACGGCAGAA GCGGCAGACT GCGCGCAGAA
251 GCC'GCAGTGT CTTTAACATC GGACTCAACG GCTTGAACCG CTTCTTAAC
301 CTC'CTGTTTG GCTTCTTGGC AACAAGCTGC CAAGGCAGCC GCCATCATTG
351 CGGCAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2330; ORF 696.a>:

```

a696.pep
1  LGCRQAASHH FCQGNKLFGG IFHFVCRFLS RVGSFVQSIF SCFSYSFFGF
51  SYSFLGTCLC ISRSIFDLVF RFFDGRSGRL GGRSRSVFNI GLNGLNRFLN
101 LLFGFLRTSC QGSRHHCNGQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 696 shows 100.0% identity over a 120 aa overlap with a predicted ORF (ORF 696.a) from *N. meningitidis*:

```

m696/a696    100.0% identity in 120 aa overlap

          10      20      30      40      50      60
m696.pep    LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
a696         LGCRQAASHHFCQGNKLFGGIFHFVCRFLSRVGSFVQSIFSCFSYSFFGFYSFLGTCLC
          10      20      30      40      50      60

          70      80      90     100     110     120
m696.pep    ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFLNLLFGFLRTSCQSRHHCNGQ
a696         ISRSIFDLVFRFFDGRSGRLGGRSRSVFNIGLNLNRFLNLLFGFLRTSCQSRHHCNGQ
          70      80      90     100     110     120

m696.pep    X
            |
a696         X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2331>:

```

g700.seq
1  ATGAGCAGCC TGATGACGTT GTTTTCGGTA TTGGTACCGA TGTTGCCCG
51  ATTTTTTATC CGTGTTCCTA AGCCTTACCT GCCCGCTTCG GACAAGGTGC
101 TGTCGGTTTT GGTGTATGCC GTGCTGCTGC TGATCGGCGT ATCGTTGTCG
151 CGCGTGGAGG ATTTGGGTTT GCGGTGGGCG GATATGGCGT TGACGGTTCT
201 TTGGCTGTTT GTTGTACGG TAGGGGCGAA CCTGCTTGCC TTGGCAGTGT
251 GTGGGAAAGT GTCCCCGTGG CGGATAGGGG GAAAAGGGAA GGGCGTTTCG
301 GTCGGCGTGT CGGGCAGTGT GAGGCAGCTC GGATGCGTAC TGCTCGGTTT
351 TGTGTCCGGC AAATTGATGT GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTACTG CCTGATGCTG CTGGTGTTCC TCATCGGCGT ACAGCTCAAA
451 AGTAGCGGCG TATCGTTGCG GCAGGTTTTC CTTAACCGGG GGGGCATCCG
501 GCTGTGCGTT TGGTTTATAT TGTCTCTCTT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGATGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATTCCCT CTCGGGTTTG GTAATGACCG AGGCTTACGG
651 GGCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTTGGCA CGAGAGCTGT
701 TTGCACTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCG GGATGCGGCG
751 GTGGGGGTCT GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTAATTCA
801 GGGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCCCGG TTTCTGATGG TGGTGTTTTC CACGCTGGGC
901 TGA

```

This corresponds to the amino acid sequence <SEQ ID 2332; ORF 700>:

```

g700.pep
1  MSSLMTLFSV LVPMFAGFFI RVPKPYLPAS DKVLSVLVYA VLLLIGVSLS
51  RVEDLGSRLG DMALTVLWLF VCTVGANLLA LAVLGKLSFW RIGGKGKGV
101 VGVSGSVRQL GCVLLGFVSG KLMCDIWMPS ENAGMYCLML LVFLIGVQLK
151 SSGVSLRQVL LNRRGIRLSV WFILSSLSGG LLFAASADGV SWTKGLAMAS

```

201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA  
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVNVIAAP FLMVVFSTLG  
 301 \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2333>:

m700.seq

1 A TGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCCG  
 51 A TTTTATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC  
 101 T ATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCTG  
 151 C GCGTGGAGG ATTTGGGTTT GCGGTTGGAC GATATGGCGT TGACGGTTCT  
 201 G TGCTGTTT GTTTGTACGG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT  
 251 T GGGAAAGTT ATTCCTGTTG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG  
 301 G TCGGCGTGT CCGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT  
 351 T GCATTCGGC AAACGTATGC GCGATATTG GATGCCGTCT GAAAGCGCGG  
 401 G CATGTATTG TCTGATGCTG CTGGTGTTC TCATCGGCGT ACAGCTCAAA  
 451 A GCAGCGGCG TATCGTTGCG GCAGGTTTGT GTCAACCGCA GGGGTATTCG  
 501 G TTGTCGGTC TGGTTTATGC TTTCATCTCT TTCGGGCGGG CTGCTGTTTG  
 551 C CGCATCGAC AGACGGTGTG TCGTGGACGA AAGGTTTGGC GATGGCTTCC  
 601 G GCTTCGGTT GGTATTCCT CTCGGGTTTG GTCATGACCG AGGCTTACGG  
 651 C GCGGTATGG GGCAGCATCA TGCTGCTGAA CGATTGGCA CGAGAGCTGT  
 701 T TGCACTGGC ATTTATCCCG CTGCTGATGA AGCGTTTTC AGATGCGGCG  
 751 G TGGGGGTTG GCGGTGCGAC CAGTATGGAT TTTACATTGC CCGTGATTCA  
 801 G GGTGCGGGC GGTTTGGAAG TCGTGCCGGT AGCGGTCAGC TTCGGCGTGG  
 851 T GGTCAATAT CGCCGCCCG TTTCTGATGG TGGTGTTC CGCTTTGGGT  
 901 TGA

This corresponds to the amino acid sequence <SEQ ID 2334; ORF 700>:

m700.pep

1 MDSLMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL  
 51 RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPW RIKGKGKVS  
 101 VGVSGSVGQL GCVLLGFAFG KLMRDIWMPES ESAGMYCLML LVFLIGVQLK  
 151 SSGVSLRQVL VNRGIRLSV WEMLSLSSGG LLFAASTDGV SWTKGLAMAS  
 201 GFGWYLSGL VMTEAYGAVW GSIMLLNDLA RELFALAFIP LLMKRFPDAA  
 251 VGVGGATSMD FTLPIQGAG GLEVVPVAVS FGVVNVIAAP FLMVVFSALG  
 301 \*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae* with *menB*

ORF 700 shows 94.7% identity over a 300 aa overlap with a predicted ORF (ORF700.ng) from *N. gonorrhoeae*:

m700/g700

	10	20	30	40	50	60
m700.pep	MDSLMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
g700	MSSLMTLFSVLVPMFAGFFIRVPKPYLPASDKVLSVLVYAVLLLIGVSLSRVEDLGSRLG					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVGQLGCVLLGFAFG					
g700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIGGKGVSVGVSGSVRQLGCVLLGFVSG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRGIRLSVWEMLSLSSGG					
g700	KLMCDIWMPSENAGMYCLMLLVFLIGVQLKSSGVSLRQVLNRRGIRLSVWFILSSLSGG					
	130	140	150	160	170	180
m700.pep	LLFAASTDGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
g700	LLFAASADGVSWTKGLAMASGFGWYLSGLVMTEAYGAVWGSIMLLNDLARELFALAFIP					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
m700.pep	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
g700	LLMKRFPDAAVGVGGATSMDFLTPVIQAGGLEVPVAVSFGVVVNIAAPFLMVVFSALG					
	250	260	270	280	290	300
m700.pep	X					
g700	X					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2335>:

```
a700.seq
1  ATGGACAGCC TGATGACGTT GCTTTCGGTA TTGATACCGA TGTTTGCCGG
51  ATTTTATATC CGTGTGCCCA AGCCTTACCT GCCCGCTTTG GATAAGGTGC
101 TATCGGTCTT GGTGTATGCT GTGCTGCTGC TGATCGGCGT CTCGTTGTCT
151 CGCGTGGAGG ATTTGGGTTT GCGGTGGGAC GATATGGCGT TGACGGTTCT
201 GTGGCTGTTT GTTGTACGCG TCGGGGCGAA CCTGCTTGCT TTGGCAGTGT
251 TGGGAAAGTT ATTCCCGTGG CGGATAAAGG GGAAAGGGAA GGGCGTTTCG
301 GTCGGTGTGT CGGGCAGTGT GGGGCAGCTC GGATGCGTGC TGCTCGGATT
351 TGCATCCGGC AAACGTATGC GCGATATTTG GATGCCGTCT GAAAACGCGG
401 GTATGTATTG TCTGATGCTG CTGGTGCTCN TCATCGGCGT ACAGCTCAAA
451 AGCAGCGGCG TATCGTTGCG GCAGGTTTTG GTCAACCGCA GGGGTATTCT
501 GTTGTCCGTC TGGTTTATGC TTTTATCTCT TTCAGGCGGG CTGCTGTTTG
551 CCGCATCGGC AGACGGTGTG TCGTGGGTGA AAGGTTTGGC GATGGCTTCC
601 GGCTTCGGTT GGTATCCCTT CTCGGGTTTG GTGATGACCG AGGCTTACCG
651 CGCGGTATGG GGCAGTATCG CGCTTTTGAA CGATTTGGCA CGAGAGCTGT
701 TCGCGTGGC ATTTATTCCG CTGCTGATGA AGCGTTTTCG CGATGCGGCA
751 GTGGGGGTCG GCGGCGCGAC CAGTATGGAT TTCACATTGC CCGTGATTCT
801 GGGTCCGGGC GGCTTGGAAG CCGTACCGGT AGCGGTGAGC TTCGGCGTGG
851 TGGTCAATAT CGCCGCTCCG TTTCTGATGG TGGTGTTCCT CGCTTTGGGC
901 TGA
```

This corresponds to the amino acid sequence <SEQ ID 2336; ORF 700.a>:

```
a700.pep
1  MDSIMTLLSV LIPMFAGFFI RVPKPYLPAL DKVLSVLVYA VLLLIGVSL
51  RVEDLGSRLD DMALTVLWLF VCTVGANLLA LAVLGKLPFW RIKGKGKGV
101 VGVSGSVGQL GCVLLGFASG KLMRDIWMP ENAGMYCLML LVLXIGVQLK
151 SSGVSLRQVL VNRRGIRLSV WFMLSSLSGG LLFAASADGV SWVKGLAMAS
201 GFGWYSLSGL VMTEAYGAVW GSIALNLNLA RELFALAFIP LLMKRFPDAA
251 VGVGGATSMDF LTPVIRGAG GLEAVPVAVS FGVVVNIAAP FLMVVFSALG
301 *
```

m700/a700 97.0% identity in 300 aa overlap

	10	20	30	40	50	60
m700.pep	MDSIMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
a700	MDSIMTLLSVLIPMFAGFFIRVPKPYLPALDKVLSVLVYAVLLLIGVSLSRVEDLGSRLD					
	10	20	30	40	50	60
m700.pep	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVGQLGCVLLGFASG					
a700	DMALTVLWLFVCTVGANLLALAVLGKLPWRIKKGKGVSVGVSGSVGQLGCVLLGFASG					
	70	80	90	100	110	120
m700.pep	KLMRDIWMPSESAGMYCLMLLVFLIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
a700	KLMRDIWMPSENAGMYCLMLLVXIGVQLKSSGVSLRQVLVNRRGIRLSVWFMLSSLSGG					
	130	140	150	160	170	180

g701.seq

1	ATGTCCTTGGC	ACATATTCCA	AGTTCAGGG	ATACCGACCG	CTTCGATGGC
51	ACAATCTACG	CCGCTCTTCG	CGACGATGCG	GAAACTTGT	TTGGAGACGT
101	C CGCGGAAGC	GGGGCTGATG	GATGGGTGCG	CGCCCACTC	TTTCGCCGGT
151	T TCAAACGGT	TTTCGTCCAT	ATCGCACACG	ATATGGCGCG	CAGGGCTATA
201	CAGTTGGGCG	GTCAACAAGG	CGGACATACC	GACAGGGCCG	GCACCTGCGA
251	TGAATACGGT	ATCGCCGGGT	TTCACTTCGC	CGTATTGCAC	GCCGATTTCG
301	TGGGCGCTGC	GTAAGCGTC	GCTCAACAGC	AGGGCGATT	CTTCGTTGAC
351	GTTGTCGTGC	GGCGGCACGA	GCTGTTGTC	GCGATAA	

g701.pap

1	MSWHIFQVAG	IPTASMAQST	PSPTMAKTC	LETSPEAGLM	VWVAPNSFAG
51	FKRFSSISHT	IMAAGLYSWA	VNKADIPTGP	APAMNTVSPG	FTSPYCTPIS
101	WAVGKASLNS	RAISSLTLS	GGTRLLSA*		

```
m701.seq
1  ATGTCCTTGGC ACATATTCGA TGTAGCAGGG ATACCGACGG CTTCGATGGC
51  CGCAATCCAGC CCGTCTTCCG CGACGATGGC AAAGACTTGT TTGGATACTT
101 CGCCGGGAAGC AGGGTTAATG GTATGGGTGC CACCAATTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACG ATGATGGCGG CGGGACTGTA
201 CAGTTGGGCG GTCAACAGGG CGGACATACC GACAGGGCCT GCCCCAGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTGC
301 TGGCGCGTGC GCAAAGCGTC GCTCAACAA AGGCGCATTT CTTCTGTTGAC
351 ATTATCGGGC AGCGGAACGA GGCTGTTGTC GGCATAAA
```

m701.pap

1 MSWHIFHVAG IPTASMAQST PSSPTMAKTC LDTSPEAGLM VVWAPNSFAS  
51 FKRFFSSISQT MMAAGLYSWA VNRADIPTGP APAMNTVSPG LTSPYCTPIS  
101 WAVGKASLNN RAISSLTLSG SGRLLISA\*

```

      10      20      30      40      50      60
m701.pep  MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g701      MSWHIFQVAGIPTASMAQSTPSSPTMAKTCLETSPEAGLMVWVAPNSFAGEKRFSISHT

```

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	10	20	30	40	50	60
	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:     :     :     :     :					
g701	IMAAGLYSWAVNKADIPTGPAPAMNTVSPGFTSPYCTPISWAVGKASLNSRAISSLTLSG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
	:
g701	GGTRLLSAX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2341>:

```
a701.seq
1  ATGCTCTGGC ACATATTCCA AGTTGCAGGG ATACCGACGG CTTCGATCGC
51  GCAGTCCACG CCGTCTTCGC CGACGATAGC GGCAACTTGC TTGCTTACAT
101 CGCCGGAAGC AGGGTTAATG GTATGGGTTG CGCCCAACTC TTTCGCCAGT
151 TTCAAACGGT TTTCGTCCAT ATCGCAAACA ATGATGGCGG CGGGGCTGTA
201 CAGTTGGGCG GTCGGCAAGG CGGACATACC GACAGGAGCG GCACCTGCGA
251 TGAATACGGT GTCGCCGGGT TTGACATCGC CGTATTGCAC GCCGATTTCG
301 TGTGCGGTCG GCAAAGCGTC GCTCAACAAC AGGGCGACTT CTTCGTTGAC
351 GTTGTGCGGC AGCGGCACGA GGCTGTTGTC GGCATAA
```

This corresponds to the amino acid sequence <SEQ ID 2342; ORF 701.a>:

```
a701.pep
1  MSWHIFQVAG IPTASIAQST PSSPTIAATC LLTSPEAGLM VVWAPNSFAS
51  FKRFSISQT MMAAGLYSWA VGKADIPTGA APAMNTVSPG LTSPYCTPIS
101 CAVGKASLNN RATSSLTSLG SGTRLLSA*
```

m701/a701 92.2% identity in 128 aa overlap

	10	20	30	40	50	60
m701.pep	MSWHIFHVAGIPTASMAQSTPSSPTMAKTCLDTSPEAGLMVWVAPNSFASFKRFSISQT					
	:     :     :					
a701	MSWHIFQVAGIPTASIAQSTPSSPTIAATCLLTSPPEAGLMVWVAPNSFASFKRFSISQT					
	10	20	30	40	50	60

	70	80	90	100	110	120
m701.pep	MMAAGLYSWAVNRADIPTGPAPAMNTVSPGLTSPYCTPISWAVGKASLNNRAISSLTLSG					
	:     :     :     :     :					
a701	MMAAGLYSWAVGKADIPTGAAPAMNTVSPGLTSPYCTPISCAVGKASLNNRATSSLTSLG					
	70	80	90	100	110	120

	129
m701.pep	SGTRLLSAX
a701	SGTRLLSAX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2343>:

```
g702.seq
1  ATGCCGTGTt ccaAAGCCAG TTGGACTTCG CCCGGAGtgg cAACGCCGGG
51  AATCAGGGGA ATGCCGCTGT TGCGGCCGGC TCTGGCGAGG GATTCTGCA
101 AACCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCCGGAT TGTTACCGT ACCTGCGCCG ATGATGGCGT TGGGCATTTC
201 TTTGGCAATC AGGCGGATGG CCTCGAGTCC GACGGGGGTG CGCAAGGTAA
251 TTTGAGGGT GGGGATGCCG CCTTCGACAA GGGCGCGGGA CAAATCGACG
301 GCGGTGCTTA AGTCGTCAAt cgCCATCACA GGCACAAC TG CGCCGGCGGT
351 CAGGATTTTC cggggggtca gttga
```

This corresponds to the amino acid sequence <SEQ ID 2344; ORF 702>:

g702.pep

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```

1  MPCSASWTS PGVATPGIRG MPLLRLPALR DSCKPGLMAK TAPASSTALS
51  C SGLVTPAP MMALGISLAI RRMASPTGV RKVISRVGMP PSTRARDKST
101 AVLKSSIAIT GTTAPAVRIS RGV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2345>:

```

m702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTC TC CGGGTGGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2346; ORF 702>:

```

m702.pep
1  MPCSASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  C SGLVTPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

ORF 702 shows 91.9% identity over a 124 aa overlap with a predicted ORF (ORF702.ng) from *N. gonorrhoeae*:

m702/g702

	10	20	30	40	50	60
m702.pep	MPCSASWISPGVATPGIRGMPELLWPALARDSCSPGLMAKTAPASSTALSCSGLVTPAP					
g702	MPCSASWISPGVATPGIRGMPELLRPALARDSCKPGLMAKTAPASSTALSCSGLVTPAP					
	10	20	30	40	50	60
m702.pep	TMALGTSIAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS					
g702	MMALGISLAIRRMASPTGVRRVISRVGMPPSTRARDKSTAVLKSSIAITGTTAPAVRIS					
	70	80	90	100	110	120
m702.pep	RGVSLDISVLRVEWGILLRWDRXL					
g702	RGVSX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2347>:

```

a702.seq
1  ATGCCGTGTT CCAAAGCCAG TTGGATTTTCG CCCGGGGTGG CAACACCGGG
51  AATCAGGGGG ATGCCGCTGT TGTGGCCGGC TTTGGCGAGG GATTCATGCA
101 GCCCGGGCT GATGGCGAAA ACCGCGCCTG CGTCTTCGAC GGCTTTGAGC
151 TGTTCGGGAT TGGTTACCGT ACCTGCGCCG ACGATGGCGT TGGGCACTTC
201 TTTGGCAATC AGGCGGATGG CATCGAGGCC GACAGGGGTG CGCAGGGTGA
251 TTTGAGGGT AGGGATGCCG CCTTCGACAA GGGCGTGGGA CAAATCGATG
301 GCGGTGCTTA AGTCGTCAAT CGCCATTACC GGCACAAC TG CGCCGGCGGT
351 CAAATTTTCG CGGGGGGTCA GTTTGGACAT TTCGGTTC TC CGGGTGGAAT
401 GGGGTATTTT ATTAAGATGG GACAGGTTGT AG

```

This corresponds to the amino acid sequence <SEQ ID 2348; ORF 702.a>:

```

a702.pep
1  MPCSASWIS PGVATPGIRG MPLLWPALAR DSCSPGLMAK TAPASSTALS
51  C SGLVTPAP TMALGTSIAI RRMASRPTGV RRVISRVGMP PSTRAWDKSM
101 AVLKSSIAIT GTTAPAVKIS RGVSLDISVL RVEWGILLRW DRL*

```

m702/a702 100.0% identity in 143 aa overlap

10	20	30	40	50	60
----	----	----	----	----	----



1128

```

m702.pep  MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      MPCSKASWISPGVATPGIRGMPLLPALARDSCSPGLMAKTAPASSTALSCSGLVTVPPAP
          10      20      30      40      50      60

          70      80      90      100     110     120
m702.pep  TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a702      TMALGTSLAIRRMASRPTGVRRVISRVGMPPSTRAWDKSMAVLKSSIAITGTTAPAVKIS
          70      80      90      100     110     120

          130     140
m702.pep  RGVSLDISVLRVEWGILLRWDR LX
          ||||||||||||||||||
a702      RGVSLDISVLRVEWGILLRWDR LX
          130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2349>:

```

g703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCG CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTTAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 CACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAGA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CACTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGGCC GTTTACGACA ATATCAGCGG TTTTATATAA
451 GGCAGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCGAAAAAA GCGGTTGCCG ATTTGAAGGC GAAAAAAGGT TTTGATGCCG
551 TTTTGAAACA ATACTCGCTC AACGACCGCA CCAAACGGAC CGGCGCGCCG
601 GACGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA
701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGcgaggTG
751 AAAGTGCCTT CTTTTCACGA AATGAAAGGA CAGATTGCCG GCAACCTTCA
801 GCGGAACGG ATTGACCGTG CCGTctgTgc gcTGTgggt aaggCAAACA
851 TCAAACCTGC AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2350; ORF 703>:

```

g703.pep
1  MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA
51 EDTPQLRQSL LENEVNTVV AQEVKRLKLD RSAEFKDALA KLRAEAKKSG
101 DDKKPSFKTV WQAVKYGLNG EAYALHIKT QPVSEQEVKA VYDNISGFYK
151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKRTGAP
201 DGYVPLKLE QGVPLYQAI KDLKKGEFTA TPLKNGDFYV VYYVNSREV
251 KVPSFDEMKG QIAGNLQAER IDRAVCALLG KANIKPAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2351>:

```

m703.seq
1  ATGAAAGCAA AAATCCTGAC TTCCGTTGCA CTGCTTGCCT GTTCCGGCAG
51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CGGTCAGAAA ATCGACAGTT
101 CCGTCATCGA TGCGCAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC
151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAAAACG AAGTGGTCAA
201 TACCGTGGTC GCACAGGAAG TGAAACGCCT GAAACTCGAC CGGTCGGCAG
251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC
301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAAATATGG
351 CTTGAACGGC GAGGCATACG CATTGCATAT CGCCAAAACC CAACCGGTTT
401 CCGAGCAGGA AGTAAAGGCC GCATATGACA ATATCAGCGG TTTTACAAA
451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA
501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAAGGT TTCGATGCCG
551 TCTTGAAACA ATATTCCCTC AACGACCGTA CCAAACAGAC CGGTGCGCCG
601 GTCGGATATG TGCCGCTGAA AGATTGGGAA CAGGGTGTTT CGCCGCTTTA
651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

```

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA  
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA  
 801 GCGGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA  
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2352; ORF 703>:

m703.pep

1 MKAKILTSVA LLACSGSLFA QTLATVNGOK IDSSVIDAQV AAFRAENSRA  
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG  
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK  
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP  
 201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSREV  
 251 KVPSEDEMKG QIAGNLQAEER IDRAVGALLG KANIKPAK\*

ORF 703 shows 98.3% identity over a 288 aa overlap with a predicted ORF (ORF703.ng) from *N. gonorrhoeae*:

m703/g703

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGOKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
g703	MKAKILTSVALLACSGSLFAQTLATVNGOKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLDRAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
g703	LENEVNTTVVAQEVKRLKLDRAEFKDALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
g703	EAYALHIAKTQPVSEQEVKAVYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
g703	FDAVLKQYSLNDRTKRTGAPDGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSREVKVPSEDEMKGQIAGNLQAEERIDRAVGALLGKANIKPAKX					
g703	VYYVNSREVKVPSEDEMKGQIAGNLQAEERIDRAVCALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2353>:

a703.seq

1 ATGAAAGCAA AAATCCTGAC TTCGTTGCA CTGCTTGCCT GTTCCGGCAG  
 51 CCTGTTTGCC CAAACGCTGG CAACCGTCAA CCGTCAGAAA ATCGACAGTT  
 101 CCGTCATTGA TGCAGAGGTT GCCGCATTCC GTGCGGAAAA CAGCCGTGCC  
 151 GAAGACACGC CGCAACTGCG CCAATCCCTG CTGGAACACG AAGTGGTCAA  
 201 CACCGTGGTC GCACAGGAAG TGAACGCCT GAACTCGAC CCGTCGGCAG  
 251 AGTTTAAAAA TGCGCTTGCC AAATTGCGTG CCGAAGCGAA AAAGTCGGGC  
 301 GACGACAAGA AACCGTCCTT CAAAACCGTT TGGCAGGCGG TAAATATGG  
 351 CTGGAACGGC GAGGCATACG CGCTGCATAT CGCCAAAACC CAACCGGTTT  
 401 CCGAGCAGGA AGTAAAAGCC GCATATGACA ATATCAGCGG TTTTACAAA  
 451 GGTACGCAGG AAGTCCAGTT GGGCGAAATC CTGACCGACA AGGAAGAAAA  
 501 TGCAAAAAAA GCGGTTGCCG ACTTGAAGGC GAAAAAGGT TTCGATGCCG  
 551 TCTTGAAACA ATATCCCTC AACGACCGTA CCAACAGAC CCGTGCGCCG  
 601 GTCGGATATG TGCCGCTGAA AGATTGGAA CAGGTGTTC CGCCGCTTTA  
 651 TCAGGCAATT AAGGACTTGA AAAAAGGCGA ATTTACGGCA ACGCCGCTGA

1130

701 AAAACGGCGA TTTCTACGGC GTTTATTATG TCAACGACAG CCGCGAGGTA  
 751 AAAGTGCCTT CTTTGTATGA AATGAAAGGA CAGATTGCGG GCAACCTTCA  
 801 GGCGGAACGG ATTGACCGTG CCGTCGGTGC ACTGTTGGGC AAGGCAAACA  
 851 TCAAACCTGC AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2354; ORF 703.a>:

a703.pep  
 1 MKAKILTSVA LLACSGSLFA QTLATVNGQK IDSSVIDAQV AAFRAENSRA  
 51 EDTPQLRQSL LENEVNTTVV AQEVKRLKLD RSAEFKNALA KLRAEAKKSG  
 101 DDKKPSFKTV WQAVKYGLNG EAYALHIAKT QPVSEQEVKA AYDNISGFYK  
 151 GTQEVQLGEI LTDKEENAKK AVADLKAKKG FDAVLKQYSL NDRTKQTGAP  
 201 VGYVPLKDLE QGVPPPLYQAI KDLKKGEFTA TPLKNGDFYG VYYVNSDREV  
 251 KVPSFDEMKG QIAGNLQAER IDRAVGALLG KANIKPAK\*

m703/a703 100.0% identity in 288 aa overlap

m703.pep	10	20	30	40	50	60
	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
a703	MKAKILTSVALLACSGSLFAQTLATVNGQKIDSSVIDAQVAAFRAENSRAEDTPQLRQSL					
	10	20	30	40	50	60
m703.pep	70	80	90	100	110	120
	LENEVNTTVVAQEVKRLKLD RSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
a703	LENEVNTTVVAQEVKRLKLD RSAEFKNALAKLRAEAKKSGDDKKPSFKTVWQAVKYGLNG					
	70	80	90	100	110	120
m703.pep	130	140	150	160	170	180
	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
a703	EAYALHIAKTQPVSEQEVKAAYDNISGFYKGTQEVQLGEILTDEENAKKAVADLKAKKG					
	130	140	150	160	170	180
m703.pep	190	200	210	220	230	240
	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
a703	FDAVLKQYSLNDRTKQTGAPVGYVPLKDLEQGVPPPLYQAIKDLKKGEFTATPLKNGDFYG					
	190	200	210	220	230	240
m703.pep	250	260	270	280	289	
	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
a703	VYYVNSDREVKVPSFDEMKGQIAGNLQAERIDRAVGALLGKANIKPAKX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2355>:

a704.seq  
 1 ATGAAAAAAA CCTGTTTCCA CTGCGGGCTG GACGTTCCCG AAAACCTGCA  
 51 TCTGACCGTC CGTTACGAAA ACGAAGACCG CGAAACCTGC TGCGCCGGTT  
 101 GTCAGGCAGT CGCACAAAGC ATTATTGACG CGGGCTTGGG CAGTTATTAC  
 151 AAACAACGCA CCGCCGACGC GCAAAAACC GAGCTGCCG CCCAAGAAAT  
 201 CCTCGACCAA ATCCGCCTGT ACGACCTGCC CGAAGTCCAG TCCGACTTTG  
 251 TGGAAACCCA CGGCGGCACG CGCGAGGCGG TTTTAATGCT CGGCGGCATC  
 301 ACCTGCGCCG CCTGCGTCTG GCTGATCGAA CAGCAGCTTT TGCGTACAGA  
 351 CGGCATCGTC CGCATCGACC TCAATTACAG CACGCACCGC TGCCGCGTCG  
 401 TCTGGGACGA CGGCAAAATC CGCCTTTCCG ACATTCTGTT GAAAATCAGG  
 451 CAGATAGGCT ACACCGCCGC ACCCTATGAC GCGCAAAAAA TCGAAGCCGC  
 501 CAACCAAAAA GAACGCAAAC AATACATCGT CCGCCTCGCC GTTGCCGGGC  
 551 TGGGGATGAT GCAGACGATG ATGTTCGCGC TGCCGACCTA CCTTTACGGC  
 601 GGCGACATCG AACCCGATTT CCTGCAAATC CTCCATTGGG GCGGCTTTTT  
 651 AATGGTGCTG CCCGTCGTAT TCTATTGCGC CGTCCCGTTT TATCAAGGCG  
 701 CGCTGCGCGA CTTGAAAAAC CGCCGCGTCG GCATGGATAC GCCGATTACC  
 751 GTCGCCATCA TCATGACCTT TATCGCCGGC GTTTACAGCC TTGCGACAAA

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801 TGCGGGGCGAG GGGATGTATT TCGAATCCAT CGCGATGCTG CTGTTTTTCC
851 TGCTGGGCGG ACCTTTTATG GAACACATTG CCCGCCGTAA GGCAGGCGAT
901 GCCGCCGAGA GGCTGGTGAA GCTGATTCTT GCGTTTTGCC ATCATATGCC
951 CGATTACCCC GATACGCAGG AAACCTGCGA GGCAGCTGTC GTCAAATTGA
1001 AGGCGGGCGA TATCGTGCTG GTCAAACCGG GCGAAACCAT CCCCGTTGAC
1051 GGCACGGTGC TGGGAAGGAAG CAGTGCCGTC AACGAATCTA TGCTGACCGG
1101 CGAGAGCCTG CCCGTCGCCA AAATGCCGTC TGAAAAAGTA ACCGCCGCGA
1151 CACTCAACAC GCAAAGCCCC CTGATTATAC GCACCGACCG CACCGGCGGC
1201 GGCACGCGAC TGTGCGACAT CGTCCGCTG CTGACCGCG CCTTAGCGCA
1251 AAAACCGCGC ACTGCCGAGT TGGCGGAACA ATACGCCTCG TCTTTCATAT
1301 TCGGCGAACT CCTGCTTGCC GTCCCGCTCT TCATCGGCTG GACGCTGTAC
1351 GCCGACGCGC ACACCGCATT GTGGATTACC GTCGCCCTGC TGGTCATTAC
1401 CTGCCCCCTG GCCTTATCGC TTGCCACGCC GACCGCGCTG GCAGCTTCTA
1451 CCGGTACGCT GGCAGCGCAA GGTATTTTAA TCGGCGGAAA GCAGGCAATC
1501 GAAACCTCG CCCAAACAC CGACATCATC TTCGACAAA CCGGCACGCT
1551 GACCCAAGGC AAACCGCCG TCCGCCGTAT CTCATTGTTG AGAGGCACAG
1601 ACGAAGCCTT TGTCTCGCG GTGGCGCAGG CTTTAGAACA ACAGTCCGAA
1651 CATCCCCCTG CCCGCCCAT CCTCAACTGC CGCATTTTCA ACAGGCGCTG
1701 CCCGACATC GCTATTAAAC AACGCCTCAA CCGCATCGGC GAAGGCGTGG
1751 GCGCGCAACT GACCGTCAAC GCGGAAACAC AGGTTTGGGC ATTGGGCAGG
1801 GCATCCTATG TCGCCGAAAT TTCAGGTAAA GAACCGCAA CAGAAGGCGG
1851 CGGCAGCGCG GTTACCTCG GCAGTCAAAG CGGTTTCCAA GCCGTGTTCT
1901 ACCTGCAAGA CCCGCTCAA GACAGCGCG CGGAGGCGGT GCGGCAGTTG
1951 GCAGGCAAAA ACCTGACGCT GCACATTCTC AGCGGCGACC GTGAAACCGC
2001 CGTTGCCGAA ACCGCACGCG CCCTGGGTGT CGCGCACTAC CGCGCCCAAG
2051 CCATGCCCGA GGACAACTG GAATACGTCA AAGCCTTGCA AAAAGAAGGG
2101 AAAAAAGTGC TGATGATAGG CGACGCGATC AACGACGCG CCGTTTTGGC
2151 GCAGGCAGAC GTATCCGCG CCGCAGCGG CGGACGGAT ATTGCGAGGG
2201 ACGGCGCGGA CATGTGTGTA TTGAACGAAG ATTTGCGTAC CGTGGCCAC
2251 CTGCTCGATC AGGCGCGCG CACCCGCCAT ATTATCCGGC AAAACCTGAT
2301 ATGGGCGGGC GCGTACAATA TCATTGCCGT ACCGCTTGCC GTTTTGGGCT
2351 ATGTCCAACC GTGGATAGCC GCACTGGGTA TGAGCTTCAG TTCGCTGGCG
2401 GTTTTGGGCA ACGCCCTGCG CCTTCAAAA CGGGGAAAA TGCAGTCTGA
2451 AAAAATGCCG TCCGAACAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2356; ORF 703>:

```

a704.pep
1 MKKTCFHCGL DVPENLHLTV RYENEDRET CAGCQAVAS IIDAGLSY
51 KQRTADAQKT ELPPQEILDQ IRLYDLPEVQ SDFVETHGGT REAVMLLGGI
101 TCAACVWLIE QQLLRTDGIV RIDLNYSTHR CRVWDDGKI RLSDILLKIR
151 QIGYTAAPYD AQKIEAANQK ERKQYIVRLA VAGLGMQTM MFALPTYLYG
201 GDIEPDLQI LHWGGFLMVL PVVFCAPVF YQALRDLKN RRVGMDTPIT
251 VAIIMTFIAG VYSLATNAGQ GMYFESIAML LFFLLGGRFM EHIARRKAGD
301 AAERLVKLIP AFCHHMPDYP DTQETCEAAV VKLKAGDIVL VKPETIPVD
351 GTVLEGSSAV NESMLTGESL PVAKMPSEKV TAGTLNTQSP LIIRTDRTGG
401 GTRLSHIVRL LDRALAQKPR TAEALAEQYAS SFIIFGELLLA VPVFIGWTLY
451 ADAHTALWIT VALLVITCPC ALSLATPTAL AASTGTTLARE GILIGGKQAI
501 ETLAQTDDII FDKTGTLTQG KPAVRRISLL RGTDEAFVLA VAQALEQQSE
551 HPLARAILNC RISDGSVPDI AIKQRLNRIG EGVGAQLTVN GETQVWALGR
601 ASYVAEISGK EPOTEGGSA VYLSQSGFQ AVFYLDPLK DSAAEAVRQL
651 AGKNLTLHL SGDRATAVAE TARALGVAHY RAQAMPEDKL EYVKALQKEG
701 KKVLMIGDGI NDAPVLAQAD VSAAAAGTD IARDGADIVL LNEDLRTVAH
751 LLDQARRTRH IIRQLIWAG AYNIIAVPLA VLGYPWPWIA ALGMSFSSLA
801 VLGNALRLHK RGKMQSEKMP SEQ*

```

m704/a704 99.8% identity in 823 aa overlap

```

      10      20      30      40      50      60
m704.pep MKKTCFHCGLDVPENLHLTVRYENEDRETCCAGCQAVASIIDAGLSYKQRTADAQKT
a704      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      10      20      30      40      50      60
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVMLLGGITCAACVWLIEQQLLRTDGIV
a704      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
      70      80      90     100     110     120
m704.pep ELPPQEILDQIRLYDLPEVQSDFVETHGGTREAVMLLGGITCAACVWLIEQQLLRTDGIV
a704      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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1132

	70	80	90	100	110	120
m704.pep	130	140	150	160	170	180
a704	RIDLNYSTHRCRVVWDDGKIRLS	DILLKIRQIGYTAAPYDAQKIEA	ANQKQYIVRLA			
	130	140	150	160	170	180
m704.pep	190	200	210	220	230	240
a704	VAGLGMQTMFALPTYLYGGDIEP	DFLQILHWGGFLMVL	PVVFYCAVPFYQ	GALRDLKN		
	190	200	210	220	230	240
m704.pep	250	260	270	280	290	300
a704	RRVGMDTPITVAIIMTFIAGV	YSLATNAGQGM	FESIAML	LLFFLLGGRFMEH	IARRKAGD	
	250	260	270	280	290	300
m704.pep	310	320	330	340	350	360
a704	AAERLVKLIPAFCHHMPDYP	DTQETCEAAV	VKLKAGDIV	LVKPGETIP	VDGTVLEGSSAV	
	310	320	330	340	350	360
m704.pep	370	380	390	400	410	420
a704	NESMLTGESLPVAKMPSEK	VTAGTLNTQSP	LIIRTDRTGG	TRL	SHIVRL	LDRALAQKPR
	370	380	390	400	410	420
m704.pep	430	440	450	460	470	480
a704	TAELAEQYASSFIFGELL	LAVPVFIGW	TLYADAHTAL	WITVALL	VITCPCAL	SLATPTAL
	430	440	450	460	470	480
m704.pep	490	500	510	520	530	540
a704	AASTGTLAREGILIGGQ	AIETLAQTTD	IIFDKTG	TLTGKPAVRR	ISLLRG	TDEAFVLA
	490	500	510	520	530	540
m704.pep	550	560	570	580	590	600
a704	VAQALEQQSEHPLARAIL	NCRISDGSVP	DAIAIKQRLN	RIGEGVGAQ	LTVNGETQ	VWALGR
	550	560	570	580	590	600
m704.pep	610	620	630	640	650	660
a704	ASYVVAEISGKEPQTEG	GSASVYLG	SGSQFQAV	FYLTDP	LKDSAAE	AVRQLAGKNLTLHIL
	610	620	630	640	650	660
m704.pep	670	680	690	700	710	720
a704	SGDRETAVAETARALG	VAHYRAQAMP	EDKLEYV	KALQKEGK	VLMIGD	GINDAPVLAQAD
	670	680	690	700	710	720
m704.pep	730	740	750	760	770	780
a704	VSAAAAGGTDIARDG	ADIVLLNED	LRTVAHLLD	QARRTRH	IIRQNLI	WAGAYNIIAVPLA
	730	740	750	760	770	780
m704.pep	790	800	810	820		
a704	VLGYVQPWIAALGMS	FS	SSLA	VLGNALRLH	KRGKMQSEK	MPSEQX
	790	800	810	820		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2357>:

```

g705.seq
1  GTGTTCAATA ATTTCTtgc CTCTCTGCCG TTTATGACGG AAACACGCGC
51  TGATATGCTC ATCAGCGCGT TTTGGCCCAT GGTAAAGCC GGCTTTACAG
101 TGTCCTTgcC TTGGCGGATC GCTTCTTTCG TTATCGGCAT GATTATTGCC
151 GTAGCCGTTG CTTTGGTAAG AATCATGCCT TCCGGCGGTA TTTTCCAAAA
201 ATGCTTGTGT AAGCTGGTGG AATTTTATAT TTCCGTCGTT CGCGGTACGC
251 CGCTGTGGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC GTCCGTCGGC
301 ATCTATATCA ATCCGATTCC CGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GCGATTTTG TCCGTGCCGA
401 AAGGCGAGTG GGAAGCAGGT TTCTCCATCG GTATGACCTA TATGCAGACG
451 TTCCGCGGCA TCGTCGCACC GCAGGCATTC CGCGTCGCGG TTCCGCGGTT
501 GAGCAACGAG TTTATCGGCT TGTTCAAAAA CACCTCGCTT GCCGCGGTGG
551 TAACGGTAAC GGAGCTTTTC CGTGTGCGAC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCTGTCTA TATCGAAGCT GCATTGGTTT ATTGGTGGTT
651 CTGTAAAGTG CTGTTTTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GTTATGTCCG CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2358; ORF 705>:

```

g705.pep
1  VFNNFLASLP FMTETRADML ISAFWPMVKA GFTVSLPLAI ASFVIGMIIA
51  VAVALVRIMP SGGIFOKCLL KLVEFYISV RGTPLLVLV IVFYGLPSVG
101 IYINPIPAAI IGFSLVNGAY ASETIRAAIL SVPRGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFDYRVAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2359>:

```

m705.seq
1  GTGTTCAATA ATTTCTTGC TTCGTCGCCG TTTATGACGG AAACACGCGC
51  CGATATGATT GTCAGCGCGT TTTTGCCAT GGTCAAAGCC GGCTTCGCGG
101 TCTCTCTGCC TTTGGCGGCA GCTTCTTTCG TTATCGGTAT GATGATTGCG
151 GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGGCGGCA TCGTCCGGAA
201 AATCCTGCTG AAATGGTGG AATTTTATAT TTCCGTCAAT CGCGGTACGC
251 CGCTGTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCCGTCGGC
301 ATCTATATCG ACCCGATTCC TGCCGCCATC ATCGGCTTTT CGCTCAATGT
351 CGGCGCATAC GCTTCCGAAA CCATACGCGC GGCAATTTTG TCCGTACCTA
401 AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451 TTCCGCGGCA TTGTGCGGCC GCAGGCATTC CGCGTTGCCG TGCCGCTTTT
501 GAGCAACGAG TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGGCACTCG
551 TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601 TATGACTTTT TGCCCGTCTA TATCGAAGCC GCTTTGGTTT ACTGGTGGTT
651 TTGTAAAGTG CTGTTCTGA TTCAGGCGCG TTTGAAAAA CGTTTCGACC
701 GCTACGTCGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2360; ORF 705>:

```

m705.pep
1  VFNNFLASLP FMTETRADMI VSAFLPMVKA GFAVSLPLAA ASFVIGNMIA
51  VAVALVRIMP AGGIVRKILL KLVEFYISVI RGTPLLVLV IVFYGLPSVG
101 IYIDPIPAAI IGFSLVNGAY ASETIRAAIL SVPRGQWEAG FSIGMTYMQT
151 FRRIVAPQAF RVAVPPLSNE FIGLFKNTSL AAVVTVTELF RVAQETANRT
201 YDFLPVYIEA ALVYWCFCVK LFLIQARLEK RFDYRVAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 705 shows 95.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. gonorrhoeae*:

```

m705/g705    95.0% identity in 238 aa overlap

          10      20      30      40      50      60
m705.pep    VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGNMIIAVALVRIMP
              |||
g705         VFNNFLASLPFMTETRADMLISAFWPMVKAGFTVSLPLAIASFVIGMIIAVALVRIMP
              |||
          70      80      90     100     110     120
m705.pep    AGGIVRKILLKLVEFYISVIRGTPPLLVLVIVFYGLPSVGIIYIDPIPAAIIGFSLVNGAY
              |||

```

```

a705.seq
1      GTGTTC AATA ATTTCC TTGC TTCGCTGCCG TTTATGACGG AAACACGCCG
51     CGATATGATT GTCAGCGCGT TTTTGCCATAT GGTCAAAGCC GGCTTCGCGG
101    TCTCTCTGCC TTTGGCGGCA GCTTCTTTTCG TTATCGGTAT GATGATTTCCG
151    GTAGCCGTGG CTTTGGTGCG GATTATGCCC GCCGCGGCCA TCGTGCGGAA
201    AATCCCTGTG AAATTTGGTG AATTTATAT TTTCCGTGAT CGCGGTACGC
251    CGCTGTTGGT TCAGCTTGTG ATTGTGTTTT ACGGGCTGCC TTCGTCGGC
301    ATCTATATCG ACCCGATTCC TCGCGCATCAT ATCGGCTTTT CGCTCAATGT
351    CGCGGCATAT GCTTCCGAAA CCATACGCGC GGAATTTTG TCCGTACCGA
401    AAGGCCAATG GGAAGCAGGT TTCTCCATCG GCATGACCTA TATGCAGACG
451    TTCCGCCGCA TCGTGCGCCC CGAGGCATT TCGGTTCCGC TGCCCGCTTT
501    GAGC ACGCGA TTTATCGGTT TGTTTAAAAA CACCTCGCTC GCGCGCATCG
551    TGACGGTAAC GGAATTATTC CGCGTCGCGC AGGAAACGGC AAACCGCACT
601    TATGATCTTTT TGCCTCGCTA TATCGAAGCC GCTTTGGTTT ACTGGTGTT
651    TTGTAAAGTT CTGTTCTCTGA TTCAGCGCGC TTTGAAAAA CGTTTCGACC
701    GCTACGTCGC CAAATAA

```

a705.pap

1	VFNNFLASLP	FMTETRADMI	VSAFLPMVKA	GFAVSLPLAA	ASFVIGMMIA
51	VAVALVRMP	AGGIVRKILL	KLVEFYISVI	RGTPLLVLQVL	IVFYGLPSVG
101	IYIDPIPAAI	IGFSLNVGAY	ASETIRAAIL	SVPKGQWEAG	FSIGHTYMQT
151	FRRI VAPQAF	RVAVPPLSNE	FIGLFKNTSL	AAVTVTVEL	RVAQETANRT
201	YDFLEVPYIEA	KLAVYQCFCKV	LFLIGLARLEK	RFDRYVAK*	

**ORF 705 shows 100.0% identity over a 238 aa overlap with a predicted ORF (ORF 705) from *N. meningitidis*:**

	10	20	30	40	50	60
a705.pep	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP					
m705	VFNNFLASLPFMTETRADMIVSAFLPMVKAGFAVSLPLAAASFVIGMMIAVAVALVRIMP					
	10	20	30	40	50	60
a705.pep	AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIIYDPIPAAIIGFSLNVGAY					
m705	AGGIVRKILLKLVEFYISVIRGTPLLVQLVIVFYGLPSVGIIYDPIPAAIIGFSLNVGAY					
	70	80	90	100	110	120
a705.pep	ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL					
m705	ASETIRAAILSVPKQWEAGFSIGMTYMQTFRRIVAPQAFRVAVPPLSNEFIGLFKNTSL					
	130	140	150	160	170	180
a705.pep	AAVVTVTTELFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFLLIQLARLEKRFDRYVAKX					
m705	AAVVTVTTELFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFLLIQLARLEKRFDRYVAKX					
	190	200	210	220	230	239
a705.pep	AAVVTVTTELFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFLLIQLARLEKRFDRYVAKX					
m705	AAVVTVTTELFRVAQETANRTYDFLPVYIEAALVYWCFCCKVLFLLIQLARLEKRFDRYVAKX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2363>:

g706.seq  
 1 ATGAACCTCT CGCAACGCAA ACGCCTTTC GgcccGCTGGC TCAACTCCTA  
 51 CGAACGCTac cGCCaccGCC GCCTCATACA TGCCGTGCGG CTCGGCGgaa  
 101 ccgttcCTGTT CGCCACCGCA CTCGCCGgc tACTCCACCT CCAacacggc  
 151 gAATGGATAG GGatgacCGT CTTCGTCGTC CTCGGCATGC TCCAGTTCCA  
 201 AGGCGcgatt tActccaacg cgggtgGAacg taTGetcggg acggtcatcg  
 251 ggcttgGGCGC GGGTTTGGGc gTTTTATGGC TGAACCAGCA TTAttccac  
 301 ggcaacTcc tcttctacct gaccatcggc acggcaagcg cactggccgg  
 351 ctGGGCGGCG GTCCGCAAAA acggctacgt ccttatgctg GCGGGGctgA  
 401 CGATGTGTCAT gctcatcggc gACAACGGCA GCGAATGGCT CGACAGCGGC  
 451 CTGATGCGCG CGATGAACGT CCTCATCGGC GCCGCCATCG CCATGCGCGC  
 501 CGC CAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG  
 551 CCGACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC  
 601 AGGCGTATGA CGCGCGAACG TTTGGAGCAG AATATGGTCA AAATGCGCCA  
 651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCACCTCGCC GCCACATCGG  
 701 GCGAAAGCCG CATCAGCCCC TCCATGATGG AAGCCATGCA GCACGCCAC  
 751 CGC AAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT  
 801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTC GACCGCCACT  
 851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGCCGCCCT CATCAACGGC  
 901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA  
 951 AGC CCTCGCC GAACACCTCC ACTACCAATG CGAGGGCTTC CTCTGGCTCA  
 1001 GCA CCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC  
 1051 ACC CGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG  
 1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2364; ORF 706.ng>:

g706.pep  
 1 MNS SQRKRLS GRWLNSYERY RHRRLIHAVR LGTVLFATA LARLLHLQHG  
 51 EWI GMTVFVV LGMLQFQAI YSNAVERMLG TVIGLGAGLG VLWLNQHYFH  
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPLM AGLTMCMLIG DNGSEWLD SG  
 151 LMRAMNVLIG AATAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG  
 201 RRMTRERLEQ NMVKMRQINA RMVKSRSRLA ATSGESRISP SMMEAMQHAH  
 251 RKI VNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTAAALING  
 301 RHA RRRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR  
 351 TRRKWLDAHE RQHLRQSILE TREHG\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2365>:

m706.seq  
 1 ATGAACACCT CGCAACGCAA CCGCCTCGTC AGCCGCTGGC TCAACTCCTA  
 51 CGAACGCTAC CGTACCGCC GCCTCATCCA CGCCGTCCGG CTCGGCGGGG  
 101 CCGTCTGTT CGCCACCGCC TCCGCCCGGC TGCTCCACCT CCAACACGGC  
 151 GAGTGGATAG GGATGACCGT CTTCGTCGTC CTCGGCATGC TCCAGTTTCA  
 201 AGGGGCGATT TACTCCAAGG CCGTGGAACG TATGCTCGGC ACGGTCATCG  
 251 GGC TGGGCGC GGGTTTGGGc GTTTTATGGC TGAACCAGCA TTATTTCAC  
 301 GGC AACCTCC TCTTCTACCT CACCGTCGGC ACGGCAAGCG CACTGGCCGG  
 351 CTGGGCGGCG GTCCGCAAAA ACGGCTACGT CCCTATGCTG GCAGGGCTGA  
 401 CGATGTGTAT GCTCATCGGC GACAACGGCA GCGAATGGCT CGACAGCGGA  
 451 CTCATGCGCG CCATGAACGT CCTCATCGGC GCGGCCATCG CCATGCGCGC  
 501 CGC CAAACTG CTGCCGCTGA AATCCACACT GATGTGGCGT TTCATGCTTG  
 551 CCGACAACCT GGGCGACTGC AGCAAAATGA TTGCCGAAAT CAGCAACGGC  
 601 AGGCGCATGA CCGCGAACG CCTCGAGGAG AACATGGCGA AAATGCGCCA  
 651 AATCAACGCA CGCATGGTCA AAAGCCGCGC CCATCTCGCC GCCACATCGG  
 701 GCGAAAGCCG CATCAGCCCC GCCATGATGG AAGCCATGCA GCACGCCAC  
 751 CGTAAAATCG TCAACACCAC CGAGCTGCTC CTGACCACCG CCGCCAAGCT  
 801 GCAATCTCCC AAATCAACG GCAGCGAAAT CCGGCTGCTT GACCGCCACT  
 851 TCACACTGCT CCAAAACGAC CTGCAACAAA CCGTCGCCCT TATCAACGGC  
 901 AGACACGCCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA  
 951 AGC CCTCGCC GAACACCTCC ACTACCAATG CGAGGGCTTC CTCTGGCTCA  
 1001 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC  
 1051 ACC CGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAAG  
 1101 CCTGCTTGAA ACACGGGAAC ACGGCTGA

This corresponds to the amino acid sequence <SEQ ID 2366; ORF 706>:

m706.pep  
 1 MNT SQRNRLV SRWLNSYERY RYRRLIHAVR LGGAFLATA SARLLHLQHG  
 51 EWI GMTVFVV LGMLQFQAI YSKAVERMLG TVIGLGAGLG VLWLNQHYFH  
 101 GNLLFYLTIG TASALAGWAA VGKNGYVPLM AGLTMCMLIG DNGSEWLD SG  
 151 LMRAMNVLIG AATAIAAAKL LPLKSTLMWR FMLADNLADC SKMIAEISNG  
 201 RRMTRERLEE NMAKMRQINA RMVKSRSRLA ATSGESRISP ANMEAMQHAH  
 251 RKI VNTTELL LTAAKLQSP KLNGSEIRLL DRHFTLLQTD LQQTVALING



1136

301 RHARRIRIDT AINPELEALA EHLHYQWQGF LWLSTNMROE ISALVILLQR  
 351 TRRKWLDAHE RQHLRQSLLE TREHG\*

m706/g706 96.5% identity in 375 aa overlap

	10	20	30	40	50	60
m706.pep	MNTSQRNRLVSRWLN	SYERYRYRRLIHAVRLGGAVLFATASARILLHLQHGEWIGMTVFVV				
g706	MNSSQRKRLSGRWLN	SYERYRHRRLIHAVRLGGTVLFATALARILLHLQHGEWIGMTVFVV				
	10	20	30	40	50	60
	70	80	90	100	110	120
m706.pep	LGMLQFQGAIYSKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVTGTASALAGWAA					
g706	LGMLQFQGAIYSNAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTIGTASALAGWAA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m706.pep	VGKNGYVPMLAGLTMCM	LIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR				
g706	VGKNGYVPMLAGLTMCM	LIGDNGSEWLDSEGLMRAMNVLIGAAIAIAAAKLLPLKSTLMWR				
	130	140	150	160	170	180
	190	200	210	220	230	240
m706.pep	FMLADNLADCSKMAIEISNGRRMT	RERLEENMAKMRQINARMVKSRS	SHLAATSGESRISP			
g706	FMLADNLADCSKMAIEISNGRRMT	RERLEQNMVKMRQINARMVKSRS	SHLAATSGESRISP			
	190	200	210	220	230	240
	250	260	270	280	290	300
m706.pep	AMMEAMQHAHRKIVNTTE	LLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTVALING				
g706	SMMEAMQHAHRKIVNTTE	LLTTAAKLQSPKLNSEIRLLDRHFTLLQTDLQQTAALING				
	250	260	270	280	290	300
	310	320	330	340	350	360
m706.pep	RHARRIRIDTAINPELEALA	EHLHYQWQGF LWLSTNMROEISALVILLQ	TRRKWLDAHE			
g706	RHARRIRIDTAINPELEALA	EHLHYQWQGF LWLSTNMROEISALVILLQ	TRRKWLDAHE			
	310	320	330	340	350	360
	370					
m706.pep	RQHLRQSLLETREHG					
g706	RQHLRQSLLETREHG					
	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2367>:

a706.seq

1	ATGAACACCT	CGCAACGCAA	CCGCCTCGTC	AGCCGCTGGC	TCAACTCCTA
51	CGAACGCTAC	CGCTACCGCC	GCCTCATCCA	CGCCGTCCGG	CTCGGCGGGG
101	CCGTCTGT	CGCCACCGCC	TCCGCCCGGC	TGCTCCACCT	CCAACACGGC
151	GAGTGGATAG	GGATGACCGT	CTTCGTCTGTC	CTCGGCATGC	TCCAGTTTCA
201	AGGGGCGATT	TACTCCAAGG	CGGTGGAACG	TATGCTCGGC	ACGGTCATCG
251	GGCTGGGCGC	GGGTTTGGGC	GTTTATGGC	TGAACCAGCA	TTATTTCAC
301	GGCAACCTCC	TCTTCTACCT	CACCGTCGGC	ACGGCAAGCG	CACTGGCCGG
351	CTGGGCGGCG	GTCGGCAAAA	ACGGCTACGT	CCCTATGCTG	GCGGGGCTGA
401	CGATGTGCAT	GCTCATCGGC	GACAACGGCA	GCGAATGGTT	CGACAGCGGC
451	CTGATGCGCG	CGATGAACGT	CCTCATCGGC	GCGGCCATCG	CCATCGCCGC
501	CGCCAACTG	CTGCCGCTGA	AATCCACACT	GATGTGGCGT	TTCATGCTTG
551	CCGACAACCT	GACCGACTGC	AGCAAAATGA	TTGCCGAAAT	CAGCAACGGC
601	AGGCGCATGA	CCCGCGAACG	CCTCGAAGAG	AACATGGCGA	AAATGCGCCA
651	AATCAACGCA	CGCATGGTCA	AAAGCCGCAG	CCACCTCGCC	GCCACATCGG
701	GCGAAAGCCG	CATCAGCCCC	GCCATGATGG	AAGCCATGCA	GCACGCCAC
751	CGTAAAATTG	TCAACACCAC	CGAGCTGCTC	CTGACCAACG	CCGCCAAGCT
801	GCAATCTCCC	AAACTCAACG	GCAGCGAAAT	CCGGCTGCTT	GACCGCCACT
851	TCACACTGCT	CCAAACCGAC	CTGCAACAAA	CCGTCGCCCT	TATCAACGGC

1137

9 01 AGACACGCC GCGCATCCG CATCGACACC GCCATCAACC CCGAACTGGA  
 9 51 AGCCCTCGCC GAACACCTCC ACTACCAATG GCAGGGCTTC CTCTGGCTCA  
 10 01 GCACCAATAT GCGTCAGGAA ATTTCCGCCC TCGTCATCCT GCTGCAACGC  
 10 51 ACCCGCCGCA AATGGCTGGA TGCCACGAA CGCCAACACC TGCGCCAAG  
 11 01 CCTGCTTGAA ACACGGGAAC ACAGTTGA

This corresponds to the amino acid sequence <SEQ ID 2368; ORF 706.a>:

a706.pep

1	MNTSQNRNLV	SRWLNSYERY	RYRRLIHAVR	LGGAVLFATA	SARLLHLQHG
51	EWIGMTVFVV	LGMLQFQGA	YSKAVERMLG	TVIGLGAGLG	VLWLNQHYFH
1 01	GNLLFYLTVG	TASALAGWAA	VGKNGYVPM	AGLTMCLIG	DNGSEWFDG
1 51	LMRAMNVLI	AAIAIAAKL	LPLKSTIMWR	FMLADNLTDC	SKMIAEISNG
2 01	RRMTRERLEE	NMAKMRQINA	RMVKSRS	SHLAATSGESRISP	AMMEAMQHAH
2 51	RKIVNTTELL	LTAAKLQSP	KLNGSEIRLL	DRHFTLLQTD	LQQTVALING
3 01	RHARRIRIDT	AINPELEALA	EHLHYQWQGF	LWLSTNMROE	ISALVILLQR
3 51	TRRKWLDAHE	RQHLRQSLE	TREHS*		

a706/m706 99.5% identity in 374 aa overlap

	10	20	30	40	50	60
a706.pep	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG	EWIGMTVFVV				
m706	MNTSQNRNLVSRWLNSYERYRYRRLIHAVRLGGAVLFATASARLLHLQHG	EWIGMTVFVV				
	10	20	30	40	50	60
	70	80	90	100	110	120
a706.pep	LGMLQFQGAISKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG	TASALAGWAA				
m706	LGMLQFQGAISKAVERMLGTVIGLGAGLGVLWLNQHYFHGNLLFYLTVG	TASALAGWAA				
	70	80	90	100	110	120
	130	140	150	160	170	180
a706.pep	VGKNGYVPMLAGLTMCLIGDNGSEWFDGSLMRAMNVLI	GAAIAIAAKLLPLKSTIMWR				
m706	VGKNGYVPMLAGLTMCLIGDNGSEWFDGSLMRAMNVLI	GAAIAIAAKLLPLKSTIMWR				
	130	140	150	160	170	180
	190	200	210	220	230	240
a706.pep	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS	HLAATSGESRISP				
m706	FMLADNLTDCSKMIAEISNGRRMTRERLEENMAKMRQINARMVKSRS	HLAATSGESRISP				
	190	200	210	220	230	240
	250	260	270	280	290	300
a706.pep	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNGSEIRLLDRHFTLLQTD	LQQTVALING				
m706	AMMEAMQHAHRKIVNTTELLLTAAKLQSPKLNGSEIRLLDRHFTLLQTD	LQQTVALING				
	250	260	270	280	290	300
	310	320	330	340	350	360
a706.pep	RHARRIRIDTAINPELEALAEHLHYQWQGF	LWLSTNMROEISALVILLQRT	TRRKWLDAHE			
m706	RHARRIRIDTAINPELEALAEHLHYQWQGF	LWLSTNMROEISALVILLQRT	TRRKWLDAHE			
	310	320	330	340	350	360
	370					
a706.pep	RQHLRQSLE	TREHSX				
m706	RQHLRQSLE	TREHGX				
	370					

g707.seq not found

g707.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2369>:

m707.seq

```

1  ATGGAATTA TTAACGATGC AGAACTTATC CGTTCCATGC AGCGTCAGCA
51  GCACATAGAT GCTGAATTGT TAACTGATGC AAATGTCCGT TTCGAGCAAC
101 CAATTGAGAA GAACAATTAT GTCTGAGTG AAGATGAAAC ACCGTGTACT
151 CGGGTAAATT ACATTAGTTT AGATGATAAG ACGGTGCGCA AATTTTCTTT
201 TCTTCCTTCT GTGCTCATGA AAGAAACAGC TTTTAAACT GGGATGTGTT
251 TAGGTTCCAA TAATTTGAGC AGGCTACAAA AAGCCGCGCA ACAGATACTG
301 ATCTGCGGTG GCTACCTCAC TTCCAAGCT ATTATCCAAC CACAGAATAT
351 GGATTCGGGA ATTCTGAAAT TACGGGTATC AGCAGCGCAA ATAGGGGATA
401 TCCGCTATGA AGAAAAACGG GATGGGAAGT CTGCCGAGGG CAGTATTAGT
451 GCATTCAATA ACAAATTTC CTTATATAGG AACAAAATTC TCAATCTTCG
501 CGATGTAGAG CAGGGCTTGG AAAACCTGCG TCGTTTGCCG AGTGTAAAAA
551 CAGATATCA GATTATACCG TCCGAAGAAG AAGGCAAAAG CGATTTACAG
601 ATCAAATGCG AGCAGAATAA ACCCATAACG TTCAGTATCG GTATAGATGA
651 TCGGGCGCGC AAAACGACCG GCAAATATCA AGGAAATGTC GCTTTATCGT
701 TCGATAACCC TTTGGGCTTA AGCGATTGT TTTATGTTTC ATATGGACGC
751 GGTTTGGCGC ACAAACGGA CTTGACTGAT GCCACCGGTA CGGAAACTGA
801 AAGCGGATCC AGAAGTTACA GCGTGCATTA TTCGGTGCCC GTAAAAAAT
851 GGCCTGTTTT TTTAATCAC AATGGACATC GTTACCACGA AGCAACCGAA
901 GGCATTATCC TCAATTACGA TTACAACGGC AAACAATATC AGAGCAGCCT
951 GCGCGCCGAG CGCATGCTTT GCGTAACAG ACTTCATAAA ACTTCAGTCG
1001 GAAATGAAAT ATGGACACGC CAAACCTATA AATACATCGA CGATGCCGAA
1051 ATCGAAGTAC AACGCCGCGC CTCTGACGGC TGGGAAGCCG AATTGCCCA
1101 CCGTGCTTAC CTCAACCGTT GGCAGCTTGA CGGCAAGTTG TCTTACAAAC
1151 GCGGGACCGG CATGCGCCAA AGTATGCCTG CACCGGAAGA AAACGCGCGC
1201 GATATTCTTC CAGGTACATC TCGTATGAAA ATCATTACTG CCAGTTTGGG
1251 CGCAGCCGCC CCATTATTT TAGGCAACA GCAGTTTTTC TACGCAACCG
1301 CCATTCAAGC TCAATGGAAC AAAACGCCGT TGGTTGCCCA AGATAAATTG
1351 TCAATCGGCA GCCGCTACAC CGTTCGCGGA TTTGATGGGG AGCAGAGTCT
1401 TTTCGGAGAG CGAGGTTTCT ACTGGCAGAA TACTTTAACT TGGTATTTTC
1451 ATCCGAACCA TCAGTTCTAT CTCGGTGCGG ACTATGGCCG CGTATCTGGC
1501 GAAAGTGCAC AATATGTATC GGGCAAGCAG CTGATGGGTG CAGTGGTCGG
1551 CTTCAGAGGA GGGCATAAAG TAGGCGGTAT GTTTGCTTAT GATCTGTTTG
1601 CCGGCAAGCC GCTTCATAAA CCCAAAGGCT TTCAGACGAC CAACACCGTT
1651 TACGGCTTCA ACTTGAATTA CAGTTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 2370; ORF 707>:

m707.pep

```

1  MEIINDAELI RSMRQOHID AELLTDANVR FEQPLEKNY VISEDETPCT
51  RVNYISLDDK TVRKFSFLPS VLMKETAFKT GMCLGSNNLS RLQKAAQQIL
101 IVRGYLTSAQ IIQPNMDSG ILKLRSAGE IGDRIYEEKR DGKSAEGSIS
151 AFNNKFPLYR NKILNLRDVE OGLENLRLRP SVKTDIQIIP SEEEGKSDLQ
201 IKWQONKPIR FSIGIDDAGG KTKGYQGNV ALSFDNPLGL SDFYVSYGR
251 GLAHKTDLTD ATGTETESGS RSYSVHYSVP VKKWLFSFNH NGHRYHEATE
301 GYSVNYDYG KQYQSSLAEE RMLWRNRLHK TSVGMKLWTR QTYKYIDDAE
351 IEVQRRRSAG WEAELRHRY LNRWLDGKL SYKRGTMGRQ SMPAPEENG
401 DILPGTSRMK IITASLDAAP PFILGKQOFF YATAIQAWN KPLVAQDKL
451 SIGSRYTVRG FDGEQSLFGE RGFYQNTLT WYFHPNHQFY LGADYGRVSG
501 ESAQYVSGKQ LMGAVVGFRG GHKVGGMFAY DLFAGKPLHK PKGFQTTNTV
551 YGFNLNYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2371>:

a707.seq

```

1  NTGAAAGAAA CAGCTTTTAA AACTGGGATG TGTTTAGGTT CCAATAATTT
51  GAGCAGGCTA CAAAAGCCG CGCAACAGAT ACTGATTGTG CGTGGCTACC
101 TCACTTCCCA AGCTATTATC CAACCACAGA ATATGGATTG GGGAATTCTG
151 AAATTACGGG TATCAGCAGG CGAAATAGGN GATATCCGCT ATGAAGAAAA
201 ACGGGATGNG AAGTCTGCCG AGGGCAGTAT TAGTGCATTC AATAACAAAN
251 TTCCCTTATA TAGGAACAAA ATTCTCAATC TTCGCGATGT AGAGCAGGGC
301 TTGGAAGAAC TCGCTCGTTT GCCGAGTGTT AAAACAGATA TTCAGATTAT
351 ACCGTCCGAA GAAGAAGGCA AAAGCGATTG ACAGATCAAA TGGCAGCAGA
401 ATAAACCCAT ACGGTTTCACT ATCGGTATAG ATGATGCGGG CGGCAAAACG
451 ACCGGCAAAT ATCAAGGAAA TGTCGCTTTA TCGTNCGATA ACCCTTTGGG
501 NNTAAGCGAT TNGTTTTATG TTTTCATATG ACGCGGTTTG GTGCACAAAA
551 CGGACTTGAC TNGTGCCACC GGTACGGAAA CTGAAAGCGG ATCCAGAAGT
601 TACAGCGTGC ATTATTCGGT GNNCGTAAAA AAATGGCTGT TTTCTTTTAA
651 TCACAATGGA CATCGTTACC ACGAAGCAAC CGAAGGCTAT TCCGTCAATT
701 ACGATTACAA CGGCAACAA TATCAGAGCA GCCTGGCCGC CGAGCGCATG

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1139

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751 CTTTGGNNNN NNAGNTTTCN TNAAACTTCA GTCNGAATGA AATTATGGAC
801 ACGCCAAACC TATAAATACA TCGACGATGC CGAAATCGAA GTGCAACGCC
851 GCCGCTCTGC AGGCTGGGAA GCCGAATTGC GCCACCGTGC TTACCTCNAC
901 CGTTGGCAGC TTGACGGCAA GTTGTCTTAC AAACGCGGGA CCGGCATGCG
951 CCAAAGTATG CCGCACCTG AAGAAAACGG CCGCGGTACT ATTCCAGNCA
1001 NATCCCGTAT GAAAATCATA ACCGCCGGAT TGGATGCAGC GGCCCCGTNT
1051 ATGTTGGGCA AACAGCAGTT TTTCTACGCA ACCGCCATTC AAGCTCAATG
1101 GAACAAAACG CCTTTGGTGT CCCAAGACAA GTTGTCTATC GGCAGCCGCT
1151 ACACCGTTCG CGGATTTGAT GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT
1201 TTCTACTGGC AGAATACTTT AACTTGGTAT TTTCATCCGA ACCATCAGTT
1251 CTATCTCGGT GCGGACTATG GCCGCGTATC TGGCGAAAGT GCACAATATG
1301 TATCGGGCAA GCAGCTGATG GGTGCAGTGG TCGGCTTCAG AGGAGGGCAT
1351 AAAGTAGGCG GTATGTTTGC TTATGATCTG TTTGCCGCA AGCCGCTTCA
1401 TAAACCCAAA GGCTTTCAGA CGACCAACAC CGTTTACGGC TTCAACTTGA
1451 ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2372; ORF 707.a>:

```

a707.pep
  1 XKETAFTKGM CLGSNNLSRL QKAAQILIV RGYLTSQAI QPONMDSGIL
 51 KLRVSAGEIG DIRYEEKRDX KSAEGSISAF NNXKPLYRNK ILNLRDVEQG
101 LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS IGIDDAGGKT
151 TGKYQGNVAL SXDNPLGLSD XFYVSYGRGL VHKTDLTXAT GTETESGSR
201 YSVHYSVXVK KWLFSFNHNG HRYHEATEGY SVNYDNGKQ YQSSLAER
251 LWXXXFXXTS VXMKLWTRQT YKYIDDAEIE VQRRRSAGWE AELRHRAYLX
301 RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPXXSRMKII TAGLDAAAPX
351 MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD GEQSLFGERG
401 FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM GAVVGFRGGH
451 KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

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a707/m707 95.3% identity in 486 aa overlap

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a707.pep                                     10      20      30
                                         XKETAFTKGMCLGSNNLSRLQKAAQILIVR
m707                                     |||
EDETPTCTRVNYSILDDKTVRKFSFLPSVLMKETAFKTMCLGSNNLSRLQKAAQILIVR
      50      60      70      80      90     100

a707.pep                                     40      50      60      70      80      90
GYLTSQAIQPONMDSGILKLRVSAGEIGDIRYEEKRDXKSAEGSISAFNNKXPLYRNKI
m707                                     |||
GYLTSQAIQPONMDSGILKLRVSAGEIGDIRYEEKRDXKSAEGSISAFNNKXPLYRNKI
      110     120     130     140     150     160

a707.pep                                     100     110     120     130     140     150
LNLRDVEQGLLENLRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
m707                                     |||
LNLRDVEQGLLENLRLPSVKTDIQIIPSEEEGKSDLQIKWQONKPIRFSIGIDDAGGKTT
      170     180     190     200     210     220

a707.pep                                     160     170     180     190     200     210
GKYQGNVALSXDNPGLGLSDLFYVSYGRGLVHKTDLTXATGTETESGSRYSVHYSVXVKK
m707                                     |||
GKYQGNVALSFDNPGLGLSDLFYVSYGRGLAHTDLTDATGTETESGSRYSVHYSVPVKK
      230     240     250     260     270     280

a707.pep                                     220     230     240     250     260     270
WLFSFNHNGHRYHEATEGYSVNYDNGKQYQSSLAERMLWXXXFXXTSVXMKLWTRQTY
m707                                     |||
WLFSFNHNGHRYHEATEGYSVNYDNGKQYQSSLAERMLWRNRLHKTSGVMKLWTRQTY
      290     300     310     320     330     340

a707.pep                                     280     290     300     310     320     330
KYIDDAEIEVQRRRSAGWEAELRHRAYLXRWQLDGKLSYKRGTMGRQSMPEENGGGTI
m707                                     |||
KYIDDAEIEVQRRRSAGWEAELRHRAYLNRWQLDGKLSYKRGTMGRQSMPEENGGDIL
      350     360     370     380     390     400

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g708.seq
1      ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TTCTTGCCTT
51     GGGCGCGTGC AGCACTTCTT ACCGCCCTCT GCGGGCAGAA AAAGCCAATC
101    AGGTTTCCAA TATCAAACC CAGTTGGCGA TGGAATATAT GCGCGGTCAG
151    GACTACCCTC AGGCAACGGC AAGTATTGAA GATGCCCTGA AATCGAACCC
201    TAAAAACGAA CTTGCTTGGC TGGTCCGTGC CAAATCTAT CAATACCTGA
251    AAGTTAAACA CAAGCGCAG GAAAGTTTCC GGCAAGCCCT TCCCATCAA
301    CCCGACCTG CCGAATCAA CAACAACATA GGCTGGTTCC TGTGCGGCAG
351    GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTCGACAAA GCCCTGGCCG
401    ACCCACCTC CCGCACCTT TATATTGCCA ACCTGAATAA AGGTATATGC
451    AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501    CCTCGCGGCC CAGCCGGCAT TCCCACCCGC ATTTAAAGAA CTGCGCGCCA
551    CCAAAATGCT GGGCGGCGAG TTGGCGGATG CCGATTACTA CTTTAAAAAA
601    TACCAAGACA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651    GAAAATTGCC AAAGCCCTCG GCAACGTGCA GCGGCATAC GAATATGAG
701    CACAATTGCA GGCAAAATTC CCCTACTCGG AAGAATTGCA AACCGTCTC
751    ACCGGTCAAT GA
```

g708.pap

1	MPFKPSKRIS	LLVLALGAC	STSYRPSRAE	KANQVSNIKT	QLAMEYMRGO
51	DYRQATASIE	DALKSNPKNE	LAWLVRAEII	QYLVNDKAO	ESFRQALSIK
101	PDSAEINNNY	GWFLCGRLLR	PAESMAYFDK	ALADPTYPTP	YIANLWKGIC
151	SAQGGQFGLA	EAYLKRSLAA	QPQFFPAFKE	LARTKMLAQO	LGDADYYFKK
201	YQSRVEVLQA	DDLLLGWKIA	KALGNVQAAY	EYEAQLQANF	PYSEELQTVL
251	GGQ*				

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708.seq
1      ATGCGCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTCG TTCTTGCCTT
51     GGGCGCGTGC AGCACTTCTT ACCGCCCTCT GCGGGCAGAA AAAGCCAATC
101    AGGTTTCCAA TATCAAACC CAGTTGGCAA TGGAATATAT GCGCGGTGAG
151    GACTTACCGT AGGCGACGCG AAGTATTGAA GACGCCCTGA AATCGGACCC
201    TAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCGTA
251    AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGCCCT TCCATCTAAA
301    CCCGACAGTG CCGAAATCAA CAACAACATA GGTGGTGTCC TATGCGGCAG
351    GCTCAACCGC CTTGCCGAAT CTATGGCATA TTTCGACAAA GCTCTGGCCG
401    ACCCCACCTA CCCGACCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451    AGCGCAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAACGTTT
501    CCTCGCGGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551    CCAAAATGCT GGCGGGCAG TTGGCGCATG CCGATTACTA CTTTAAAAAA
601    TACCAAGACA GGGTAAGAAT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651    GAAATATTCC AAAGCCCTCG GCAACGCACA GCGCGCATAC GAATATGAAG
701    CCAAATTGCA GCGGAATTTC CCCTACTCGG AGAATTGCA AACCGTCTC
751    ACCGCTCAAT GA

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**m708.pap**

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1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQATASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAO ESFRQALSIK
101 PDSAEINNNY GWFLCGRILNR PAESMAYFDK ALADPTYPTP YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 TGQ*

```

m708/g708 99.2% identity in 253 aa overlap

```

      10      20      30      40      50      60
m708.pep MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
|||||
g708      MPFKPSKRISLLLVLAGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE
      10      20      30      40      50      60

      70      80      90     100     110     120
m708.pep DALKSDPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRILNR
|||||
g708      DALKSNPKNELAWLVRAEIYQYLVNDKAQESFRQALSIKPDSEINNNYGWFLCGRILNR
      70      80      90     100     110     120

      130     140     150     160     170     180
m708.pep PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
|||||
g708      PAESMAYFDKALADPTYPTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPQFPAPFKE
      130     140     150     160     170     180

      190     200     210     220     230     240
m708.pep LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNAQAAYEYEAQLQANF
|||||
g708      LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLGWKIAKALGNVQAAYEYEAQLQANF
      190     200     210     220     230     240

      250
m708.pep PYSEELQTVLTGQX
|||||
g708      PYSEELQTVLTGQX
      250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2377>:

```

a708.seq
1  ATGCCTTTTA AGCCATCCAA ACGAATCTCT TTATTACTTG TCCTTGCCTT
51  GGGCGCGTGC AGCACTTCCT ACCGCCCCCTC GCGGGCAGAA AAAGCCAATC
101 AGGTTTCCAA TATCAAAACC CAGTTGGCAA TGGAAATATAT GCGCGGTCAG
151 GACTACCGTC AGGNGACGGC AAGTATTGAA GACGCCTTGA AATCAGACCC
201 TAAAAACGAG CTTGCCTGGC TGGTCCGTGC CGAAATCTAT CAATACCTGA
251 AAGTTAACGA CAAGGCGCAG GAAAGTTTCC GGCAAGNCCT CTCCATCAAA
301 CCCGACAGTG CCGAAATCAA CAACAACCTAC NGCTGGTTCC TGTGCGGCAG
351 GCTCAACCGC CCTGCCGAAT CTATGGCATA TTTGACAAA GCCCTGGCCG
401 ACCCCACNTA CCCGANCCCT TATATTGCCA ACCTGAATAA AGGCATATGC
451 AGCGCAAAAC AGGGGCAATT CGGATTGGCG GAAGCCTATT TGAAACGTTT
501 CCTCGCCGCC CAGCCGCAGT TCCCACCCGC ATTTAAAGAA CTGGCGCGCA
551 CCAAAATGCT GGCCGGGCAG TTGGGCGATG CCGATTACTA CTTTAAAAAA
601 TACCAAAGCA GGGTAGAAGT CCTTCAGGCC GATGATTTCG TGCTAGGCTG
651 GAAAATTGCC AAAGCCCTCG GCAACGCACA GGCGGCATAC GAATATGAAG
701 CACAATTGCA GCGAATTTC CCTACTCGG AAGAATTGCA AACCGTCCTC
751 ATCGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2378; ORF 708.a>:

```

a708.pep
1  MPFKPSKRIS LLLVLALGAC STSYRPSRAE KANQVSNIKT QLAMEYMRGQ
51 DYRQXTASIE DALKSDPKNE LAWLVRAEIY QYLVNDKAO ESFRQXLSIK
101 PDSAEINNNY XWFLCGRILNR PAESMAYFDK ALADPTYXPX YIANLNKGIC
151 SAKQGQFGLA EAYLKRSIAA QPQFPAPFKE LARTKMLAGQ LGDADYYFKK
201 YQSRVEVLQA DDLLGWKIA KALGNAQAAY EYEAQLQANF PYSEELQTVL
251 IGQ*

```

a708/m708 98.0% identity in 253 aa overlap

1142

	10	20	30	40	50	60
a708.pep	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQXTASIE					
m708	MPFKPSKRISLLLVLALGACSTSYRPSRAEKANQVSNIKTQLAMEYMRGQDYRQATASIE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a708.pep	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQXLSIKPDSAEINNXYWFLCGRINR					
m708	DALKSDPKNELAWLVRAEIQYLKVNDKAQESFRQALSIPKPSAEINNXYWFLCGRINR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a708.pep	PAESMAYFDKALADPTYXPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
m708	PAESMAYFDKALADPTYTPYIANLNKGICSAKQGQFGLAEAYLKRSIAAQPFPPAFKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
a708.pep	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
m708	LARTKMLAGQLGDADYYFKKYQSRVEVLQADDLLLGWKIAKALGNAQAAYEYEAQLQANF					
	190	200	210	220	230	240
	250					
a708.pep	PYSEELQTVLIGQX					
m708	PYSEELQTVLTGQX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2379>:

g709.seq

```

1  ATGTTTGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC
51  CGTCGTGCTC GCTCTGATTG CCGCAATGGG CTATACCATC ATTTTCATTG
101 AGTGGCTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGG CAGGGATGAT
201 AGGCGCGTGT AATCAGGTA TGGCGCGGTT TACCTGTTT TTCTTCATCG
251 GGC TGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGGCTGAT TTCCCGGACT TATTTTATT TTCCGCGCTT
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCGCCT
401 GCGCCACTGT CGCGCTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC
451 GATATGGCGA TGACGcgggg cgcgattgTT tccggTGTGT TTTTCGGCGA
501 TAAATGTGCC CCGCTTTCGG ACACCACGGG CATTTCGCGG TCCATCGTCG
551 GTATCGACCT GTTGAACAC ATCAAAAACA TGATGTACAC CACCATCCCT
601 CCGTGGCTTA TCAGCGCGGC ACTGATGCTT TGGCTTCTTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACGGCTAT TCGCTGATTC CGTTTGCATC GTTGGTCTGT
751 TTGGCATTGA TCGCGCTCAA TGGCGTGGTC GCCATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACTG ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTATGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA
901 GACATTGCCA AACTGATTTC GCGCGGCGGC TTGGAGAGTA TGTCTTTAC
951 GCAGACCATC GTTATCCTCG GTATGAGTTT GGGCGGGCTG CTGTTTGGCG
1001 TCGGTGTGAT TCCTTCCTTG CTGGAGGCGG TCCGTACCTT CTGACGAAT
1051 GCCGGACGCG CGACGTTTCA GCTTGCCATG ACTTCGGTCTG GGGTCAATTT
1101 CCTGATTGGA GAGCAATATT TGAGCATCCT GCTTTCGGGA GAAACGTTCA
1151 AACCCTTTTA CGACAACTC GGCCTGCATT CGTGCAACCT GTCGCGGACT
1201 CTGGAAGATG CGGGGACGGT GATTAACCCG CTCGTGCGGT GGAGCGTGTG
1251 CGGCGTATTT ATCAGCCACG CCCTTGGCGT ACCCGTTTGG GAATATCTGC
1301 CTTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTAACCCT GTTATTCGGC
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2380; ORF 709.ng>:

g709.pep

```

1  MFAFKSLDDM PRGEALAVVV ALIAMGYTI ISLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMQAGMIGAL NOGMGAVYLF FFIGLMVSAL MMSGAIPTLM
101 YYGFLISPT YFYFSAFALC SVIGVSISS LTACATVGVA FMGMAAFQA
151 DMAMTAGAIV SGVFFGDKMS PLSDTTGISA SIVGIDLFH IKNNMYTTIP
201 AWLISAALML WLFPSVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVV
251 LALMRVNAV AVLEFVIAAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK
301 DIAKLISRGG LESMFFTQTI VILGMSLGL LFALGVIPSL LEAVRTFLTN

```

351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT  
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG  
451 WTGLTSLKK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2381>:

m709.seq  
1 ATGTTGCTT TCAATCCTT ACTCGATATG CCGCGCGGTG AGGCACTTGC  
51 CGTCTGCTG GCTCTGATTG CCGCGATGGG CTATACCATC ATTTTCATTG  
101 AGTGGTTGCC GCATATGTCC ATTATTGCCG CCATCGTCGT GCTGATTTTG  
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT  
201 AGGCGCGGTG AATCAGGGTA TGGGCGCGAT TTACCTGTTT TTCTTCATCG  
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG  
301 TATTACGTTT TCGGACTGAT TTCCCGGACT TATTTTATT TTCTCTCCTT  
351 CGCGCTGTGT TCCGTCATCG GCGTGTCCAT CGGCAGCAGC CTGACCACCT  
401 GCGCCACTGT CGGCGTTGCC TTTATGGGGA TGGCGGCGGC GTTTCAGGCC  
451 GATATGGCGA TGACGGCGGG CGCGATTGTT TCGGGCGCAT TTTTGGCGA  
501 CAAAATGTCC CCGCTTTCGG ATACGACGGG TATTTCGCGT TCCATCGTCG  
551 GCATCGACTT GTTTGAGCAC ATCAAAAATA TGATGTACAC CACCATCCCC  
601 GCGTGGCTCA TTAGTGCGGC ACTGATGCTT TGGCTTTTGC CGAATGTCGC  
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA  
701 CGGGATTGGT GCACGGCTAT TCGCTGATTG CGTTGCGGCT GTTGGTCATT  
751 TTGGCATTGA TGGCATCAA CGCGTCTGTC GCCATGCTCT TTACCGTCAT  
801 GGTGTCGGTT GCTGTAACGT ATCTGCACAG CACGCGCGAT CTGCGTCAGC  
851 TCGGTGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTTTAAA  
901 GATGTTGTCA AACTGATTTC GCGCGGCGGT TTGGAAGTA TGTTTTCAC  
951 GCAAAACATC GTGATTCTCG GGATGAGTTT GGGCGGACTG TTGTTGCGC  
1001 TCGGTGTGAT TCCTTCCCTG TTGGAGGCCA TCCGTACCTT CTTGACGAAT  
1051 GCGCGACGCG CGACGTTTCA CGTTGCCATG ACTTCGGTCG GGGTTAATTT  
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTGCGGT GAAACGTTCA  
1151 AACCCGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG  
1201 CTGGAAGATG CGGGGACGGT GATTAAACCG CTCGTACCGT GGAGCGTATG  
1251 CGGCGTGTTC ATCAGCCACG CGCTGGGCGT GCCGGTTTGG GAATATCTGC  
1301 CGTATGCCCT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT  
1351 TGGACGGGGC TGACTTTGAG CAAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 2382; ORF 709>:

m709.pep  
1 MFAFKSLDDM PRGEALAVVV ALIAAMGYTI ISLEWLPHMS IIAAIVVLIL  
51 YGLARGLKYN DMQQGMIGAL NQMGAIYLF FFIGLMVSAL MMSGAIPTLM  
101 YYGFGSLIPT YFYFSSFALC SVIGVSIGSS LTTTCATVGA FMGMAAFQA  
151 DMAMTAGAIV SGAFFGDKMS PLSDTTGISA SIVGIDLFEH IKNMYYTIP  
201 AWLISAALML WLLPNVAAQD LNSVESFRSQ LEATGLVHGY SLIPFALLVI  
251 LALMRINAVV AMLFTVMVAV AVTYLHSTPD LRQLGAWFYG GYKLEGEAFK  
301 DVVKLISRGG LESMFFTQTI VILGMSLGLL LFALGVIPSL LEAIRTELTN  
351 AGRATFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSCNLSRT  
401 LEDAGTVINP LVPWSVCGVF ISHALGVPVW EYLPYAFFCY LSLALTLLFG  
451 WTGLTSLKK\*

m709/g709 96.9% identity in 459 aa overlap

	10	20	30	40	50	60
m709.pep	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
g709	MFAFKSLDDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
m709.pep	DMQQGMIGALNQMGAIYLFFFIGLMVSALMMSGAIPTLMYYGFGSLISPTYFYFSSFALC					
g709	DMQAGMIGALNQMGAVYLFFFIGLMVSALMMSGAIPTLMYYGFGSLISPTYFYFSAFALC					
	70	80	90	100	110	120
m709.pep	SVIGVSIGSSLTTCATVGVAFMGMAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
g709	SVIGVSIGSSLTACATVGVAFMGMAAFQADMAMTAGAIVSGVFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
m709.pep	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
g709	SIVGIDLFEHIKNMYYTIPAWLISAALMLWLLPSVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240



1144

	250	260	270	280	290	300
m709.pep	SLIPFALLVILALMRINAVVAMLFVTVMVAVVLYLHSTPDLRQLGAWFYGGYKLEGEAFK					
g709	SLIPFALLVVLALMRVNAVVMFLFTVIAAVAVVLYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
m709.pep	DVVKLISRGGLSEMFQTIVILGMSLGGLLFALGVIPSLLEAIRFTLTNAGRATFSVAM					
g709	DIAKLISRGGLSEMFQTIVILGMSLGGLLFALGVIPSLLEAVRTLTNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m709.pep	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
g709	TSVGVNFLIGEQYLSILLSGETFKPVYDKLGLHSCNLSRTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
m709.pep	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKX					
g709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2383>:

```

a709.seq
1  ATGTTTCGCTT TCNAATCCTT ACTCGATATG CCGCGCGGTG AGGCNCTTGC
51  CGTCGTCGTC GCTCTGATTG CCGCGATGGG CTATACCATC ATTTNNTTGG
101 AGTGGCTGCC GCATATGTCC ATTATTGCGG CCATCGTNGT GCTGATTTTG
151 TACGGCTTGG CGCGCGGTTT GAAATACAAC GATATGCAGC AGGGCATGAT
201 AGGCGCGTTG AATCAGGGTA TGGGCGCGAT TTACCTNNTT TTCTTCATCG
251 GGCTGATGGT CAGCGCGCTG ATGATGAGCG GCGCGATTCC GACGCTGATG
301 TATTACGGTT TCGGACTGAT TTCCCGGACT TATTTTATT TTTCCGCCCTT
351 CCGCTGTGT TCCGTCATCG GCGTGTCAT CCGCAGCAGC CTGACCACCT
401 GCGCCACTGT CGGCGTTGCC TTNATGGGTA TNNNGNCGGC GTTTCNGGCC
451 NANATGGNGN NGNNGNNGGN CNNGATTGTN NNGGNCGCAT TTTTNGGCGN
501 CAAAATGTCN CCGCTTCCG ATACGNCGGG CATNTCCGCG TCCATTGTCTG
551 GTATCGACCT GTTGAACAC ATCAAAAATA TGATGTACAC NACCATTCCC
601 GCGTGGCTCA TCAGTGNNNC ACTGATGCTG TNGCTTCTC CCAGCGTCGC
651 CGCGCAGGAT TTGAACAGCG TCGAATCCTT CCGCAGCCAG CTTGAAGCCA
701 CGGGATTGGT GCACTGCTAT TCGCTGATTC CGTTTGGCGT GTTGGTCGTT
751 TTGGCATTGA TGCGCGTCAA TGCCGTGGTC GCTATGCTCT TTACCGTCAT
801 TGCCGCCGTT GCCGTAACGT ATCTGCACAG CACGCCCGAT CTGCGTCAGC
851 TCGGCGCGTG GTTTTACGGC GGCTACAAAC TCGAAGGCGA AGCGTNTANA
901 GACATTGCCA AACTCATTTT TCGCGGCGGT TTGAAAGTA TGTTTTTCAC
951 GCAGACCATC GTGATTCTTG GGATGAGCCT TGGCGGGCTG CTGTTTGCAC
1001 TGGGCGCGAT TCCTTCCCTG CTGGATGCCG TCCGCAGCTT TTTGACGAAT
1051 GCCGGGCGTN CCACATTGAG CGTTGCCATG ACTTCGGTCG GGGTTAATTT
1101 CCTGATCGGC GAGCAATATT TGAGTATTTT GTTGTCTGGT GAAACGTTCA
1151 AACCTGTTTA CGATAAGCTC GGTCTGCATT CGCGCAATCT GTCGCGGACG
1201 CTGGAAGATG CGGGGACGGT CATCAACCCG CTCGTACCGT GGAGCGTATG
1251 CGGCGTGTTT ATCANCCACG CGCTGGGCGT GCCGTTTTGG GAATATCTGC
1301 CGTATGCCTT TTTCTGCTAT TTGAGTTTGG CTTTGACCCT GTTATTCGGT
1351 TGGACGGGGC TGACTTTGAG CAAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2384; ORF 709.a>:

```

a709.pep
1  MFAFXSLDM PRGEALAVVV ALIAAMGYTI IXLEWLPHMS IIAAIVVLIL
51  YGLARGLKYN DMOQGMIGAL NOGMGAIYLF FFIGLMVSAL MMSGAIPTIM
101 YYGFLISPT YFYSAFALC SVIGVSIGSS LTTCATVGVA XMGXXXAFXA
151 XMXXXXXIV XXAXGKXMS PLSDTXGXA SIVGIDLFEH IKNMMYTTIP
201 AWLISXXLML XLLPSVAAQD LNSVESFRSQ LEATGLVHCY SLIPFALLVV
251 LALMRVNAV VAMLFVIAAV AVTYLHSTPDL RQLGAWFYG GYKLEGEAXX
301 DIAKLISRG LSEMFQTIV ILGMSLGG LFGALGAIPL LDAVRSFLT N
351 AGRXTFSVAM TSVGVNFLIG EQYLSILLSG ETFKPVYDKL GLHSRNLST

```

1145

401 LEDAGTVINP LVPWSVCGVF IXHALGVPVW EYLPYAFFCY LSLALTLLFG  
 451 WTGLTSLKK\*

a709/m709 91.1% identity in 459 aa overlap

	10	20	30	40	50	60
a709. pep	MFAFXSLDMPRGEALAVVVALIAAMGYTIIXLEWLPHMSIIAAIVVLILYGLARGLKYN					
m709	MFAFXSLDMPRGEALAVVVALIAAMGYTIISLEWLPHMSIIAAIVVLILYGLARGLKYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a709. pep	DMQOGMIGALNQGMGAIYILFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSAFALC					
m709	DMQOGMIGALNQGMGAIYILFFFIGLMVSALMMSGAIPTLMYYGFGGLISPTYFYFSSFALC					
	70	80	90	100	110	120
	130	140	150	160	170	180
a709. pep	SVIGVSIGSSLTTCATVGVAIXMXXXXXAFAXMXXXXXIVXXAXXGXKMSPLSDTXGXA					
m709	SVIGVSIGSSLTTCATVGVAIFMGAFAAFQADMAMTAGAIVSGAFFGDKMSPLSDTTGISA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a709. pep	SIVGIDLFEHIKNMYYTTPAWLISXXLMXLPLPSVAAQDLNSVESFRSQLEATGLVHCY					
m709	SIVGIDLFEHIKNMYYTTPAWLISAAALMLWLLPNVAAQDLNSVESFRSQLEATGLVHGY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a709. pep	SLIPFALLVVLALMRVNAVAMLFVIAAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAXX					
m709	SLIPFALLVILALMRINAVAMLFVMAVAVTYLHSTPDLRQLGAWFYGGYKLEGEAFK					
	250	260	270	280	290	300
	310	320	330	340	350	360
a709. pep	DIAKLISRGGLESMTTQTIVILGMSLGGLLFGALGAIPLSDAVRSFTLNAGRXTFSVAM					
m709	DVVKLISRGGLESMTTQTIVILGMSLGGLLFGALGVIPSLLEAIRTFTLNAGRATFSVAM					
	310	320	330	340	350	360
	370	380	390	400	410	420
a709. pep	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
m709	TSVGVNFLIGEQLSILLSGETFKPVYDKLGLHSRNLSTLEDAGTVINPLVPWSVCGVF					
	370	380	390	400	410	420
	430	440	450	460		
a709. pep	IXHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
m709	ISHALGVPVWEYLPYAFFCYLSLALTLLFGWTGLTSLKKX					
	430	440	450	460		

g710.seq not found

g710.pep not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2385>:

m710.seq  
 1 ATGGAAACCC ACGAAAAAT CCGCCTGATG CGCGAATTGA ATAAATGGTC  
 51 CCAGGAGGAT ATGGCGGAAA AGCTGGCGAT GTCGGCAGGC GGGTATGCCA  
 101 AAATCGAACG GGGCGAACG CAGTTAAATA TCCCGCGTTT GGAGCAGTTG  
 151 GCTCAGATT TCAAATCGA TATGTGGGAC TTGCTCAAAT CGGGCGGTGG  
 201 TGGGATGGTG TTTGAGATTA ATGAAGGTGA TAGTGGTGGC GATATTGCGT  
 251 TGTATGCGTC GGGTGATGTT TCGATGAAAA TAGAATTTTT AAAAATGGAG

m710.pep

a710.seq

a710.pwp

	10	20	30	40	50	60
a710.pep	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
m710	METHEKIRLMRELNKWSQEDMAEKLAMSAGGYAKIERGETQLNIPRLEQLAQIFKIDMWD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a710.pep	LLKSGGGMVLQINDVDTNSGEFAIYTAQDASGKAGFVKMELKHCKEMLEHKDKKEIELLR					
	:     :   :   :   :   :   :   :   :   :   :   :   :   :   :					
m710	LLKSGGGMVFQINEGDSG-GDIALYASGDVSMKIEFLKMELKHCKEMLEQKDKKEIELLR					
	70	80	90	100	110	

```

a710.pep      KLTETVX
               |||||
m710          KLTETVX
               120

```

g711.seq not found

g711.pap not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2389>:

m711.seq

```

1 ATGCCCAGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAGGC
51 AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
1 01 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
1 51 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
2 01 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
2 51 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
3 01 CCAGCCACCG GCGAGGTATT CGGTTCGCGG CGGAGGTTGG AGACGATTTA
3 51 CCGTACCAAT ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
4 01 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
4 51 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
5 01 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
5 51 GCTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
6 01 ATTGTGGGCA AAAGCACGGC GGACAATCTG GTCGAGACCC ATAAATCTA
6 51 CAACAAAAAA GGCATACTT ATCTGACCCT TGCTATAAAA GCACCGGATG
7 01 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
7 51 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
8 01 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
8 51 TTGAAAAAGA GTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG
9 01 CCCGATAAAG AGCAGAAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
9 51 TAAATTTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
10 01 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
10 51 GACAGCCGTG AGGGGCAGAA TTTGATGATG TCCTACTATG CTTTTTTGCC
11 01 GGATATGCTG CAAAACCCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
11 51 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
12 01 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
12 51 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2390; ORF 711&gt;:

m711.pap

```

1 MFAPDLGFAL SLPPKAIEW LESKKVTAES YRNLTAIEIA KVTIARMTD
51 LDMLNDIKTS MVESAKSQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
1 01 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
1 51 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
2 01 IVGQSTADNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYDYNAGRM
2 51 NYRPDLDRYD RALAHQFAKA EMGGADFKTS FKQLEKEFYE VKQRDLIDGK
3 01 PDKEQKIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
3 51 DSREGQNFDD SYIAFLPDML QNPEHVIRDN RELIFTARYK GSALWAVLKY
4 01 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2391>:

a711.seq

```

1 ATGCCCAGCGC CTGATTTGGG ATTTGCCTTA AGTCTGCCGC CAAAAAGGC
51 AATCGAGTGG CTGGAAAGTA AAAAGGTTAC GGCGGAGAGC TACCGCAATC
1 01 TGACAGCCTC CGAAATTGCC AAAGTCTATA CGATTGCCCG CATGACCGAC
1 51 TTGGATATGC TCAACGACAT CAAAACTTCG ATGGTTGAAT CGGCAAAAAG
2 01 TGGACAGTCG TTTGACGATT GCGGAAAAGG TATCTTGAAT CTGCTCAGCA
2 51 ACAAGGGCTG GCTGCATCCG AACGGGCATA ACGGTAAGGA TATCATCGAC
3 01 CCAGCCACCG GCGAGGTATT CGGTTCGCGG CGGAGGTTGG AGACGATTTA
3 51 CCGTACCAAC ATGCAAACTG CCTACAACGC CGGTCAATAT CAAGGATATA
4 01 TGGCAAATAT TGATGCACGA CCTTATTGGA TGTATGACGC GGTAGGCGAC
4 51 AGCCGCACCC GTCCGGCGCA TTCGGCAATA GACGGGCTGG TGTACCGCTA
5 01 CGACGACCCG TTTTGGGCAA CGTTTTACCC GCCCAACGGC TACAACTGCC
5 51 GTTGCTCGGT CATCGCGCTG TCGGAGCGGG ATGTGGAACG CCAGGGGCGG
6 01 ATTGTGGGCA AAAGCACGTC GGACAATCTT GTTGAGACCC ATAAATCTA
6 51 CAACAAAAAA GGCATACTT ATCTGACCCT TGCTATAAAA GCACCGGATG
7 01 GCAGTCTGTA CACGACCGAT CGAGGATTTG ATTACAACGC CGGACGAATG
7 51 AACTACCGCC CCGATTTAGA CAAGTACGAC CGTGCGTTGG CGCATCAATT
8 01 TGCCAAAGCG GAAATGGGTG GTGCGGATTT TAAAACAGC TTTAAACAGC
8 51 TTGAAAAAGA GTTTATGAA GTCAAGCAAC GTTTGGATAT TGATGGCAAG

```

1148

```

901 CCCGATAAAG AGCAGAAAAT CAAAATCCGA AATGCGCTAT CAAGACAGCT
951 TAAATTGCT GCGGGTGTAT TGAGCAAGGA AACGCAAGAA TTGGCAGGTA
1001 TGACACGAGC GACGGTGTGG CTGTCTGATG ATACGTTGGT TAAACAGGTA
1051 GACAGCCGTG AAGGGCAGAA TTTTCGATGAC TCCTACTATG CTTTTCGCTC
1101 GGATATGCTG CAAAACCCTG AACATGTCAT CCGCGACAAT CGTGAATTGA
1151 TTTTCACAGC TCGCTATAAA GGCTCGGCAT TGTGGGCAGT TTTAAATAT
1201 ATTAAGGAGG TGGATGAGAT TTATCTACAG TCGTACCGAA TCAGTAACGA
1251 CAAAGAGATT GCCAAATTTA TGGCGAAGAA GAAAGTATTG AAATAG

```

This corresponds to the amino acid sequence <SEQ ID 2392; ORF 711.a>:

## a711.pep

```

1 MPAPDLGFAL SLPPKKAIEW LESKKVTAES YRNLTAIEIA KVTIARMTD
51 LDMLNDIKTS MVESAKSGQS FDDWRKGILN LLSNKGWLHP NGHNGKDIID
101 PATGEVFGSP RRLETIYRTN MQTAYNAGQY QGYMANIDAR PYWYDAVGD
151 SRTRPAHSAI DGLVYRYDDP FWATFYPPNG YNCRCSVIAL SERDVERQGR
201 IVGQSTSDNL VETHKIYNKK GDTYLTLAYK APDGSLYTTD RGFYNAGRM
251 NYRPLDKYD RALAHQFAKA EMGGADFCTS FKQLEKEFYE VKQRLDIDGK
301 PDKEQIKIR NALSRLKFA AGVLSKETQE LAGMTRATVW LSDDTLVKQV
351 DSREGQNFDD SYAFLPDM LONPEHVIRDN RELIFTARYK GSALWAVLKY
401 IKEVDEIYLQ SYRISNDKEI AKFMAKKKVL K*

```

a711/m711 99.8% identity in 431 aa overlap

a711.pep	10	20	30	40	50	60
m711	10	20	30	40	50	60
a711.pep	70	80	90	100	110	120
m711	70	80	90	100	110	120
a711.pep	130	140	150	160	170	180
m711	130	140	150	160	170	180
a711.pep	190	200	210	220	230	240
m711	190	200	210	220	230	240
a711.pep	250	260	270	280	290	300
m711	250	260	270	280	290	300
a711.pep	310	320	330	340	350	360
m711	310	320	330	340	350	360
a711.pep	370	380	390	400	410	420
m711	370	380	390	400	410	420

1149

a711.pap

AKFMAKKKVLKX

m711

|||||||

AKFMAKKKVLKX  
430

1150

g712.seq not found yet

g712.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2393>:

```

n712.seq
1  ATGATGCCCC ATATTGATTT TGACACGATT CCGGGCAGCA TCCGCGTGCC
51  CCGGCAGTAT ATTGAATTTA ACACCCGCAA TGCCGTACAA GGTTTGCCGC
101 AAAATCCGCA AAAGGTATTG ATGGTTGCAC CCATGCTGAC CGCGGCATA
151 CAGCCCGCCT TAGAGCCGGT GCAACTATTT AGCGATGCCG AGGCGGCCGA
201 TTGTTCGGA CAAGGCTCGC TGGCGCATT GATGGTGCGC CAAGCATTTG
251 CCAACAACCC TTATTTGGAT TTGACCGTTA TCGGTATTGC CGACCACAGC
301 GCAGGCGTGC AGGCAACCGC AACCGTTACC CTTTCCGGCA CGGCCACCGC
351 GCCGGGCGTG GTGGAATCA CGATTGGCGG CAAGCAGGTA AGCACGGCCG
401 TTAACACCGG CGAGACCGCC GCCACAGTGG CAGACCGTCT GAAAACCGCC
451 ATCACTGCCG CCGATGTAAC CGTTACCGCA TCCGGCAGCG GCGCAGCCGT
501 TACGCTGACG GCCAAACACA AAGGCGAGAT CGGCAACGAG AGCGGCTTAA
551 CCGTGAGCAC CGGCAATACC GGCCTAACTT ATCAAGCCAA TGCCTTTACC
601 GCGCGTGCCA AAAATGCGGA CATTGCCACG GCCTTGTCCTA AAGTGGCGGG
651 CAAGCATTAT CACATTATTT GCAGCCCGTT TAGCGATGAC GCCAACGCCA
701 AAGCCTTGAG CAACCATATT ACCAACGTAT CCAACGCCAT CGAGCAGCGC
751 GGCTGTATCG GCGTATTGGG TATGAGTGGC GCCTTGAGCA CGGCCACCAC
801 CGTACCGGC GAAATCAACG ACGGCCGCAT GACCTGTGCT TGGTACAAAG
851 GTCGGGTAGA GCCAACCGGC ATCATCGCCG CAGGTTATGC GGCGGTGTTG
901 GCCTTTGAAG AAGACCCTGC CAAGCCGCTG AACACGCTGG AAATCAAAGG
951 GCTGGCCGTT ACACCTGATG CGCAATGGCC GCTGTTGCA GAATGCAACA
1001 ATGCGCTGTA CAACGGCTTG ACCCGCTCA CAGTGGTCAA CAACCGCGTG
1051 CAGATTATGC GTGCCGTATC CACCTATACC AAGTCGGCCA ACAACACCGA
1101 CGACCCGGCA TACTCGACA TTACCACCAT CCGCACGCTG GATTATGTGC
1151 GCCGCAGCGT TAAAGAGCGC ATTGCCCTGC GTTTTCCGCG CGACAAATTG
1201 AGCGACCGCC TGCTGCCCAA GGTAAAGAGC GAGATTTTGG ACGTGTGTAT
1251 TAAGCTCGAC CAAGCCGAAA TCATCGAAAA CGCCGAGGCC AACAAAGGCA
1301 AGCTGGTGGT GCGCGGTGCG CAAAACGACC CCAACCGTGT TAATGCCATT
1351 ATCCCGCCG ATGTGGTCAA CGGCCTGCAC GTCTTTGCCG GCGCATTTGA
1401 TTTGATTTTG TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2394; ORF 712&gt;:

```

n712.pep
1  MMPHIDFDTI PGSIRVPGQY IEFNTRNAVQ GLPQNPKVL MVAPMLTAGI
51  QPALEPVQLF SDAEAADLFG QGSLAHLNVR QAFANNPYLD LTVIGIADHS
101 AGVQATATVT LSGTATAPGV VEITIGGKQV STAVNTGETA ATVADRLKTA
151 ITAADVTVTA SGSGAAVTLT AKHKGEIGNE SGLTVSTGNT GLTYQANAFT
201 GGAKNADIAT ALSKVAGKHY HIICSPFSDD ANAKALSNHI TNVSNAIEQR
251 GCIGVLGMSA ALSTATTATG EINDGRMTCA WYKGAVEPNG IIAAGYAAVL
301 AFEEDPAKPL NTLEIKGLAV TPDAQWPLFA ECNNALYNGL TPLTVVNNRV
351 QIMRAVSTYT KSANNTDDPA LLDITTIRTL DYVRRSVKER IALRFPKDKL
401 SDRLLPKVKS EILDVLKLD QAEIENAEA NKGKLVVRA QNDPNRVNAI
451 IPADVNLGH VFAGRIDLIL *

```

a712.seq not found yet

a712.pep not found yet

g713.seq not found yet

g713.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2395>:

```

m713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCA
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 CCGAAAACAA CCCCCTTTG GCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGCGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CTGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CCGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGTGACACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCCTGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CCCGCATGGA TGGTACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG
1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GCGGTGTTT GAATGA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2396; ORF 713&gt;:

```

m713.pap
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLGSECE VVIDGQIVMT GIIGSQRHGK SKGSRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTLVDAAKKL AAPWPQIKAV VLKAENNPAL GKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGAD YSSPPVATLC WSRTDSRCNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDLLWVYKD PTMTLHRPKT
251 VVVSADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVLWQPLR
301 VHVIDDEHGI DAVFFLMGRR FMLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGR KGVSHKGKKG GKKQAETAVF E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2397>:

```

a713.seq
1  ATGCAAAATA ATTCATACGG CTATGCCGTG TCGGTGCGCG TGGGCGGTAA
51  AGAGCACCGC CACTGGGAGC GCTACGACAT CGACAGCGAC TTTTAAATCC
101 CTGCCGACAG CTTTCGATTTT GTCATCGGCA GGTGGGGACC GGAGGCGGCC
151 ATACCCGATT TAAGCGGAGA GAGCTGCGAG GTAGTGATAG ACGGGCAAAT
201 CGTGATGACG GGCATCATCG GCAGCCAGCG CCACGGCAAA AGCAAGGGCG
251 GCCGCGAGTT GAGCTTGAGC GGGCGTGATT TGGCCGTTT TTTGGTGGAT
301 TGCTCCGCGC CGCAGCTCAA TGTAAGGGC ATGACGGTAT TGGATGCAGC
351 CAAAAGCTG GCCGCGCCGT GGCCGAGAT TAAAGCGGTG GTGCTTAAGG
401 TCGAAAACAA CCCCCTTTG GCAAAATCG ACATCGAGCC GGGCGAAACC
451 GTATGGCAGG CATTAAACCA TATTGCCAAC TCGGTGCGGC TGCATCCGTG
501 GCTGGAGCCG GACGGCACGT TGGTGGTGGG CGGTGTGGAT TACAGCAGCC
551 CGCCGGTGGC GACATTGTGT TGGAGCCGCA CCGACAGCCG CCGCAATATC
601 GAGCGCATGG ACATTGAGTG GGATACCGAC AACCGCTTTT CTGAGGTTAC
651 TTTTTTGGCG CAATCGCACG GCCGAGCGG CGACAGCGCC AAACACGATT
701 TAAAGTGGGT GTACAAAGAC CCGACGATGA CGTGACACCG CCTAAAACG
751 GTGGTGGTGT CCGATGCCGA CAATTGGGCC GCATTGCAAA AGCAGGCTAA
801 AAAGCAGCTG GCCGACTGGC GGCTGGAGGG ATTTACTCTC ACGATAACCG
851 TGGGCGGCCA TAAACCCGCG GACGGCGTAT TGTGGCAACC TGGCAGCGT
901 GTGCATGTGA TCGACGACGA GCACGGTATC GATGCGGTGT TTTTCTGAT
951 GGGGCGGCGG TTTATGCTAT CTCGCATGGA TGGCACGCAA ACCGAGCTGC
1001 GGCTCAAAGA GGACGGTATT TGGACACCCG ACGCTTACCC CAAAAGGCC
1051 GAGGCGGCGC GCAAGCGCAA AGGCAAACGC AAAGGCGTGA GCCATAAGGG

```



1152

1101 CAAAAAAGGC GGCAAAAAC AAGCAGAAAC GGCGGTGTTT GAATGA

This corresponds to the amino acid sequence &lt;SEQ ID 2398; ORF 713.a&gt;:

## a713.pep

```
1  MQNNSYGYAV SVRVGGKEHR HWERYDIDSD FLIPADSFDF VIGRLGPEAA
51  IPDLSGESCE VVIDGQIVMT GIIGSQRHGK SKGGRELSLS GRDLAGFLVD
101 CSAPQLNVKG MTLVDAKKL AAPWPQIKAV VLKVENNPAL DKIDIEPGET
151 VWQALTHIAN SVGLHPWLEP DGTLLVVGVD YSSPPVATLC WSRTDSRRNI
201 ERMDIEWDTD NRFSEVTFLA QSHGRSGDSA KHDWKVYKD PTMTLHREPKT
251 VVVSADADNLA ALQKQAKKQL ADWRLEGFTL TITVGGHKTR DGVWLWQPGQR
301 VHVIDDEHGI DAVFFLMGRR FLSRMDGTQ TELRLKEDGI WTPDAYPKKA
351 EAARKRKGRK KGVSHKGGKG GKKQAETAVF E*
```

a713/m713 98.4% identity in 381 aa overlap

	10	20	30	40	50	60
a713.pep	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
m713	MQNNSYGYAVSVRVGGKEHRHWERYDIDSDFLIPADSFDFVIGRLGPEAAIPDLSGESCE					
	10	20	30	40	50	60
	70	80	90	100	110	120
a713.pep	VVIDGQIVMTGIIGSQRHGKSKGGRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
m713	VVIDGQIVMTGIIGSQRHGKSKGSRELSLSGRDLAGFLVDCSAPQLNVKGMTVLDAKKL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a713.pep	AAPWPQIKAVVLKVENNPALDKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVVGVD					
m713	AAPWPQIKAVVLKAENNPALGKIDIEPGETVWQALTHIANSVGLHPWLEPDGTLLVVGAD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a713.pep	YSSPPVATLCWSRTDSRRNIERMDIEWDTNRFSEVTFLAQSHGRSGDSAKHDLKWYKD					
m713	YSSPPVATLCWSRTDSRCNIERMDIEWDTNRFSEVTFLAQSHGRSGDSAKHDLKWYKD					
	190	200	210	220	230	240
	250	260	270	280	290	300
a713.pep	PTMTLHREKTVVVSADADNLAALQKQAKQLADWRLEGFTLTITVGGHKTRDGVWLWQPGQR					
m713	PTMTLHREKTVVVSADADNLAALQKQAKQLADWRLEGFTLTITVGGHKTRDGVWLWQPGLR					
	250	260	270	280	290	300
	310	320	330	340	350	360
a713.pep	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
m713	VHVIDDEHGIDAVFFLMGRRFMLSMDGTQTELRLKEDGIWTPDAYPKKAEAAARKRKGR					
	310	320	330	340	350	360
	370	380				
a713.pep	KGVS HKGKGGKKQAETAVFEX					
m713	KGVS HKGKGGKKQAETAVFEX					
	370	380				

1153

g714.seq not found yet

g714.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2399>:

```

m714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGCCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 CGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CCGTACGGGC AAAAACC GCCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGCTA A

```

This corresponds to the amino acid sequence &lt;SEQ ID 2400; ORF 714&gt;:

```

m714.pap
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVA DA VDP
51  RSAGQMLADW ERLGLDGTG KNRQHRVLAV MAKLN ETGGL SIPYFVRLAE
101 AAGYQIQIDE POPFRAGVNR AGDRLAPQEI MWVWHVNV RG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2401>:

```

a714.seq
1  ATGAGCTATC AAGACATCTT GCGGGGTCTG TTGCCCCCGG TGTCGTATGC
51  CCGCAATGCC CCGCGTGTGC GGGCGCAGGC AGAAATAGAC GGCGCAGCGC
101 TGGATGCGGT GCGGGAATCG GCTCAAAGCG TTGCCGATGC CGTCGACCCG
151 AGCAGCGCCG GCCAAATGCT GGCCGATTGG GAGCGCGTAT TAGGTTTGGA
201 CCGTACGGGC AAAAACC GCCACCGTGT GTTGGCCGTC ATGGCCAAGC
251 TAAACGAAAC AGGCGGCTTG AGTATTCCTT ATTTTGTGCG TTTGGCCGAG
301 GCGGCGGGCT ATCAAATCCA AATCGACGAA CCGCAGCCGT TCCGCGCCGG
351 TGTAACCGC GCCGGCGACC GTCTTGCGCC GCAGGAAATC ATGTGGGTGT
401 GGCACGTTAA CGTGCGCGGC GGCAACAACC GCATTACCCG ATTCCGCGCC
451 GGTATCTCGG CGGCGGGCGA CAGGCTGACC GATTACAGCG ATGCCGTGAT
501 CGAGAGCCTG TTCAACCGCC TCAAGCCCGC CCACACCGCT ATCCGATTTA
551 CCTACCGATA A

```

This corresponds to the amino acid sequence &lt;SEQ ID 2402; ORF 714.a&gt;:

```

a714.pap
1  MSYQDILRGL LPPVSYARNA PRVRAQAEID GAALDAVAES AQSVA DA VDP
51  SSAGQMLADW ERLGLDGTG KNRQRRVLAV MAKLN ETGGL SIPYFVRLAE
101 AAGYQIQIDE POPFRAGVNR AGDRLAPQEI MWVWHVNV RG GNNRITRFRA
151 GISAAGDRLT DYSDAVIESL FNRLKPAHTA IRFTYR*

```

a714/m714 98.9% identity in 186 aa overlap

	10	20	30	40	50	60
a714.pap	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVA DA VDPSSAGQMLADW					
m714	MSYQDILRGLLPPVSYARNAPRVRAQAEIDGAALDAVAESAQSVA DA VDPSPSAGQMLADW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a714.pap	ERVLGLDGTGKNRQRRVLAVMAKLN ETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
m714	ERVLGLDGTGKNRQHRVLAVMAKLN ETGGLSIPYFVRLAEAAAGYQIQIDEPOPFRAGVNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a714.pap	AGDRLAPQEI MWVWHVNV RG GNNRITRFAGISAAGDRLTDYSDAVIESL FNRLKPAHTA					

1154

m714 AGDRLAPQEIMVWHVNVVRGGNNRITRFRAGISAAGDRLTDYSDAVIESLFNRLKPAHTA  
 130 140 150 160 170 180

a714.pep IRFTYRX

|||||||

m714 IRFTYRX

g715.seq not found yet

g715.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2403>:

m715.seq  
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
 151 CCGAAATGGG TTGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC  
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC  
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG  
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
 401 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2404; ORF 715>:

m715.pep  
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
 51 PKWVGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM  
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2405>:

a715.seq  
 1 ATGATTGATG TCAAAATAGA CAATATCTTT GTCGTCCTAA ACCAAATCGA  
 51 GCGGCTTGGC AACGGGATCG AAAACCGCTA CCTGCTGATG CGCCGACTGT  
 101 CCGAAACCAT GCACACGGCG GTCAAGCTCA ATTTCCGCTA CGCAGGCCGT  
 151 CCGAAATGGT TGGGGCTAAA ATACCGCGAC GGCAAGCCGC TTTCGGATTC  
 201 GGGTCGTCTG AAAGACAGTT TTTCCACACT GTCAGACAAC GATACAGCCC  
 251 TTGTCGGTAC GAATATCGTC TATGCCGCCA TCCACAACCT CGGCGGTATG  
 301 GCGGGGCGCA ACCGCAAAGT TCGGATTCCG CAACGGGAAT TTTTGACGCT  
 351 GACGGACGAC GACAAACAGG CTTTGATGGA CGATGTGCAG GATTATTTTT  
 451 CGGGTCTGAT ACCGTGA

This corresponds to the amino acid sequence <SEQ ID 2406; ORF 715.a>

a715.pep  
 1 MIDVKIDNIF VVLNQIERLG NGIENRYLLM RRLSETMHTA VKLNFRYAGR  
 51 PKWLGLKYRD GKPLSDSGRL KDSFSTLSDN DTALVGTNIV YAAIHNFGGM  
 101 AGRNRKVRIP QREFLTLTDD DKQALMDDVQ DYFSGSLIP\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2407>:

g716.seq  
 1 ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT  
 51 GGCCGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCAAAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC  
 201 TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA  
 251 AAAAAAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC  
 301 GAAGGCAAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

This corresponds to the amino acid sequence <SEQ ID 2408; ORF 716.ng>:

g716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVQKSAQG SCGASKSAEG  
 51 SCGASKSAEG SCGAAASKAG EGKCGEGKCG ATVKAHKHT KASKAKARSA

101 EGKCGEGKCG SK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2409>:

m716.seq  
 1 ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT  
 51 GGCCGCGCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG  
 201 CAAATGCGGT GCGACCGTAA AAAAAACCA CAAACACACC AAAGCATCTA  
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT  
 301 TCTAATAA

This corresponds to the amino acid sequence <SEQ ID 2410; ORF 716>:

m716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG  
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG  
 101 SK\*

m716/g716 86.6% identity in 112 aa overlap

	10	20	30	40	50	
m716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGA-----					
g716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVQKSAQSGASKSAEGSCGASKSAEG					
	10	20	30	40	50	60
	60	70	80	90	100	
m716.pep	----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
g716	SCGAAASKAGEGKCGEGKCGATVKKAHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2411>:

a716.seq  
 1 ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT  
 51 GGCCGCGCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG  
 101 TTCATAAATC CGCCCATGGC TCTTGCGGCG CGTCCAAATC TGCCGAAGGT  
 151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG  
 201 CAAATGCGGT GCGACCGTAA AAAAAACCA CAAACACACC AAAGCATCTA  
 251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT  
 301 TCTAATAA

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2412.a>:

a716.pep  
 1 MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSAGH SCGASKSAEG  
 51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG  
 101 SK\*

a716/m716 100.0% identity in 102 aa overlap

	10	20	30	40	50	60
a716.pep	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
m716	MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSAGHSCGASKSAEGSCGAAGSKAG					
	10	20	30	40	50	60
	70	80	90	100		
a716.pep	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
m716	EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2413>:

g717.seq  
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC

```

51  GGT'TTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCcccgCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  ACTGACGGTG
151  TCGGTATTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CGCGCCGAC  AAAGACACTT  TGTTCAAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGT'TTTCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGT'TTTCGCT  CGACGATGCC  GCCGCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGT'TTTC
401  GTATGGAAGG  GCGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAA
451  CTCGCCATTG  TGCTGCTGTT  GCCGCTGACG  GTCGGGCTGC  TGCAC'TTTC
501  GCGGAACACC  TCCGTCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CGCGCCGCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CGCGCGCCGT  TTTGCGCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGCTCGCA  CTGAGCAGCC  TTGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGCTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGTGC  AATCGAAGAA  AACGCCACGC
851  CGCGCCGCTT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGAAT  TTTCTCGCCC  CTCGCCTCCC  TCCTGCTGCC
951  GGAAAACTAC  GCGCCGCTCC  GGT'TTACCGT  CGTATCGTGT  ATGCTGCCcg
1001  cgcTGT'TTA  CACGCTGACC  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GTCGATCGC  GCTTGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTACCGTC  CGGCGGCACG  CGCGGCGCGG
1151  CGG'TTGCCTG  TGCCGCCTCA  TTCTGGTTGT  TTTTGT'TTT  CAAGACAGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATATGCA
1251  CACAT'TGTT  TGCTGCGCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACAC
1301  CGGCAAACTA  CCCctgttt  gccggcgTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCA'TCCTGC  GCCACCGGAA  AAATTGAC  AACTGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2414; ORF 717.ng>:

g717.pep

```

1  MDTKEILGYA  AGSIGSAVLA  VIILPLLSWY  FPADDIGRIV  LMQTAAGLTV
51  SVLCGLGDOA  YVREYYAAD  KDTLEKTLFL  PLLLFSAAIA  ALLLSRPSLP
101  SEILFSLDDA  AAGIGLVLFE  LSFLPIRFL  LVLMEGRAL  AFSSAQLVPK
151  LAILLLLPLT  VGLLHFPANT  SVLTAVYALA  NLAAAELLF  QNRCRLKAVR
201  RAPFSFAVLH  RGLRYGIPLA  LSSLAYWGLA  SADRLFLKXY  AGLEQLGVYS
251  MGISFPGAAL  LLOSIFSTVW  TPYIFRAIEE  NATPARLSAT  AESAAALLAS
301  ALCLTGIFSP  LASLLLPENY  AAVRFTVWSC  MLPPLFYTLT  EISGIGLNVV
351  RKTRPIALAT  LGALANLLL  LGLAVPSGGT  RGAAVACAAS  FWLFFVFKTE
401  SSCRLWQPLK  RLPLYMHTLF  CLASSAAYTC  FGTPANYPLF  AGVWAAYLAG
451  CILRHRKNLH  KLFHYLKKQG  FPL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2415>:

m717.seq

```

1  ATGGACACAA  AAGAAATCCT  CGGCTACGCG  GCAGGCTCGA  TCGGCAGCGC
51  GGT'TTTAGCC  GTCATCATCC  TGCCGCTGCT  GTCGTGGTAT  TTCCCGCCCG
101  ACGACATCGG  GCGCATCGTG  CTGATGCAGA  CGGCGGCGGG  GCTGACGGTG
151  TCGGTGTTGT  GCCTCGGGCT  GGATCAGGCA  TACGTCCGCG  AATACTATGC
201  CACCGCCGAC  AAAGACACCT  TGTTCAAAAC  CCTGTTCTTG  CCGCCGCTGC
251  TGTCTGCCGC  CGCGATAGCC  GCCCTGCTGC  TTTCCCGCCC  GTCCCTGCCG
301  TCTGAAATCC  TGT'TTCACT  CGACGATGCC  GCCGCGGCA  TCGGGCTGGT
351  GCTGTTTGAA  CTGAGCTTCC  TGCCCATCCG  CTTTCTCTTA  CTGGT'TTTC
401  GTATGGAAGG  ACGCGCCCTT  GCCTTTTCGT  CCGCGCAACT  CGTGCCCAAG
451  CTCGCCATCC  TGCTGCTGCT  GCCGCTGACG  GTCGGGCTGC  TGCAC'TTTC
501  AGCGAACACC  GCCGTCTGA  CCGCCGTTTA  CGCGCTGGCA  AACCTTGCCG
551  CGCGCCGCTT  TTTGCTGTTT  CAAAACCGAT  GCCGTCTGAA  GGCCGTCCGG
601  CACGACCCGT  TTTGCGCCGC  CGTCTGCAC  CGGGGGCTGC  GCTACGGCAT
651  ACCGATCGCA  CTGAGCAGCA  TCGCCTATTG  GGGGCTGGCA  TCCGCCGACC
701  GTTTGTTCCT  GAAAAAATAT  GCGGGCTGG  AACAGCTCGG  CGTTTATTCG
751  ATGGGTATTT  CGTTCGGCGG  GCGGCGATTA  TTGTTCCAAA  GCATCTTTTC
801  AACGGTCTGG  ACACCGTATA  TTTTCCGCGC  AATCGAAGAA  AACGCCCCGC
851  CGCGCCGCTT  CTCGGCAACG  GCAGAATCCG  CCGCCGCCCT  GCTTGCCCTC
901  GCCCTCTGCC  TGACCGGCAT  TTTCTCGCCC  CTTGCCTCCC  TCCTGCTGCC
951  GGAAAACTAC  GCGCCGCTCC  GGT'TTATCGT  CGTATCGTGT  ATGCTGCCCG
1001  CGCTGTTTTC  CACGCTGGCG  GAAATCAGCG  GCATCGGTTT  GAACGTCGTC
1051  CGCAAAACGC  GCCCGATCGC  GCTCGCCACC  TTGGGCGCGC  TGGCGGCAAA
1101  CCTGCTGCTG  CTGGGGCTTG  CCGTCCCGTC  CGGCGGCGCG  CGCGGCGCGG
1151  CGGTTGCCTG  TGCCGCCTCA  TTCTGGCTGT  TTTTGCCTT  CAAGACCGAA
1201  AGCTCCTGCC  GCCTGTGGCA  GCCGCTCAA  CGCCTGCCGC  TTTATCTGCA
1251  CACATTGTTT  TGCTGACCT  CCTCGGCGGC  CTACACCTGC  TTCGGCACGC
1301  CGGCAAACTA  TCCCCTGTTT  GCGGGGTAT  GGGCGGCATA  TCTGGCAGGC
1351  TGCA'TCCTGC  GCCACCGGAA  AGATTGAC  AACTGTTTC  ATTATTGAA
1401  AAAACAAGGT  TTCCATTAT  GA

```

This corresponds to the amino acid sequence <SEQ ID 2416; ORF 717>:

m717.pep  
 1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV  
 51 SVLCGLGDDA YVREYYATAD KDTLFTKTLF PPLLSAAAIA ALLLSRPSLP  
 101 SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLMEGRAL AFSSAQLVPE  
 151 LAIILLLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR  
 201 HAPFSPAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS  
 251 MGISFGGAAL LFQSFSTVW TPYIFRAIEE NAPPARLSAT AESAAALLAS  
 301 ALCLTGIFSP LASLLPENY AAVRFIVVSC MLPPFLCTLA EISGIGLNVV  
 351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFAFKTE  
 401 SSCRLWQPLK RLPLYLHTLF CLTSSAAYTC FGTPANYPLF AGVWAAAYLAG  
 451 CILRHRKDLH KLFHYLKKQG FPL\*

m717/g717 96.4% identity in 473 aa overlap

	10	20	30	40	50	60
m717.pep	MDTKEILGYAAGSIGSAVLA VIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLGDDA					
g717	MDTKEILGYAAGSIGSAVLA VIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCGLGDDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m717.pep	YVREYYATADKDTLFTKTLF PPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF					
g717	YVREYYAADKDTLFTKTLF PPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m717.pep	LSFLPIRFLLLVLRMEGRALAFSSAQLVPEKLA ILLLLPLTVGLLHFPANTAVLTAVYALA					
g717	LSFLPIRFLLLVLRMEGRALAFSSAQLVPEKLA ILLLLPLTVGLLHFPANTSVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m717.pep	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
g717	NLAAAFLLFQNRCLKAVRRAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
g717	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEENAPPARLSATAESAAALLAS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m717.pep	ALCLTGIFSPLASLLPENYAAVRFIVVSCMLPPFLCTLA EISGIGLNVVRKTRPIALAT					
g717	ALCLTGIFSPLASLLPENYAAVRFIVVSCMLPPFLCTLA EISGIGLNVVRKTRPIALAT					
	310	320	330	340	350	360
	370	380	390	400	410	420
m717.pep	LGALANLLLGLAVPSGGARGA AVACAASFWLFFAFKTESSCRLWQPLKRLPLYLHTLF					
g717	LGALANLLLGLAVPSGGTRGA AVACAASFWLFFVFKTESSCRLWQPLKRLPLYMHTLF					
	370	380	390	400	410	420
	430	440	450	460	470	
m717.pep	CLTSSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLH KLFHYLKKQG FPLX					
g717	CLASSAAYTCFGTPANYPLFAGVWAAAYLAGCILRHRKDLH KLFHYLKKQG FPLX					
	430	440	450	460	470	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2417>:

a717.seq  
 1 ATGGACACAA AAGAAATCCT CGGCTACGCG GCAGGCTCGA TCGGCAGCGC  
 51 GGTTTTAGCC GTCATCATCC TGCCGCTGCT GTCGTGGTAT TTCCCTGCCG  
 101 ACGACATCGG ACGCATCGTG CTGATGCAGA CGGCGGCGG GCTGACGGTG  
 151 TCGGTGTTGT GCCTCGGGCT GGATCAGGCA TACGTCCGCG AATACTATGC  
 201 CGCCGCGGAC AAAGACACTT TGTTCAAAAC CCTGTTCTG CCGCCGCTGC

1158

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251 TGTCTGCCGC CGCGATAGCC GCCCTGCTGC TTTCCCGCCC ATCCCTGCCG
301 TCTGAAATCC TGTTTTCTGCT CGACGATGCC GCCGCCGGCA TCGGGCTGGT
351 GCTGTTTGAA CTGAGCTTCC TGCCCATCCG CTTTCTCTTA CTGGTTTTCG
401 GTATGGAAGG ACGCGCCCTT GCCTTTTCGT CCGCGCAACT CGTGCCAAG
451 CTCGCCATCC TGCTGCTGCT GCGCGTGACG GTCGGGCTGC TGCACTTTCC
501 GGCGAACACC GCCGTCCTGA CCGCCGTTTA CCGCTGGCA AACCTTGCCG
551 CCGCGCCCTT TTTGCTGTTT CAAAACCGAT GCCGCTGAA GGCCGTCGGG
601 CGCGCACCGT TTTATCCGC CGTCCTGCAT CGCGGCTGC GCTACGGCAT
651 ACCGATCGCA CTAAGCAGCA TCGCTATTG GGGGCTGGCA TCCGCCGACC
701 GTTTGTTTCT GAAAAAATAT GCCGCTTAG AACAGCTCGG CGTTTATTCG
751 ATGGGTATTT CGTTCGGCGG AGCGGCATTA TTGTTCCAAA GCATCTTTTC
801 AACGGTCTGG ACACCGTATA TTTCCGCGC AATCGAAGCA AACGCCCGGC
851 CCGCCCGCCT CTCGGCAACG GCAGAATCCG CCGCCGCCCT GCTTGCCCTC
901 GCCCTCTGCC TGACCGGCAT TTTCTGCCC CTCGCTCCC TCCTGCTGCC
951 GGAAACTAC GCCGCCGCTC GGTATATCGT CGTATCGTGT ATGCTGCCTC
1001 CGCTGTTTTG CACGCTGGTA GAAATCAGCG GCATCGGTTT GAACGTCGTC
1051 CGAAAAACAC GCCCGATCGC GCTCGCCACC TTGGGCGCGC TGGCGGCAAA
1101 CCGTCTGCTG CTGGGGCTTG CCGTACCGTC CGGCGGCGCG CGCGGCGCGG
1151 CGGTTGCTCG TGCCGCTCA TTTGCGCTGT TTTTGTGTTT CAAGACCGAA
1201 AGCTCTGCC GCCTGTGGCA GCCGCTCAA CGCCTGCCGC TTTATATGCA
1251 CACATTGTTT TGCCTGGCCT CCTCGGCGGC CTACACCTGC TTCGGCACTC
1301 CGGCAAACTA CCCCCTGTTT GCGGCGGTAT GGGCGGTATA TCTGGCAGGC
1351 TGCATCCTGC GCCACCGGAA AGATTGTCAC AAACGTGTTT ATTATTTGAA
1401 AAAACAAGGT TTCCATTAT GA

```

This corresponds to the amino acid sequence <SEQ ID 2418; ORF 717.a>:

a717.pep

```

1 MDTKEILGYA AGSIGSAVLA VIILPLLSWY FPADDIGRIV LMQTAAGLTV
51 SVLCLGLDQA YVREYYAAAD KDTLEKTLFL PPLLSAAAIA ALLLSRPSLP
101 SEILFSLDDA AAGIGLVLEF LSFLPIRFL LVLMEGRAL AFSSAQLVSK
151 LAILLLLPLT VGLLHFPANT AVLTAVYALA NLAAAFLLF QNRCRLKAVR
201 RAPFSSAVLH RGLRYGIPIA LSSIAWGLA SADRLFLKKY AGLEQLGVYS
251 MGISFGGAAL LFQSFSTVW TPYIFRAIEA NAPPARLSAT AESAAALLAS
301 ALCTGIFSP LASLLPENY AAVRFIVVSC MLPPLFCTLV EISGIGLNVV
351 RKTRPIALAT LGALANLLL LGLAVPSGGA RGAAVACAAS FWLFFVFKTE
401 SSCLRWQPLK RLPLYMHTLF CLASSAAYTC FGTPANYPLF AGVWAVYLAG
451 CILRHRKDLH KLFHYLKKQG FPL*

```

a717/m717 97.9% identity in 473 aa overlap

	10	20	30	40	50	60
a717.pep	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
m717	MDTKEILGYAAGSIGSAVLAVIILPLLSWYFPADDIGRIVLMQTAAGLTVSVLCLGLDQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a717.pep	YVREYYAAADKDTLEKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF					
m717	YVREYYATADKDTLEKTLFLPPLLSAAAIAALLLSRPSLPSEILFSLDDAAAGIGLVLEF					
	70	80	90	100	110	120
	130	140	150	160	170	180
a717.pep	LSFLPIRFLLLVLMEGRALAFSSAQLVSKLAILLLLPLTVGLLHFPANTAVLTAVYALA					
m717	LSFLPIRFLLLVLMEGRALAFSSAQLVSKLAILLLLPLTVGLLHFPANTAVLTAVYALA					
	130	140	150	160	170	180
	190	200	210	220	230	240
a717.pep	NLAAAFLLFQNRCLKAVRRAPFSSAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
m717	NLAAAFLLFQNRCLKAVRHAPFSPAVLHRLRYGIPIALSSIAWGLASADRLFLKKY					
	190	200	210	220	230	240
	250	260	270	280	290	300
a717.pep	AGLEQLGVYSMGISFGGAALLFQSFSTVWTPYIFRAIEANAPPARLSATAESAAALLAS					

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|||||
m717      AGLEQLGVYSMGISFSGGAALLFQSI FSTVWTPYIFRAIEENAPPARLSATAESAAALLAS
           250       260       270       280       290       300

           310       320       330       340       350       360
a717.pep  ALCLTGIFSPLASLLLPENYA AAVRFIVVSCMLPPLFCTLVEISGIGLNVVRKTRPIALAT
           |||||
m717      ALCLTGIFSPLASLLLPENYA AAVRFIVVSCMLPPLFCTLAEISGIGLNVVRKTRPIALAT
           310       320       330       340       350       360

           370       380       390       400       410       420
a717.pep  LGALAANLLLGLAVPSGGARGA AVACAASFVWFFVKT ESSCRLWQPLKRLPLYMHTLF
           |||||
m717      LGALAANLLLGLAVPSGGARGA AVACAASFVWFFA FKT ESSCRLWQPLKRLPLYLHTLF
           370       380       390       400       410       420

           430       440       450       460       470
a717.pep  CLASSAAYTCFGTPANYPLFAGVWAVYLAGCILRHRKDLHKL FHYLKKQGFLX
           ||:|||||
m717      CLTSSAAYTCFGTPANYPLFAGVWAAYLAGCILRHRKDLHKL FHYLKKQGFLX
           430       440       450       460       470

```

g718.seq not found yet

g718.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2419>:

```

m718.seq
1   TCAGACGGCC TTTACGTACC CCGAAACTTT ATCCACCGCC CGCAAAGCTG
51  GTTCAAATGG GACAAAGACA ACGGGCTGCT GCTGCGTACC CGCGAAAATC
101 CGGAAGGCCG AGCGTTGTGG CCGCTGGGCT GGGTCGTTCA TACCCAAAAA
151 TCGCGCAGCG TCCAGCAGGC GCGCAACGGG CTTTTCGCA CGCTTTCCTG
201 GCTGTATATG TTCAAACACT ACGCCGTCCA CGATTTTGCC GAGTTTGTG
251 AGCTGTACGG CATGCCCATC CGTATCGGCA AATACGGCGC GGGCGCAACC
301 AAAGAGGAAA AAAACACCCT GCTTCGAGCG GTGGCGGAAA TCGGTCACAA
351 CGCGGCAGGC ATCATGCCAG AAGGTATGGA AATAGAGCTC CACAACGCGG
401 CAAACGGTAC GACGGCAACC AGCAATCCGT TTTTGAGAT GGCCGACTGG
451 TCGGAAAAAT CGGCGGCGCG GCTGATTTTG GGGCAAACGC TGACCAGCGG
501 TGCGGACGGA AAATCCAGCA CCAACGCGCT GGGCAATATC CACAACGAGG
551 TACGCCGCGA TTTGCTGGTG TCGGACGCAA AACAGGTGGC GCAAACCATC
601 ACAAGCCAAA TCATCGGACC GTTCTTGCAA ATCAACTATC CCCATGCCGA
651 CCCAAACCGC GTGCCGAAAT TTGAATTGTA CACGCGCGAG CCGAAAGACA
701 TCGCGGTCTT TGCCGACGCT ATCCCGAAAC TGGTGGATGT CGGCGTACAA
751 ATCCCGAAA GCTGGGTGCG CGACAACTG GTCATTCCAG ATGTGCAGGA
801 GGGTGAGGCT GTGTTGGTGC GGCAGGTACC GGACAATCCG GTAAACAGAA
851 CTGCATTGGC GGCTTTATCC GCCCACACCG TACCATCTAA GGCTACGGGC
901 AGGCATCAGG AAATATTGGA CGGCGCGTTG GATGACGCGC TGTTGAGCC
951 CGATTTCAAT TCTCAGCTCA ACCCGATGGT GCGTCAGGCG GTTGCCGCAC
1001 TTAATGCTTG CAACAGCTAC GAGGAGGCAG ATGCCGCACT GAATGCGCTT
1051 TATCCGAATT TGGACAACGC GAAACTGCGT ACCTATATGC AGCAGGCCTT
1101 GTTTATCAGC GATATTTTGG GACAAGACCA TGCCCGCGCC TGA

```

This corresponds to the amino acid sequence <SEQ ID 2420; ORF 718>:

```

m718.pep
1   SDGLYVPRNF IHRPQSWFKW DKDNGLLLRT RENPEGEALW PLGWVVHTQK
51  SRSVQQARNG LFRTLSWLYM FKHYAVHDFE EFLELYGMPY RIGKYGAGAT
101 KEEKNTLLRA VAEIGHNAAG IMPEGMEIEL HNAANGTTAT SNPFLOMADW
151 CEKSAARLIL GQTLTSGADG KSSTNALGNI HNEVRDLIV SDAKQVAQTI
201 TSQIIGPFLQ INYPHADPNR VPKFEFDTRF PKDIAVFADA IPKLVDVGVO
251 IPESWVRDKL VIPDVQEGEA VLVQRQVDNP VNRTALAALS AHTVPSKATG
301 RHQEILDGAL DDALVEPDFN SQLNPMVRQA VAALNACNSY EEADAALNAL
351 YPNLDNAKLR TYMQQALFIS DILGQDHARA *

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2421>:



1160

## a718.seq

```

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTCGAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAT ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 GCGACGCCCG AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCCTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCTGC TTCGAGCGGT GCGGGAATC GGTCAACACG CCGCAGGCAT
801 CATTCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCCGG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTA ACCAGCGGTG CCGACGGA
951 ATCCAGCACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2422; ORF 718.a>:

## a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHFLFADI EERDS DIAAN MGTRKRALLT LNW RVAPPRN
101 ATP EEKLS D QAYEMMDSL P TLEDLIMDL M DAVGHGFSAL EWEV VFS DGL
151 YLPRNF IHRP QSWFKWDKDN GLLRLTREN P EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLLRAVAEI GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMA DWCEKS
301 AARLILQOTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGFFLQINYP HADPNRVPKF EFDTREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNR TALAALSAHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAA L NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718 98.4% identity in 380 aa overlap

	120	130	140	150	160	170
a718.pep	DSLPTLEDLIMDLMDAVGHGFSALEVEWVSDGLYLPRNF IHRPQSWFKWDKDNGLLLRT					
m718	SDGLYVPRNF IHRPQSWFKWDKDNGLLLRT					
				10	20	30
	180	190	200	210	220	230
a718.pep	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
m718	RENPEGEALWPLGWVVHTQKRSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPI					
	40	50	60	70	80	90
	240	250	260	270	280	290
a718.pep	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAA NGMTSAGNPF LQMA DW					
m718	RIGKYGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAA NGTTATSNPFLQMA DW					

1161

	100	110	120	130	140	150
	300	310	320	330	340	350
a718.pep	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLO					
m718	CEKSAARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLO					
	160	170	180	190	200	210
	360	370	380	390	400	410
a718.pep	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVIPDVQEGEA					
m718	INYPHADPNRVPKFEFDTREPKDIAVFADAI PKLVDVGVIQIPESWVRDKLVIPDVQEGEA					
	220	230	240	250	260	270
	420	430	440	450	460	470
a718.pep	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
m718	VLVRQVPDNPVNRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQA					
	280	290	300	310	320	330
	480	490	500	510	520	
a718.pep	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
m718	VAALNACNSYEEADAALNALYPNLDNAKLRTYMQQALFISDILGQDHARAX					
	340	350	360	370	380	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2423>:

m718-1.seq

```

1  ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51  CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACGGCG ACCGGTCGGG
101 TTATCGCCGA GCATCCGTCC AATTTATTA CGCCGCAAAA GATGCGGGCC
151 CTCTTCGAGG ACGCAGAAAG CGGCGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAA ATGGGGACGC
251 GCAAACGCGC GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCGCGAAAT
301 CGGACGCCCC AGAAGAAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGGTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCTACCCC GAAACTTTAT CCACCGCCCG CAAAGCTGGT TCAAATGGGA
501 CAAAGACAAC GGGCTGCTGC TCGGTACCCG CGAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGGCGC GCAACGGGCT TTTCCGCACG CTTTCTTGGC TGTATATGTT
651 CAAACACTAC GCCGTCCACG ATTTTGCCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCCCTG TTCGAGCGGT GCGGGAATC GGTCAACAAC CGGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TAGAGCTCCA CAACGCGGCA AACGGTACGA
851 CGGCAACCAG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGGCGCGGC TGATTTTGGG GCAAACGCTG ACCAGCGGTG CGGACGGAAA
951 ATCCAGCACG AACGCGCTGG GCAATATCCA CAACGAGGTA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCGCGT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCCGAAACTG GTGGATGTCG GCGTACAAAT CCCGAAAGC
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCGG CAGGTACCGG ACAATCCGGT AAACGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGCAG GCATCAGGAA
1351 ATATTGGACG GCGCGTTTGA TGACGCGCTG GTTGAGCCCG ATTTCATTC
1401 TCAGCTCAAC CCGATGCTGC GTCAGGCGGT TGCCGCACCT AATGCTTGCA
1451 ACAGCTACGA GGAGGCAGAT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCCTTGT TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2424; ORF 718-1>:

m718-1.pep.

```

1  MEPIMAKKNN KTKIQPEAA LQDVAQITA TGRVIAEHPS NFITPQKMRA
51  LFEDAESGDI RAQHLEFADI EERDSIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEEKLS QAYEMMDSL P TLEDLINDLM DAVGHGFSAL EWEVVFSDGL
151 YLPRNFIHRP QSWFKWDRDN GLLLRTRNRP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRLRAVAEI GHNAAGIMPE GMEIELHNA NGTTATSNPF LQADWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEV RRDLLVSDAK QVAQTITSQI

```

```

351 IGPFLQINYP HADPNRVKPF EFDTPREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2425>:

a718.seq

```

1 ATGGAGCCGA TAATGGCAAA AAAGAACAAT AAAACTAAAA TCCAAAAGCC
51 CGAAGCTGCA TTGCAGACGG ACGTGGCTCA AATTACAGCG ACCGGTGCAG
101 TTATCGCCGA GCATCCATCC AATTTTATTA CGCCGCAAAA GATGCGCGCC
151 CTCTTCGAGG ACGCAGAAAG CGGTGACATC CGCGCCCAAC ACGAGCTTTT
201 CGCGGACATT GAGGAGCGCG ACAGCGACAT CGCGGCAAAAT ATGGGGACGC
251 GCAACGCGCG GCTGCTGACG CTCAACTGGC GCGTCGCCCC GCCCGGAAAT
301 GCGACGCCCC AAGAAGAAAA GCTGTCCGAC CAAGCCTACG AAATGATGGA
351 CAGCCTGCCT ACCCTCGAAG ACCTGATTAT GGATTGTATG GACGCGGTAG
401 GGCACGGATT TTCTGCGTTG GAGTTCGAGT GGGTATTTTC AGACGGCCTT
451 TACCT'ACCCC GAAACTTTAT CCACGCCCCG CAAAGCTGGT TCAATATGGG
501 CAAAGACAAC GGGCTGCTGC TGCATACCCG CGAAATCCG GAAGGCGAAG
551 CGTTGTGGCC GCTGGGCTGG GTCGTTTATA CCCAAAAATC GCGCAGCGTC
601 CAGCAGCGCG GCACGCGGCT TTTCCGACG CTTTCTCTGGC TGTATATGTT
651 CAAACACTAC CCGTCCACG ATTTTGCGA GTTTTGGAG CTGTACGGCA
701 TGCCCATCCG TATCGGCAAA TACGGCGCGG GCGCAACCAA AGAGGAAAAA
751 AACACCTGCG TTCGAGCGGT GGCAGAAATC GGTCAACAAC GCGCAGGCAT
801 CATGCCAGAA GGTATGGAAA TCGAGCTGCA CAACGCGGCA AACGGCATGA
851 CTTCCGCGCG CAATCCGTTT TTGCAGATGG CCGACTGGTG CGAAAAATCG
901 GCGCGCGCGG TGATTTTGGG GCAAACGCTA ACCAGCGGTG CGGACGGAAA
951 ATCCAGTACC AACGCGCTGG GCAATATCCA CAACGAGATA CGCCGCGATT
1001 TGCTGGTGTC GGACGCAAAA CAGGTGGCGC AAACCATCAC AAGCCAAATC
1051 ATCGGACCGT TCCTGCAAAAT CAACTATCCC CATGCCGACC CAAACCCGCT
1101 GCCGAAATTT GAATTTGACA CGCGCGAGCC GAAAGACATC GCGGTCTTTG
1151 CCGACGCTAT CCGGAAACTG GTGGATGTCG GCGTACAAAT CCCCAGAAAG
1201 TGGGTGCGCG ACAAACTGGT CATTCCAGAT GTGCAGGAGG GTGAGGCTGT
1251 GTTGGTGCAG CAGGTACCGG ACAATCCGGT AAACAGAACT GCATTGGCGG
1301 CTTTATCCGC CCACACCGTA CCATCTAAGG CTACGGGACG GCATCAGGAA
1351 ATATTGGACG GCGCGTTGGA TGACGCGCTG GTTGAGCCCG ATTTCAATTC
1401 TCAGCTCAAC CCGATGGTGC GTCAGGCGGT TGCCGCACTT AATGCTTGCA
1451 ACAGCTACGA GGAGGCGAGT GCCGCACTGA ATGCGCTTTA TCCGAATTTG
1501 GACAACGCGA AACTGCGTAC CTATATGCAG CAGGCTTGTG TTATCAGCGA
1551 TATTTTGGGA CAAGACCATG CCCGCGCCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2426; ORF 718-1.a>:

a718.pep

```

1 MEPIMAKKNN KTKIQKPEAA LQTDVAQITA TGRVIAEHPS NFITPQKMRA
51 LFEDAESGDI RAQHELFAEI EERDSIDIAAN MGTRKRALLT LNWRVAPPRN
101 ATPEEEKLSD QAYEMMDSLP TLEDLIMDLN DAVGHGFSAL EVEWVFSDDL
151 YLPRNFIHRP QSWFKWDKDN GLLLTRENTP EGEALWPLGW VVHTQKRSRV
201 QQARNGLFRT LSWLYMFKHY AVHDFAEFLE LYGMPIRIGK YGAGATKEEK
251 NTLRAVAEII GHNAAGIMPE GMEIELHNAA NGMTSAGNPF LQMDWCEKS
301 AARLILGQTL TSGADGKSST NALGNIHNEI RRDLLVSDAK QVAQTITSQI
351 IGPFLQINYP HADPNRVKPF EFDTPREPKDI AVFADAIPKL VDVGVQIPES
401 WVRDKLVIPD VQEGEAVLVR QVPDNPVNRT ALAALSHTV PSKATGRHQE
451 ILDGALDDAL VEPDFNSQLN PMVRQAVAAAL NACNSYEEAD AALNALYPNL
501 DNAKLRTYMQ QALFISDILG QDHARA*

```

a718/m718-1 99.0% identity in 526 aa overlap

	10	20	30	40	50	60
a718.pep	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRA					
m718-1	MEPIMAKKNNKTKIQKPEAALQTDVAQITATGRVIAEHPSNFITPQKMRA					
	10	20	30	40	50	60
a718.pep	RAQHELFAEIERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
m718-1	RAQHELFAEIERDSIDIAANMGTRKRALLTLNWRVAPPRNATPEEEKLSDQAYEMMDSLP					
	70	80	90	100	110	120
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
	130	140	150	160	170	180
a718.pep	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					
m718-1	TLEDLIMDLMDAVGHGFSALEVEWVFSDDLGLYLPRNFIHRPQSWFKWDKDNGLLLRTRENTP					

a718.pep	190	200	210	220	230	240
	EGEALWPLGWVVHTQKSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
m718-1	EGEALWPLGWVVHTQKSRVQQARNGLFRTLSWLYMFKHYAVHDFAEFLELYGMPIRIGK					
	190	200	210	220	230	240
a718.pep	250	260	270	280	290	300
	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGMTSAGNPFLQMAWCEKS					
m718-1	YGAGATKEEKNTLLRAVAEIGHNAAGIMPEGMEIELHNAANGTTATSNNPFLQMAWCEKS					
	250	260	270	280	290	300
a718.pep	310	320	330	340	350	360
	AARLILGQTLTSGADGKSSTNALGNIHNEIRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
m718-1	AARLILGQTLTSGADGKSSTNALGNIHNEVRRDLLVSDAKQVAQTITSQIIGPFLQINYP					
	310	320	330	340	350	360
a718.pep	370	380	390	400	410	420
	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEAVLVR					
m718-1	HADPNRVPKFEFDTREPKDIAVFADAIPKLVDPVGVQIPESWVRDKLVIPDVQEGEAVLVR					
	370	380	390	400	410	420
a718.pep	430	440	450	460	470	480
	QVPDPNPVRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
m718-1	QVPDPNPVRTALAALSAHTVPSKATGRHQEILDGALDDALVEPDFNSQLNPMVRQAVAAL					
	430	440	450	460	470	480
a718.pep	490	500	510	520		
	NACNSYEEADAALNALYPNLDNAKLRITYMQQALFISDILGQDHARAX					
m718-1	NACNSYEEADAALNALYPNLDNAKLRITYMQQALFISDILGQDHARAX					
	490	500	510	520		

g719.seq not found yet

g719.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2427>:

m719.seq

```

1  ATGGCAAACG GGAACATGAA ACTGTCGTTG GTGTTAACCG CCCGAGATGA
51  CGGAGCGAGA CGGCTACTGG CTGATACTCA ACGACAATTA GATCGTACCG
101 CGAATCGCGG GCGCAACTT GAACGGCAAA GCCATACTTA TGCCTTGACC
151 GGCATCCGCT CAGAAAAACA GATTCAACGC GAAATCATGC TGACACAGGC
201 TGCCTTTAAC CGTTTGCGCG GCAGCGGCAA GGCATCACAA AATGATTTGG
251 CACGGGCGGC GGTGCTACG CGTAACCGAA TTCGCGAGCT GAACCGGAA
301 CTGAAACAGG GCACGGGATT TGGCGACAAG ATGGGAAAAA TCGGAAGATT
351 CGGTGCAGCT GCGGTGGCTG GTGGCGCGGC AGCGTATACG GTGCTTAAGC
401 CTGCTATGGA CAACAGAAAG CAGCTTGATG AGAACATCAA CCGCGTGTCC
451 AGACAGGCAT TTATTGAGGA TAACAGTAAA TCGGCAGCGT GGATTGCAAC
501 TGAAGGTGCG CAACAGATCA AGGATTTGGC ACTTGAACCT GTCGAGAAAA
551 ATGGCGGGAC CCACGATAAG GCTTTGGATT TAATCAGCGG CATGATGACC
601 ACCGGTCTGA ATTTTGCCCA AACCAAGAAT GAAGCGCAGG CGGCATATGC
651 TTTTGCACCT GCCTCAGAAG GCAGTGGCGA GGATACGGCA AAACCTGATTA
701 AAACCTTGAA AGATGGCGGC ATGAGCGGTA AAGACCTGCA ACTCGGGCTT
751 GAGCACGTCT TGCAATCGGG TTTAGACGGC ACTTTCAGAG TCGGGGATAT
801 GGTTCGGGAG CTGCCGAGCC TGCTCTCTGC CGCGCAACAG GCAGGGATGA
851 ATGTGTCTCG CGGTTTGAC TACCTGCTCT CACTCTTACA ATCTGCGGCG
901 AATAAATCGG GCAGTCTGCT CGAAGCGGCG ACTAATGTGC AAAATCTTTT
951 GAGTAAAACT CTGTCGCTCT ACACGATAGG TCGTCTGAAG AAGATGGCAA
1001 ATCCGAATGA CCCGAAGAAA GGTGTCGATT GGATAGGCTC GGTGTGCGAA
1051 GGCAAGCAAA ACGGCGAAAA CGCAGTGCAG GTGTTGTCCT GTCTTGCCGA
1101 TGCCATGCTA GTAAAGGATA AGCAATACCA AGATTATAAG AAACGCGCGG
1151 CTGCAGGCGA TAAGACGGCG GCGGAGCAGG CAAATATGCT TAAGGCGCGC
1201 CTTTGGCGC AACTGCTGCC TGATTGTCAG GCAAAACAAG GTTTGCTGGC
1251 TGCAACGGAT ATGACGCAAA TCCGTGAATA TATGGCTTCG TTGGCTGGCG

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1164

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1301 TAACGTTGGA TAACGGAAAA ATTGCTAAGA ACAACGAGGC GCGAATGTTG
1351 TCGGCAGCGG CGCAACAAGA GCAACAGGAA TCGCTGGCAA TGTTGCGGGA
1401 AAGTCTGACG GGAACATTGG TGGATATGGA AACCTCGTTT AAAAAGCTGG
1451 CAGCGGAATA CCCTAATGCC ACTCTAGCCC TGCAAGCATT GACGACGGCG
1501 GCAACAGCGG CGTCTGCCGC AATGTTATTA ACCGCCGGTG GCGGTAAAGG
1551 TGCAGGCTTT CTGAAAGATG TAGGTAGTAA AGCGTTGGGA TGGGGTAAGG
1601 CTTCCGCAGG CGGCGTGGCA GCAGGTGCCA CAGCGGCAGG CGGTAAGTTG
1651 CTGTCATGGG GAAAATCTGC CGGTAGCGGG CTCATGAATA ATCCAGCGTT
1701 AGTTAAACGG GCGGGTTTGT TAGGTATGTT GCTGTATTCC GAGTCTTTGG
1751 GTGACGGCAC ATTGCCAAAG GGTTCGCGTG GTACCAAGAC AACTCCTGAA
1801 ATGATTAATC GTCTGAAAA CAACGGTATC CGATTGAAC CTGCGCCGAA
1851 GCGGGAACAG GCGCGGGGTG GTGTCCCTCA GTATTGGCT GTCCTGTCAG
1901 CGCAGCCTAC CGATAAGATG TTGTCTCCGT TGTTTTCAAC TCAGACGGCG
1951 GCGTATCAGG CAGCCATTCA GCAGCAGACG GCGGCGTATC AGGCAGCATT
2001 GCGCGAGGAT ACGGCTGCAG TTACAACAGG TTTGGCACAA GTGCAAAATG
2051 CGATGGCGTC GGCAAGTCAG ACCATCAATA CCAATGTGAG CCTGAATATC
2101 GACGGACGTG TTATCGCGAA TGAGGTATCG CCGTATCAAG TGGCCATGTT
2151 CCGCCGTGGA GCGGGTCAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2428; ORF 719>:

m719.pap

```

1 MANGNMKLSL VLTARDDGAR RLLADTQRQL DRTAKSRAQL ERQSHTYALT
51 GIRSEKQIQR EIMLTQAAFN RLARSGKASQ NDLARAATVAT RNRIRELNAE
101 LKQGTGFADK MGKIGRFGAA AVAGGAAAYT VLKPPAMDNRK QLDENINRVS
151 RQAFIEDNSK SAAWIATEGA QQIKDLALEL VEKNGGTHDK ALDLISGMMT
201 TGLNFAQTKN EAQAAYAFAL ASEGSGEDTA KLIKTLKDG MSKDLQLGL
251 EHVLSGLDGF TFEVRDMVRE LPSLLSAAQQ AGMNGVGGLD YLLSLLQSA
301 NKSGPSAEAA TNVQNLLSKT LSPDTIGRLK KMANPNDPKK GVDWIGSVVQ
351 GKQNGENAVQ VLSRLADAML VKDKQYQDYK KRAAAGDKTA AEQANMLKGA
401 LLAQLLPDLQ AKQGLLAATD MTQIREYMAS LAGVTLDNKG IAKNNEARML
451 SAAQQEQQE SLAMLRSLT GTLVDMETSF KKLAEYPNA TLALQALTTA
501 ATAASAAMLL TAGGGKGAGF LKDVGSKALG WGKASAGGVA AGATAAGGKL
551 LSWGKSAGSG LMNPNALVKR AGLLGMLLYS ESLGDGTLPK GLRGTKTTPE
601 MINRLKNNGI RFEPAPKREQ ARGGVPOYLA APSAQPTDKM LSPLFSTQTA
651 AYQAAIQQT AAYQAALAQD TAAVTGLAQ VQSAMASASQ TINTNVSLNI
701 DGRVIANEVS RYQVAMFGRG AGQ*

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a719.seq not found yet

a719.pap not found yet

g720.seq not found yet

g720.pap not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2429>:

m720.seq

```

1 ATGAGCGGAT GGCATACCTT ATTGCAGGAC GCATCTTACA AGGGCGTCCG
51 CTTTGATATT GAGGTGGTGG ACGAGAGCAA CGGCAAGGCA TTGGCCGAGC
101 ATGCGCGGCC GTTGTGTCAG GGTATCGACC TTGAAGACAT GGGCATGACC
151 GGGCGGCAGG TGCAGATTAA TGCGGTGTTT TGGGGCAAGG GCTATGCAGG
201 CCGTCTGAAA AAGCTGCTGG ATGCGCTGGA GCAGCCGGGC GCGCGCTGC
251 TGGTGACCCC TGTTGGGGGG CGGATGCACA ACATGATTGC GGCATCATGG
301 AGTTACCGAC ATGAGGCCGA TTATGTGGAT TATGCGGGCA TCGATATTAC
351 TTTCCGCGAG GCGGCCGAAG CGCAGGAAAT CTTTGTTTT GAAAACGCCT
401 TTTGGTCTGA GCTTGAGGCG TTGATTGCTA ATATCGACAC CTACCGCGAG
451 GCGGCTATCG GCTTTGTTGA TGCGGTGTTG GCGGTGGATG CCGGCGTATC
501 AGCTTTATGG GGCAGCGCGC TGGGCATTG GAGTGGCGCA TCGGTACGT
551 TTGGCGCGGT GCGCCGTTTG TTTGATTGG ACAAAATTGC CTTTCCCGAT
601 CGGGGCGGAT ACGTGCAGC GCGGTTTAAA AACGGCTCGG CCAAGCTGTT
651 TCGGGATATA TCGGTATGAG TAGATACTGG CATACGCCGT GAGGCGGGTT
701 TGGCCGATAA TGCCATGCAC CATGCCGTT GGTCCGCGC ACAGCGGTTT
751 GACGGGGCTG CGGCTGTTGC CGACCGGCC GCGCTATCC CTGATAATTT
801 GCTGACCGGC CGCTTTTCAG ACGGCCTGCA AAACCGCCTG AACCGGTAA

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1165

```

851 CCGCCAAACA GGTGCAGCCG GTAGCGCAGG CGGTGCGCCT GTTATCCACG
901 TCATCGCTGT TGTGCGGTGGC AACGGCATTG ATCGAGGCGC ATGGCGGAAGA
951 GATGACCGCG CCCGATTGTA TTGAGGTTAA CCGCGCCATG CGCCGCCGTA
1001 TGCAGGCCGA GATTGCCGCC TTGCGGGCGG TGCAGACGGC TGCTGCCGAG
1051 TCTGGTGGGC TGACGGCCAA CGCCGTGTAT ACCGAGGCTT ACCAAACGGC
1101 AGAATCCCTG CGCGCGGCGG CAGGCCGTCT GAATGCGTTG GTTGCGGCGG
1151 TCATCAACCA AAAGCCGCGC CTGATTGTGC GCCAAGCCCC AATCGACGGT
1201 ACGATACACC AAATCGCCCA CGAGTTTAC GCGGATATAG CCCGCGCAGC
1251 AGAGCTGGTG CGGCTCAATC CCCATATCCA CCACCCGCG TTTATCAAGC
1301 GCGGCACTTT GGTCAACAGC TATGCAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2430; ORF 720>:

```

m720.pep
1 MSGWHTLLQD ASYKGVGFDI EVVDESNGKA LAEHARPFVQ GIDLEDMGMT
51 GRQVQINAVF WGKGYAGRLK KLLDALEQPG GGVLVHPVWG RMHNMIAASW
101 SYRHEADYVD YAGIDITFRE AAEAQEIFVF ENAFLEVELEA LIANIDTYRE
151 AAIGFVDAVL AVDAGVSALW GSALGIWSAA SGTFGAVRRL FDLDKIAFPD
201 RGGYSAAAFK NGSAKLFADI SVMVDTGIRR EAGLADNAMH HAGWSPQRQF
251 DGAAAVADRA AAIPDNLLTG RFSDDLQNLRL NRLTAKQVOP VAQAVRLLST
301 SLLSVATAL IEAHGEEMTA PDLIEVNRAM RRRMQAEIAA LRAVQTAAAE
351 SGLTANAVY TEAYQTAESE RAAAGRLNAL VAAVINQKPP LIVRQAPIDG
401 TIHQIAHEFY GDIARAAELV RLNPHIHHPA FIKRGTLVNS YAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2431>:

```

a720.seq (partial)
1 GGCCTGCAAA ACCGCCTGAA CCGGTTAACC GCCAAACAGG TGCAGCCCGT
51 AGCGCAGGCG GTGCGCCTGT TATCCACGTC ATCGCTGTTG TCGGTGGCAA
101 CGGCATTAAT CGAGGCGCAT GCGGAAGAGA TGACCGCGCC CGATTGTATT
151 GAGGTTAACC GCGCCATGCG CCGCCGTATG CAGGCCGAGA TTGCCGCCTT
201 ACGGGCGGTG CAGACGGCTG CTGCCGAGTC TGGTGGGCTG ACGGCCAACG
251 CCGTGTATAC CGAGGCTTAC CAAACGGCAG AATCCCTGCG CGCGGCGCA
301 GGCCGTCTGA ATGCGTTGGT TCGGGCGGTC ATCAACCAAA AGCCGCGGCT
351 GATTGTGCGC CAAGCCCCAA TCGACGGTAC GATACACCAA ATCGCCACG
401 AGTTTTACGG CGATATAGCC CGCGCAGCAG AGCTGGTGCG GCTCAATCCC
451 CATATCCACC ACCCGCGGTT TATCAAGCGC GGCACCTTGG TCAACAGCTA
501 TGCAAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2432; ORF 720.a>:

```

a720.pep (partial)
1 GLQNLRLNLT AKQVQVPAQA VRLSTSSLL SVATALIEAH GEEMTAPDLI
51 EVNRAMRRRM QAEIAALRAV QTAAESGGL TANAVYTEAY QTAESELRAA
101 GRNLALVAHV INQKPLIVR QAPIDGTIHQ IAHEFYGDIA RAAELVRLNP
151 HHHHPAFIKR GTLVNSYAK*

```

m720 / a720 100.0% identity in 169 aa overlap

```

250 260 270 280 290 300
m720.pep SPRQRFDGAAAVADRAAAIPDNLLTGRFSDGLQNLRLNLTAKQVQVPAQAVRLLSTSSLL
a720 GLQNLRLNLTAKQVQVPAQAVRLLSTSSLL
10 20 30

310 320 330 340 350 360
m720.pep SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
a720 SVATALIEAHGEEMTAPDLIEVNRAMRRRMQAEIAALRAVQTAAESGGLTANAVYTEAY
40 50 60 70 80 90

370 380 390 400 410 420
m720.pep QTAESELRAAAGRLNALVAHVINQKPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
a720 QTAESELRAAAGRLNALVAHVINQKPLIVRQAPIDGTIHQIAHEFYGDIAARAAELVRLNP
100 110 120 130 140 150

430 440
m720.pep HHHHPAFIKRGTLVNSYAKX

```

a720  
 |||||  
 HIHHPAFIKRGTLVNSYAKX  
 160 170

g721.seq not found

g721.pap not found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2433>:

m721.seq  
 1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT  
 51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG  
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
 201 TGTCGATTAT GAACACCAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA  
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG  
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT  
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GACCTGCCTG  
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGAAGCC  
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA  
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
 701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCAA  
 851 AAGGCGTATT GAAACAGCCG GCGCGCTTGG CATTTTGTAC CGGCTTTATT  
 901 GAAAACGCCC AGCCGGTCCG TGCACTGGCA GGCTCGCAAA CGGGCGGCAA  
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG  
 1001 CAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC  
 1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2434; ORF 721&gt;:

m721.pap  
 1 MSKNAQKILL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAYLLEE  
 51 NGHDVALLAN SSRNQLVVDY EHQTLYKEKN GQPAPAGWM RWLEFTPKGM  
 101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG  
 151 MDEVLAASA QILKPETEQN PMKELLQOLF DLPDAGEEEL KAALSALVEA  
 201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLTXYAPI SVVQELQSKV  
 251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAKGVLRQP GGLAFLTGFI  
 301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES  
 351 EGK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2435>:

a721.seq  
 1 ATGTCCAAAA ATGCACAAAA AACCTACTT GCCGTGTGCA GTTTCGAGGT  
 51 GCAGCCAAAA GACGGGCGAA TCCAACCTGCT GCCATATGGC GAATTTTCGCG  
 101 CAGTAGACGG TCGTCCGACT GATGTCCCTG CGTGGTATCT GACCGAAGAA  
 151 AACGGTCATG ATGTCGCGTT GTTGGCCAAC AGCTCGCGCA ATCAGTTGGT  
 201 TGTCGATTAT GAACACTAGA CGCTCTACAA AGAGAAAAAC GGACAACCTG  
 251 CACCTGCCGC CGGTTGGATG CGTTGGCTGG AGTTCACGCC TAAAGGCATG  
 301 TTTGCCGAAG TGGAGTGGAC GGACAAGGCG GCTGCGGCAA TTGCCGCAAA  
 351 AGAGTATCGC TACATCTCTG CTGTGTTTTC CTATGACACA AAGGGATATG  
 401 TAAGCAAAAT TTTTCACGCC GCGCTGACAA ATTTCCCCGC GTTGGACGGT  
 451 ATGGACGAGG TGCTGGCGGC AGCGTCGGCG CAAATTTTAA AACCGGAAAC  
 501 GGAGCAAAAC CCTATGAAAG AGTTGTTACA GCAACTGTTC GGTCTGCCTG  
 551 ATGCGGGCGA AGAAGAACTG AAGGCGGCAT TGTCCGCGCT CGTGAAGCC  
 601 AAGCCGAAAG ACGTGGCATT GTCTGCCGAC GTGTTTCGCGC AGCTGGCGGA  
 651 AAAAGACAGC CGCATCGCGG CATTGACGGC GCAAACCGCC AAGCCTGATT  
 701 TGACTAAATA CGCGCCTATC TCAGTGGTTC AAGAGCTGCA AAGCAAAGTC  
 751 GCCGCGCTGA CTGCCAAGCA GGAAGCAGAC AAAGGCAACG AATTGATTAC  
 801 CGCCGCGCTG ACTTCAGGCA AATTGCTGCC TGCTCAGAAG GAGTGGGCGA  
 851 AAGGCGTATT GAAACAGCCG GCGCGCTTGG CATTTTGTAC CGGCTTTATT  
 901 GAAAACGCCC AGCCGGTCCG TGCACTGGCA GGCTCGCAAA CGGGCGGTAA  
 951 AGCACCCGAC GAACGCGTCG CCGCACTGAC TGCGGAAGAG GCAGCCGCAG  
 1001 CAAAATGCT GGGCATGTCC GGCGAAGAAT TTGTAAAAAT CAAAGAAAGC

1167

1051 GAAGGTAAGT AA

This corresponds to the amino acid sequence &lt;SEQ ID 2436; ORF 721.a&gt;:

a721.pep

```

1  MSKNAQKTL AVCSFEVQPK DGRIQLLPYG EFRAVDGRPT DVPAWYLTEE
51  NGHDVALLAN SSRNQLVVDY EH*TLYKEKN GQPAPAAGWM RWLEFTPKGM
101 FAEVEWTDKA AAAIAAKEYR YISAVFSYDT KGYVSKIFHA ALTNFPALDG
151 MDEVLAASA QILKPETEON PMKELLQOLF GLPDAGEEEL KAALSALVEA
201 KPKDVALSAD VFAQLAEKDS RIAALTAQTA KPDLT KYAPI SVVQELQSKV
251 AALTAKQEAD KGNELITAAL TSGKLLPAQK EWAEGVLKQP GGLAFLTGFI
301 ENAQPVAAAL GSQTGGKAPD ERVAALTAEE AAAAKMLGMS GEEFVKIKES
351 EGK*

```

a721/m721 99.2% identity in 353 aa overlap

	10	20	30	40	50	60
a721.pep	MSKNAQKTLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
m721	MSKNAQKTLAVCSFEVQPKDGRIQLLPYGEFRAVDGRPTDVPAWYLTEENGHDVALLAN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a721.pep	SSRNQLVVDYEHXTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
m721	SSRNQLVVDYEHQTLYKEKNGQPAPAAGWMRWLEFTPKGMFAEVEWTDKAAAAIAAKEYR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a721.pep	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
m721	YISAVFSYDTKGYVSKIFHAALTNFPALDGMDEVLAASAQILKPETEONPMKELLQOLF					
	130	140	150	160	170	180
	190	200	210	220	230	240
a721.pep	GLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
m721	DLPDAGEEELKAALSALVEAKPKDVALSADVFAQLAEKDSRIAALTAQTAKPDLTKYAPI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a721.pep	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAGVLKQPGGLAFLTGFI					
m721	SVVQELQSKVAALTAKQEADKGNELITAALTSGKLLPAQKEWAGVLKQPGGLAFLTGFI					
	250	260	270	280	290	300
	310	320	330	340	350	
a721.pep	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESEGGKX					
m721	ENAPVAAALAGSQTGGKAPDERVAALTAEEAAAAAKMLGMSGEEFVKIKESEGGKX					
	310	320	330	340	350	

g722.seq not found yet

g722.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2437>:

m722.seq

```

1  GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51  TACCAAAGC CTGTGCGCGG ATGCCGATAT CAGCCCCGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCGCAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCTT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCTCCA TCGCGGCTT GAGCCGCGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGACCTGC AAGTGCATAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG

```



1168

```

401 AGCCGGGCGC GGCCGCCAAT GTGGGCGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGGCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG TCGTCGGAAG
701 AAACGTGCGC CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GTATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCTGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCGCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2438; ORF 722>:

m722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLSRR NPTTASGTLT VSGIAQSMLS
101 DDLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VGDGEAQLMA
151 APAGVATECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAIV YPLRRGLGTG DIAITSADGV SSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDRR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2439>:

a722.seq

```

1 GTGTTTGAAA CGCCGACATT TGAGCAAATC CGCGAGCGTA TCCTGCGCGA
51 TACCAAAAGC CTGTGGCCCG ATGCCGATAT CAGCCCGGAC AGCGACCATT
101 ATGTGCACGC CAGCCGTTTG GCCAGCTGCG CCGAAGGGCA ATATGCCGAT
151 CAAAGCTGGA TTGTGCGGCA GATTTTCCCT GATACCGCCG ACCGCGAGTA
201 TTTGGAGCGG CATGCCCTCA TCGCGGGCTT GCGCCGCGGC AATCCTACCA
251 CGGCCAGCGG CACGCTGACC GTAAGCGGTA TTGCGCAATC CATGCTTTCA
301 GACGCGCTGC AAGTGCGTAT CGGCCAGCGT TTTTACCGCA CTACCGCCCG
351 CGCCGTTATC GGCAGCGGCG GCACGGCGGA AATACCGGCA ATCGCCGACG
401 AGCCGGGCGC GGCCGCCAAT GTGCGGACG GCGAGGCGCA ACTGATGGCC
451 GCCCCGCGCG GTGTGTCCAC CGAATGCCGC CTTACCGTAC AAGGCGGCAC
501 CGACCGAGAA AGCGATGCCT CACTGCTGGC GCGTCTGTTG GAAATCATCC
551 GCCGACCGCC CGCAGGCGGC AACCCTTACG ACTATAAAAA CTGGGCGTTG
601 AGTGTGACG GCGTAACCAG CGCATATGTT TATCCGCTGC GCCGCGGCTT
651 GGGTACGGTG GATATTGCCA TTACCTCCGC CGACGGTGTG CCATCGGAAG
701 AAACGTGCGC CCGCGTACAG GCTTATATCG ACGAGATGCG CCCGGTAACG
751 GCAAAAAATG CGCTGGTACT CAAGCCAACC GTAACGGCGG TGCCTGTTAC
801 CGTGCAAGTC AAGCTCGACG GCATCGACTT GGACGAGGCC AAGCGCCGCA
851 TACGGACGGC CCTAAAAGAA TATTTCGACA CCCTGATCCC CGGCGACGGC
901 CTGACTGTGT CGCAAATCGA GGCGGCTATC AGCAATGTGG ATGGTGTGAT
951 CGACCTCCGT CTGACTGCGC CGACGGCCAA CCGTGCCGCC GATACGGTTA
1001 ACCGCATCGA GTGGTTTAAA GCGGGCGCGA TTAATGTAAC GGAGATGCCG
1051 TCATGA

```

This corresponds to the amino acid sequence <SEQ ID 2440; ORF 722.a>:

a722.pep

```

1 VFETPTFEQI RERILRDTKS LWPADISPD SDHYVHASRL ASCAEGQYAH
51 QSWIVRQIFP DTADREYLER HASMRGLRRR NPTTASGTLT VSGIAQSMLS
101 DGLQVRIGQR FYRTTARAVI GSGGTAEIPA IADEPGAAAN VRDGEAQLMA
151 APAGVSTECR LTVQGGTDRE SDASLLARLL EIIRRPAGG NRYDYKNWAL
201 SVDGVTSAIV YPLRRGLGTG DIAITSADGV PSEETVRRVQ AYIDEMRPVT
251 AKNALVLKPT VTAVPVTQV KLDGIDLDEA KRRIRTALKE YFDTLIPGDG
301 LTVSQIEAAI SNVDGVIDLR LTAPTANRAA DTVNRIEWFK AGAINVTEMP
351 S*

```

g723.seq not found yet

g723.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2441>:

m723.seq

```

1  ATGCGACCCA AGCCCCGTTT CAGACGGTCT GTTATCGCTT GCTCAATATC
51  AGTGATCACG CCCGAACACC TTATTTTAC  CGTTTACAAA CACAATACCG
101 TCTTCGCCCC CGGCCACTTC TTCGCCGCTA TCATCCACGC CCAGCTGCAC
151 TTCGCCTTTG GCCATAGCAC GCAGCAGGTC GAGCACGTCG ATTTGTAGC
201 GGTTCGGGAT TTCGTCGGTA ATCAACACGC CCTGAGCCGC CGTCAGACGG
251 TAGCGGGCAA TGTCGCAGCA AAGGCGCACC AAGATGGGCG GCAGATCCTC
301 AAAAGGTCGT CTGAACCGCC CCAGATACGC GTCGATTTCG GCAGTGGCGT
351 CCACCAGCGC GGTTCGTGCG ACCTCGCGGT CAATCAGCCC CTCGTTGTTG
401 CGGTGCGTGA GCTGCAAGAC TTCCAGCTCA CCGAAACGCG CAACCATATC
451 CTAACCGTTC GCGTATGCCA TTAATCGACC GCCTTGCCTT GCAGCATAGG
501 CTCGGCGCAG ATTGCCTTCC ACACCGCTTC GCCGACTTCG GCGCGCTTCA
551 CTTGCGGCCA GCCGCCGTC AACAGCAGGC CGCCGCGCCA AAATTCTTTG
601 CCGTCTGCGC CGGTACTGAC GAGCATCACA TCGCGGCTGT CCGCCAAAGC
651 GTCGGCGGCA CGTTGCGTAT GCTGCACTTT GAGTTCGGCA AGTTCGGCGG
701 ACAGTGCCTT TTTGTCGTCT TCGGCTTTTT CCAAGGCTGT GGTCAGCATT
751 TCGACATCGT TTCGGGCGGC GGCAAGCTCT GCCTGCACGG CGTCCAATTC
801 GGCTTTGATG TCTTCAAACG ACGGGGCGGC GGTTCGGCG GTTTCTGGTT
851 TGTGTTGGT TTTTGCCATG ATGACTCCTT GTTTCAGACG GCGGCGGATT
901 CGCATTGGA

```

This corresponds to the amino acid sequence <SEQ ID 2442; ORF 723>:

m723.pep

```

1  MRPKPRFRRS VIACISVIT PEHLIFTVYK HNTVFARGHF FAIIHAQLH
51  FAFGHSTQOV EHVDFVAVAD FVGNQHALSR RQTVAGNVAA KAHQDGRQIL
101 KRSSEPPQIR VDFGSGVHOR GLCDLAVNQP LVVAVGELQD FOLTETRNHI
151 LNRRVCHYST ALRCSIGSAQ IAFHTASPTS ARFTSRQPPS NSRPPRQNSL
201 PSAPVLTSIT SRLSAKASAA RCVCTLSSA SSADSAFLSS SAFSKAVVSI
251 STSFRAAASS ACTASNSALM SSNDGA AVSA VSGLLLVFAM MTPCFRRRRI
301 RI*

```

a723.seq not found yet

a723.pep not found yet

g724.seq not found yet

g724.pep not found yet

The following partial DNA sequence, shown with its encoded amino acid sequence, was identified in *N. meningitidis* <SEQ ID 2443>:

m724.map

```

ATGAGTTTGAGTAAATTGGCGAAAAAACCGGCACAACTGCTAAAAATATCGGCGAAACC
1  -----+-----+-----+-----+-----+-----+-----+ 60
TACTCAAACCTCATTTAACCCTTTTTTTGCGGTGTTGACGATTTTTATAGCCGCTTTGG
a  M S L S K L A K K T A Q T A K N I G E T -
CTGCGCGCGGCCTTTGCGGGAAAAATCACGCTGGTGGTGTGCTCCGAGCCGATACAGCGC
61  -----+-----+-----+-----+-----+-----+-----+ 120
GACGCGCGCGGAAAGCCCTTTTTAGTGCGACCAACACAGCAGGCTCGGCTATGTCGCG
a  L R A A F R G K I T L V V S S E P I Q R -
GTGCAGTTGAGCGGCTTGCGCGACGAAACCCTGCAAGACCTGAACATTTGCAGGAATAC
121  -----+-----+-----+-----+-----+-----+-----+ 180
CACGTCAACTCGCGAACCCTGCTTTGGGACGTTCTGGAACCTGTAAACGTCCTTATG
a  V Q L S G L A D E T L Q D L E H L Q E Y -
GGCTTTGCCAGCCATCCGCCCCGACGGCAGCGAAGCGGTAGTGATACCGCTGGGCGGCAAT
181  -----+-----+-----+-----+-----+-----+-----+ 240
CCGAACCGGTGCGTAGGCGGGCTGCCGTCGCTTCGCCATCACTATGGCGACCCGCCGTTA
a  G F A S H P P D G S E A V V I P L G G N -

```

```

      ACTTCGCACGGTGTGATTGTGTGCAGCCAGCACGGCAGCTACCGCATCAAAAACCTTAAG
241  -----+-----+-----+-----+-----+-----+-----+ 300
      TGAAGCGTGCCACACTAACACACGTGCGTCGTGCCGTGCGTAGTTTTTGGAATTCT
a      T S H G V I V C S Q H G S Y R I K N L K -

      CCCGGCGAGACGGCGATTTTTAATCATGAGGGTGCAAAAATCGTGATTAAGCAAGGCAAA
301  -----+-----+-----+-----+-----+-----+-----+ 360
      GGGCCGCTCTGCCGCTAAAAATTAGTACTCCACGTTTTTAGCTAATTTCGTTCCGTTT
a      P G E T A I F N H E G A K I V I K Q G K -

      ATCATTGAGGCCGATTGCGACGTGTACCGGGTAACTGCAACAATACGAGGTTAATGCG
361  -----+-----+-----+-----+-----+-----+-----+ 420
      TAGTAACTCCGGCTAACGCTGCACATGGCCCAATTGACGTTTGTATGCTCCAATTACGC
a      I I E A D C D V Y R V N C K Q Y E V N A -

      GCCACGGATGCCAAATTTAACGCTCCGTTGGTGGAGACCAGTGCACTGTTGACGGCGCAA
421  -----+-----+-----+-----+-----+-----+-----+ 480
      CCGTGCCCTACGGTTTAAATTGCGAGGCAACCACCTCTGGTCACGTCACAACCTGCCGCGTT
a      A T D A K F N A P L V E T S A V L T A Q -

      GGCCAAATCAACGGCAACGGCGGCATGGCCGTCGAGGGCGGCGACGGAGCCACCTTTAGC
481  -----+-----+-----+-----+-----+-----+-----+ 540
      CCGGTTTAGTTGCCGTTGCCGCGTACCGGCAGCTCCCGCCGCTGCCTCGGTGGAATCG
a      G Q I N G N G G M A V E G G D G A T F S -

      GGCGATGTTAACCAACGGGCGGCAGCTTTAACACCGACGGCGACGTGGTGGCCGGCAAT
541  -----+-----+-----+-----+-----+-----+-----+ 600
      CCGCTACAATTGGTTTGCCCGCCGTCGAAATTGTGGCTGCCGCTGCACCACCGGCCGTTA
a      G D V N Q T G G S F N T D G D V V A G N -

      ATATCGTTGCCCGAGCACCCGCATACCGACAGCATCGGCGGCAAAACCTTACCGGCGGAA
601  -----+-----+-----+-----+-----+-----+-----+ 660
      TATAGCAACGCGGTCTGTTGGCGTATGGCTGTCTAGCCGCGTTTTGGAATGGCCGCGTT
a      I S L R Q H P H T D S I G G K T L P A E -

      CCGGCATAG
661  ----- 669
      GGCCGTATC
a      P A * -

```

Enzymes that do cut: NONE

Enzymes that do not cut: BamHI BglII EcoRI HindIII KpnI NdeI NheI PstI SacI  
Sall SmaI SphI XbaI XhoI

This corresponds to the amino acid sequence <SEQ ID 2444; ORF 724>:

m724.pep

```

1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSIYRIKNLK
101 PGETAIFNHE GAKIVIKQK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2445>:

a724.seq

```

1  ATGAGTTTGA GTAAATTGGC GAAAAAACG GCACAACTG CTAAAAATAT
51  CGGCGAAACC CTGCGCGCGG CCTTTCGGGG AAAAATCACG CTGGTGGTGT
101 CGTCCGAGCC GATACAGCGC GTGCAGTTGA GCGGCTTGGC CGACGAAACC
151 CTGCAAGACC TTGAACATTT GCAGGAATAC GGCTTTGCCA GCCATCCGCC
201 CGACGGCAGC GAAGCGGTAG TGATACCGCT GGGCGGCAAT ACTTCGCACG
251 GTGTGATTGT GTGCAGCCAG CACGGCAGCT ACCGCATCAA AAACCTTAAG
301 CCCGGCGAGA CGCGGATTTT TAATCATGAG GGTGCAAAA TCCTGATTAA
351 GCAAGGCAAA ATCATTGAGG CCGATTGCGA CGTGTACCGG GTTAAGTGCA
401 AACAATACGA GGTAAATGCG GCCACGGATG CCAAATTTAA CGCTCCGTTG
451 GTGGAGACCA GTGCAGTGTT GACGGCGCAA GGCCAAATCA ACGGCAACGG

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1171

```

501 CGGCATGGCC GTCGAGGGCG GCGACGGAGC CACCTTTAGC GGCGATGTTA
551 ACCAAACGGG CGGCAGCTTT AACACCGACG GCGACGTGGT GGCCGGCAAT
601 ATATCGTTGC GCCAGCACCC GCATACCGAC AGCATCGGCG GCAAAACCTT
651 ACCGGCGGAA CCGGCATAG

```

This corresponds to the amino acid sequence <SEQ ID 2446; ORF 724.a>:

```

a724.pep
1  MSLSKLAKKT AQTAKNIGET LRAAFRGKIT LVVSSEPIQR VQLSGLADET
51  LQDLEHLQEY GFASHPPDGS EAVVIPLGGN TSHGVIVCSQ HGSYRIKNLK
101 PGETAIFNHE GAKIVIKQGK IIEADCDVYR VNCKQYEVNA ATDAKFNAFL
151 VETSAVLTAQ GQINGNGGMA VEGGDGATFS GDVNQTGGSF NTDGDVVAGN
201 ISLRQHPHTD SIGGKTLPAE PA*

```

a724/m724 100.0% identity in 222 aa overlap

	10	20	30	40	50	60
a724.pep	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
m724	MSLSKLAKKTAQTAKNIGETLRAAFRGKITLVVSSEPIQRVQLSGLADETLQDLEHLQEY					
	10	20	30	40	50	60
	70	80	90	100	110	120
a724.pep	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
m724	GFASHPPDGS EAVVIPLGGNTSHGVIVCSQHGSYRIKNLKPGETAIFNHEGAKIVIKQGK					
	70	80	90	100	110	120
	130	140	150	160	170	180
a724.pep	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
m724	IIEADCDVYRVNCKQYEVNAATDAKFNAFLVETSAVLTAQGQINGNGGMAVEGGDGATFS					
	130	140	150	160	170	180
	190	200	210	220		
a724.pep	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
m724	GDVNQTGGSFNTDGDVVAGNISLRQHPHTDSIGGKTLPAEPAX					
	190	200	210	220		

g725.seq not found yet.

g725.pep not found yet.

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2447>:

```

m725.seq
1  ATGGTGCGCA CGGTTAAAAG CTACAACGGC GAGGCCGACG ATTTGGCGGG
51  GCAAATCCAT ACGCTGCCTG CGGTTTGGGT AACGTATGGC GGCAGCAAAG
101 TTGAGCCTGC CAGCACCAGC GCGTATGCG GACGTTATCA GGATACCGCC
151 GAATTTGTGG TGATGGTGGC GGCCCGCAAT CTGCGCAACG AGCAGGCGCA
201 GCGGCAAGGC GGCATCGACA GCCGCGAAAT CCGCAGCAAC GATTTAATCC
251 GCGCTGTTTC CCGCTGCTT GACGGCCAGC GGCTCGGTTT TGCCGATAGC
301 CGCGGCTTGG TGCCCAAAGC GGTGCGCGCG ATTGCCAATC ATGTGCTGGT
351 GCAAACGCC GCAGTAAGCA TATATGCGGT TGAGTATGCC ATCCGCTTTA
401 ACACCTGCGG GTTGGAAAT GACCGCTACC CCGAACGCAC CGACAATCCC
451 GACGACCCCA ACCATATCTT TACCAAGTAT CAGGGTACAT TGAGCGAGCC
501 GTGGCCTGAT TTCGAGGGGT TGGACGGCAA AATTACGAC CCGCAATCCG
551 CCGATGAAAT ACCTGTAAAC CTAACCCTTA AGGATAAGCA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 2448; ORF 725>:

```

m725.pep
1  MVRTVKSUNG EADDLAQIHL TPAVWVTYG GSKVEPASTG GVCGRYQDTA
51  EFVVMVAARN LRNEQAQRQG GIDSREIGSN DLIRAVRRLD DGQRLGFADS
101 RGLVPKAVRA IANHVLVQNA AVSIYAVEYA IRFNTCGLEN DRYPERTDNP
151 DDPNHIFTKY QGTLSEFPWD FEGLDGKIYD PQSADEIPVN LTLKDKQ*

```

a725.pap not found yet

q726.seq not found yet

q726.pdf not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2449>:

**m726.seq**

1	ATGACCATCT	ATTTCAAAAA	CGGCTTTTAC	GACGACACAT	TGGGCGGCAT
51	CCCCGAAGGC	GCGGTTGCCG	TCCGGCGCCGA	AGAATACGCC	GCCCTTTTGG
101	CAGGACAGGC	CGCGCGCGGG	CAGATTGCCG	CAGATTCCGA	CGGCGGCCCC
151	GTTTTAAACC	GCAGCGCGCC	GTCGATTAC	CAGCAATTGG	ACGGCAAAAA
201	ATGGAATAATC	AGCAAAGCCG	CCGCGCCCGC	CCGTTTCGCC	AAACAAAAAA
251	CCGCTTGGC	ATTCCGCCTC	GCGGAAAAGG	CGGACGAACT	CAAAAACAGC
301	CTCTTGCGCG	GCTATCCCCA	AGTGGAATC	GACAGCTTTT	ACAGGCAAGGA
351	AAAAGAAGCC	CTCGCGCGGC	AGGCGGACAA	CAACGCCGCC	ACCCCGATTGC
401	TGGCGCAAAT	CGCCGCGCCA	AGGGGCGTGG	AATTGACAGT	TTTGATTGAA
451	AAAGTTATCG	AAAAATCCGC	CCGCTTGGCT	GTTGCCGCGC	GCGCGATTAT
501	CGGAAGCGT	CAGCAGCTCG	AAGACAAATT	GAACACCATC	GAAACCGCGC
551	CCGGATTGGA	CGCGCTGGAA	AAGGAAATCG	AAGAATGGAC	GCTAAACATC
601	GGCTGA				

**This corresponds to the amino acid sequence <SEQ ID 2450; ORF 726>:**

И  
Д726.рер

1	MTIYFKNGFY	DDTLGGIPEG	AVAVRAEYYA	ALLAGQAQGG	QIAADSDGRP
51	VLTPPRPSDY	HEWDGKKWKI	SKAAAAARFA	KOKTALAFRL	AEKADELKNS
101	LLAGYPQVEI	DSFYRQEKEA	LARQADNNAP	TPMLAQIAAA	RGVELDV LIE
151	KVIEKSARLA	VAAGAIIGKR	QQLEDKLN TI	ETAPGLDALE	KEIEEWTLNI
201	G*				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2451>:

**a726.seq**

1	ATGACCATCT	ATTTCAAAAA	CGGCTTTTAC	GACGACACCT	TGGGCAGCAT
51	CCCCGAAGGC	GCGGTTGCCG	TCCGCGCCGA	AGAATACGCC	GCCCTTTTGG
101	CAGGACAGGC	CGAGGGCGGG	CAGATTGCCG	CAGATTCCGA	CGGCGCCGCC
151	GTTTTTAACCC	GCAGCGCCCT	TCGCCAATAC	CAGCAATGGG	ACGCCAAGAA
201	ATGGGAAATC	GGCGAAGCCG	CTGCCGCCGC	CCGTTTGCGC	GAACAAAAAA
251	CCGCGACGGC	ATTCCGCCTC	GCGGCAAAAG	CGGACGAACT	CAAAAAACAG
301	CTCTTGCGCG	GCTATCCCCA	AGTGGAAATC	GACAGCTTTT	ACAGGCGAGGA
351	AAAAGAAGCC	CTCGCGCGCG	AGGCGGACAA	CAACGCCCCG	ACCCCGATTG
401	TGGCGCAAAT	CGCGCGCGCA	AGGGGCGTGG	AAATTGACGT	TTTGATTGAA
451	AAAGTTGTCT	AAAAATCCGC	CCGCCTGGCC	GTTGCCGCCG	GCGCGATTAT
501	CGGAAGCGCG	CAGCAGCTCG	AAGACAAATT	GAACACCATC	GAAACCGCGC
551	CAGGATTGGA	CGCGCTGGAA	AAGGAAATCG	AAGAATGGAC	GCTAAACATC
601	GGCTGA				

This corresponds to the amino acid sequence <SEQ ID 2452; ORF 726.a>:

g726.pap

1	MTIYFKNGFY	DDTLGSIPEG	AVAVRAEEYA	ALLAGQAQGG	QIAADSDGRP
51	VLTPPRPSEY	HEWDGKKWEI	GEAAAAARFA	EQKTATAFRL	AAKADELKNS
101	LLAGYPQVEI	DSFYRQEKEA	LARQADNNAP	TPMLAQIAAA	RGVELDVLIE
151	KVVEKSARLA	VAAGAIIGKR	QQLEDKLNTI	ETAPGLDALE	KEIEEWTLNI
201	G*				

**a726/m726 95.5% identity in 201 aa overlap**

```

          10          20          30          40          50          60
a726.pep  MTIYFKNGFYDDTLGSIPEGAVAVRAEYYAALLAGQAQGGQIAADSDGRPVLTTPRPSEY
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m726      MTIYFKNGFYDDTLGGIPEGAVAVRAEYYAALLAGQAQGGQIAADSDGRPVLTTPRPSED
          10          20          30          40          50          60

```

1173

```

              70      80      90      100      110      120
a726.pep      HEWDGKKWEIGEEAAAAARFAEQKTATAFRLAAKADELKNSLLAGYPQVEIDSFYRQEKEA
              |||||:|:|:|||||:||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          HEWDGKKWKISKAAAAARFAKQKTALAFRLAEKADELKNSLLAGYPQVEIDSFYRQEKEA
              70      80      90      100      110      120

              130      140      150      160      170      180
a726.pep      LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQOLEDKLNIT
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          LARQADNNAPTMLAQIAAARGVELDVLEIKVVEKSARLAVAAGAIIGKRQOLEDKLNIT
              130      140      150      160      170      180

              190      200
a726.pep      ETAPGLDALEKEIEEWTLNIGX
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m726          ETAPGLDALEKEIEEWTLNIGX
              190      200

```

g727.seq not found yet

g727.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2453>:

```

m727.seq
1  ATGAATCTCG TGAAACTGCT GCGGAATAAC TGGCAACCGA TTGCCATTAT
51 CGCGCTTGTC GGCACGGGCT TGGCTGTGTC GCACCATCAA GGCTACAAGT
101 CGGCATTGTC GAAGCAGCAG GCGGTCATCG ACAAGATGGA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TATGCGCGCG AACTGGAAC
201 GGCACGCGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCTGTCGGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAGA
301 GACCTTTGCA AAATTCCTTT CCCTCCCGAC AGCCGAAACC CAAACACAGG
351 TTTTCGCGTG TTTTCGCCCC AAATACCGCC TAATTTTACC CAAATACCCC
401 CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2454; ORF 727>:

```

m727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK
51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTER
101 DLCKIFPPPD SRNPNTGFRL FSPQIPPNFT QIPP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2455>:

```

a727.seq
1  ATGAATCTCG TGAAACTGCT GCGGAATAAC TGGCAACCGA TTGCCATCAT
51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT
101 CGGCTTTTGC GAAGCAGCAG GCGGTCATTG AGAAAATGAA GCGCGACAAG
151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA
201 GGCAGCGTGC GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCCGCA
251 TGGCTTTGGC GAAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAAT
301 AAAAAGGAAA TCGAAAATGT CCTTACTCAA GACCGTAAAA ATGCAGGCGG
351 CGGTTGTATT GACGGCTTGT GCCATCACGG CTTGCAGCTC TACAAGCGCG
401 CCCTCGGCTA CGGAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2456; ORF 727.a>:

```

a727.pep
1  MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK
51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN
101 KKEIENVLTQ DRKNAGGCCI DGFHGHGLQL YKRALGYGN*

```

a727/m727 83.2% identity in 119 aa overlap

```

              10      20      30      40      50      60
a727.pep      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

1174

```

m727      MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN
              10      20      30      40      50      60

              70      80      90      100     110     119
a727.pep   YARELEQARAEAKKYEYVKAHAVGMALAKKQAEVSRKKTENKKEIENV-LTQDRKNAGGGC
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
m727      YARELELARAEEAKKYEYVKAHAVGMALAKKQAEVSRKTE--RDLCKIPFPDSDRNPTGTF
              70      80      90      100     110

              120     130     140
a727.pep   IDGFGHHGLQLYKRALGYGNX

m727      RLFSPQIPPNFTQIPPX
              120     130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2457>:

```

g728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CGGGGAATAAT TATGAAACGA CAGGAGAATA TCGGTTTGTG TGGCAACCGG
551 ACGGTTCCGGT ATTTGATGCG GCGGGGCGCG GGAAATCCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG GATTGCATCG GACTCGCGCG ATTATGTGTT TTATCAGAA
751 ATGCGGGAAT TGATGCCCGG GGGGATGAAG GCGAACAGTC TTGTGTCGG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGGCGGA
1001 TTATCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAGATT TGGAAAAGA GGTGAGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG GCCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2458; ORF 728>:

```

g728.pep
1  MFKKFKPVLL SFFALVFVFW LGTGIAYEIN PRWFLSDTAT EVPENPNFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PFAFVNAEYL
151 YRNDRPFVSN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGCMQ AOVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVIFYQN
251 MRELMPRGMK ANSLVVGIDA DGLPQKVYWS FDNGKKRQSF EYYLKNGNLF
301 IAQSSTVALK ADGVTADMQT YHAQQTWYLD GGRIIREEKQ GDRLPDFPLN
351 LEDLEKEVSR YAEAAARRSG GRRGLSH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2459>:

```

m728.seq
1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACCG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAACG GTGGATGACG
251 GTCCGTTGCA GTCGGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCGAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTTTCGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA

```

1175

```

501  CGGGGAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCAG
551  ACGGTTCCGT ATTTGATGCG GCGGGGCGCG GGAAATCGG GGAAGATGTT
601  TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651  ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCAAAG
701  AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751  ATGCGGGAAT TGATGCCCCG AGGGATGAAG GCGAACAGTC TTGTGGTCGG
801  CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851  GAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901  ATTGACAAT CTTCGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951  TATGCAGACC TATCATGCGC AACAGACGTG GTATTGGAT GGCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAAAATT TGGAAAAGA GGTGCCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTTCTCA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 2460; ORF 728>:

```

m728.pep
1  MEKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFVSU VYGGTVHGEN YETTG EYRVV WQPDGSVFDA AGRKGIGEDV
201 YEHLGCGYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
251 MRRLMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYLLKNGNLF
301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN
351 LENLEKEVRR YAEAAARRSG GRRDLSH*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 728 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF728.a) from *N. gonorrhoeae*:

m728 / g728

```

          10      20      30      40      50      60
m728.pep  MEKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA
          |||
g728      MEKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPEPNPNAFVAKLARLFRNA
          10      20      30      40      50      60

          70      80      90      100     110     120
m728.pep  DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV
          |||
g728      DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV
          70      80      90      100     110     120

          130     140     150     160     170     180
m728.pep  WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFVSU VYGGTVHGENYETTG EYRVV
          |||
g728      WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDRPFVSU VYGGTAHGENYETTG EYRVV
          130     140     150     160     170     180

          190     200     210     220     230     240
m728.pep  WQPDGSVFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFRKNRIAS
          |||
g728      WQPDGSVFDAAGRGKIGEDVYEHCLGCGYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
          190     200     210     220     230     240

          250     260     270     280     290     300
m728.pep  DSRNSVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF
          |||
g728      DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYLLKNGNLF
          250     260     270     280     290     300

          310     320     330     340     350     360
m728.pep  IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR
          |||

```



1176

g728           IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIIREEKQGDRLPDFPLNLEDLEKEVSR  
                   310           320           330           340           350           360

                  370

m728.pep       YAEAAARRSGGRRDLSHX  
                   |||||           |||||

g728           YAEAAARRSGGRRGLSHX  
                   370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2461>:

a728.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTGTG	CACTTGTATT
51	TGCCTTTTGG	CTGGGAACGG	GTATTGCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTGTAGCGA	TACGGCAACT	GAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCCGCCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCCAGGTA	TATTTGGCGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGACTCGCGC	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC
951	CTATCATGCG	CAACAGACGT	GGTATTTAGA	TGGCGGGCGG	ATTGTCCCGG
1001	AAGAGAAACA	GGGGACAGA	CTGCCTGATT	TTCTTTTGAA	CTTGGAAGAT
1051	TTGGAAAAAG	AGGTGAGCCG	TTATGCAGAG	GCTGCGGCGA	GACGTTCCGG
1101	CGGCAGGCGC	GACCTTTCTC	ACTGA		

This corresponds to the amino acid sequence <SEQ ID 2462; ORF 728.a>:

a728.pep

1	MFKKFKPVLL	SFFALVFAFW	LGTGIAYEIN	PRWFLSDTAT	ENPNAFVAKL
51	ARLFRNADRA	VVIVKESMRT	EESLAGAVDD	GPLQSEKDYL	ALAVRLSRLK
101	EKAKWFHVTE	QEHGEEVWLD	YYIGEGGLVA	VLSQRSPEA	FVNAEYLYRN
151	DRPFSVNVYG	GTVHGENYET	TGEYRVVWQP	DGSVFDASGR	GKIGEDVYEH
201	CLGCQMAQV	YLAKYRDVAN	DEQKVWDFRE	ESNRIASDSR	DSVIFYQNMRE
251	LMPRGMKANS	LUVGYDADGL	PQKVYWSFDN	GKKRQSFEYY	LKNGNLFIAQ
301	SSTVALKADG	VTADMQTYHA	QQTWYLDGGR	IVREEKQGDR	LPDFPLNLED
351	LEKEVSRYAE	AAARRSGGRR	DLSH*		

a728 / m728    96.3% identity in 377 aa overlap

	10	20	30	40	50	
a728.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATE---NPNAFVAKLARLFRNA					
m728	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNAFVAKLARLFRNA					
	10	20	30	40	50	60
a728.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAVRLSRLKEKAKWFHVTEQEHGEEV					
m728	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
a728.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
m728	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLYRNDPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180

1177

	180	190	200	210	220	230
a728.pep	WQPDGSVFDASGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m728	WQPDGSVFDAAAGRGKIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
	240	250	260	270	280	290
a728.pep	DSRDSVFYQNMRELMPRGMKANSILVVGVDADGLPQKVYWSFDNGKKRQSFHEYLLKNGNLF					
m728	DSRNSVFYQNMRELMPRGMKANSILVVGVDADGLPQKVYWSFDNGKKRQSFHEYLLKNGNLF					
	250	260	270	280	290	300
	300	310	320	330	340	350
a728.pep	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLEDEKEVSR					
m728	IAQSSTVALKADGVTADMQTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENEKEVRR					
	310	320	330	340	350	360
	360	370				
a728.pep	YAEAAARRSGGRRDLSHX					
m728	YAEAAARRSGGRRDLSHX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2463>:

g729.seq

1	AT GAATACTA	CATTGAAAAC	TACCTTGACC	TCTGTTGCAG	CAGCCTTTGC
51	AT TGTCTGCC	TGCACCATGA	TTCCTCAATA	CGAGCAGCCC	AAAGTCGAAG
101	TT GCGGAAAC	CTTCCAAAAC	GACACATCGG	TTTCTTCCAT	CCGCGCGGTT
151	GATTTGGGTT	GGCATGACTA	TTTGGCCGAC	CCGCGCCTGC	AAAAGCTGAT
201	CGACATCGCA	CTCGAGCGCA	ATACCAAGTT	GCGTACAGCC	GTATTGAACA
251	GC GAAATCTA	CCGCAACAA	TACATGATCG	AGCGCAACAA	CCTCCTGCC
301	AC GCTTGCCG	CCAATGCGAA	CGGCTCGCGC	CAAGGCAGCT	TGAGCGGCGg
351	ca aTGTCAGC	AGCAGCTACA	ATGTCGGACT	GGGTGcGGca	tCTTACGAAC
401	TCGATCTGTT	CgGGCGCGTG	CGCagcaacA	GcgaagcAGC	ACTGcaggGC
451	tATTTTGCCA	GCGTTGCCAA	CcgcGATGCG	GCACATTGa	ttCtGATTGC
501	CACCGTTGCC	AAAGCCTATT	TCAAcgaGcG	TTATGCCGAA	AAAGcgaTgT
551	CT TTGGCGCa	gcGTGTCTTG	AAAACGCGCG	AGGAAACCTA	CAAGCTGTCC
601	GAATTGCGGT	ACAAGGCAGG	CGTGATTTC	GCCGTGCCCC	TGCGCCAGCA
651	GGAAAGCCTTG	ATTGAATCTG	CCAAAGCCGA	TTATGCCCAT	GCCGCGCGCa
701	gc CGCGAACA	GGCGCGCAAT	GCCTTGCCAA	CCTTGATTAA	ccGTCCGATA
751	CCCGAagaCC	TGCCCCCGG	TTTGCCGTTG	GACAagcAGT	TTTTTGTTGA
801	AAAACCTGCCT	GCCGTTTGA	GTTCCGAAGT	ATTGCTCGAC	CGTCCCGACA
851	TC CGCGCCCG	CGAACACGCG	CTCAAACAGG	CAAACGCCAA	TATCGGTGCG
901	gcgCGCGCCg	ccTTTTTCCC	GTCCATCCGC	CTGACCGGAA	GCGTCGGTAC
951	GGGTTCTGTC	GAATTGGGCG	GGCTGTTCAA	AAGCGGCACG	GGCGTTTGGG
1001	CGTTCGCTCC	GTCTATTACC	CTGCCGATT	TTACTTGGGG	AACGAACAAG
1051	GC GAACCTTG	ATGTGGCAAA	ACTGCGCCAA	CAGGCACAAA	TTGTGCTTA
1101	TGAATCCGCC	GTCCAATCCG	CCTTTCAAGA	CGTGGCAAAC	GCATTGGCGG
1151	CGCGCGAGCA	GCTGGATAAA	GCCTATGACG	CTTTAAGCAA	ACAAAGCCGC
1201	GCCTCTAAAG	AAGCGTTGCG	CTTGGTCGGA	CTGCGTTACA	AACACGGCGT
1251	ATCCGGCGCG	CTCGATTGTC	TCGATGCGGA	ACGCATCAGC	TATTCGGCGG
1301	AAGGTGCGGC	TTTGTGCGCA	CAACTGACCC	GCGCCGAAAA	CCTTGCCGAT
1351	TTGTACAAGG	CGCTCgacGG	CGGATTGAAA	CGGGATACCC	AAACCGGCAA
1401	ATAA				

This corresponds to the amino acid sequence <SEQ ID 2464; ORF 729>:

g729.pep

1	MNTTLKTTLT	SVAAAFALSA	CTMIPQYEQP	KVEVAETFQN	DTSVSSIRAV
51	DLGWHDYFAD	PRLQKLIDIA	LERNTSLRTA	VLNSEIYRKQ	YMIERNLLP
101	TLAANANGSR	QGSLSGGNVS	SSYNVGLGAA	SYELDLFGRV	RSNSEAALQG
151	YFASVANRDA	AHLILIAIVA	KAYFNERYAE	KAMSLAQRLV	KTREETYKLS

1178

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201 EL RYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINRPI
251 PE DLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 AR AAFPSIR LTGSVGTGSV ELGGLFKSGT GVWAFAPSIT LPIFTWGTNK
351 AN LDVAKLRQ QAQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 AS KEALRLVG LRYKHVSGA LDLLDAERIS YSAEGAALSA QLTRAENLAD
451 LY KALDGLK RDTQTK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2465>:

```

m729.seq
1 ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTTGC
51 ATTGTCTGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGCGCCGTC
151 GATTTTAGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAAGTT GCGTACCGCC GTATTGAACA
251 CGGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TC GATCTGTT CGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTTCGCC GCACCGCCAA CCGCGATGCG GCACATTGTA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTACGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGTTTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCC GCCGTCGCC TACGTCAGCA
651 GGAAGCCCTG ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCCGCGAACA GCGCGCAAT GCCTTGCAA CCTTGATTAA CCAACCGATA
751 CCCGAAGACC TGCCTGCCGG TTTGCCGCTG GACAAGCAGT TTTTGTGTA
801 AAAACTGCCG GCCGGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTCC ATCCATCCGC CTGACCGGAA CCGTCCGTAC
951 GGGTTCTGCC GAATTGGGTG GGTGTTCAA AAGCGGCACG GGCCTTGGT
1001 CGTTTCGCGC GTCTATTACC CTGCCGATT TTACCTGGGG TACGAACAAG
1051 CGGAACCTTG ATGTAGCCAA GCTGCGCCAA CAGGTACAAA TCGTGCCTA
1101 TGAATCCGCC GTCCAATCCG CATTTCAGA CGTGGCAAAC GCATTGGCGG
1151 CGCGCGAGCA GCTGGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG CTTGGTCGGC CTGCGTTACA AGCACGGCGT
1251 ATCCGCGCGC GTCGACTTGC TCGATCGGGA ACGCAGCAGC TATGCGGCGG
1301 AGGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2466; ORF 729>:

```

m729.pep
1 MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDYFAD PRLQKLIDIA LERNLSLRTA VLNSEIYRQ YMIERNLLP
101 TLAANANDSR QGSLSGNV SSVKVLGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PEDLPAGLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGTVGTGSA ELGGLFKSGT GVWSFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QVQIVAYESA VQSAFQDVAN ALAAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHVSGA LDLLDAERSS YAAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

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Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 729 shows 95.7% identity over a 467 aa overlap with a predicted ORF (ORF729.a) from *N. gonorrhoeae*:

m729 / g729 95.7% identity in 467 aa overlap

```

          10      20      30      40      50      60
m729.pep  MDTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDYFAD
          1:|||||:|||||:|||||:|||||:|||||:|||||:
g729      MNTTLKTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTSVSSIRAV DLGWHDYFAD
          10      20      30      40      50      60

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1179

	70	80	90	100	110	120
m729.pep	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANDSRQGSLSGGNVS					
g729	PRLOKLIDIALERNTSLRTAVLNSEIYRKQYMIERNNLLPTLAANANGSRQGSLSGGNVS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m729.pep	SSYKVGLGAASYELDLFGRVRSSEAAALQGYFASTANRDAAHLSLIATVAKAYFNERYAE					
g729	SSYNVGLGAASYELDLFGRVRSNSEAAALQGYFASVANRDAAHLILIATVAKAYFNERYAE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m729.pep	EAMSLAQRVLKTRREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
g729	KAMSLAQRVLKTRREETYKLSELRYKAGVISAVALRQOEALIESAKADYAAHAARSREQARN					
	190	200	210	220	230	240
	250	260	270	280	290	300
m729.pep	ALATLINQPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
g729	ALATLINRPIPEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m729.pep	ARAAFFPSIRLTGTGTGSSELGGLFKSGTGVWFSFAPSITLPIFTWGTNKANLDVAKLRQ					
g729	ARAAFFPSIRLTGSVGTGSSELGGLFKSGTGVWAFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
	370	380	390	400	410	420
m729.pep	QVQIVAYESAVQSAFQDVANALAAEQDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
g729	QAQIVAYESAVQSAFQDVANALAAEQDKAYDALSKQSRASKEALRLVGLRYKHGVSQA					
	370	380	390	400	410	420
	430	440	450	460		
m729.pep	LDLLDAERSSYAEGAALSAQLTRAENLADLYKALGGGLKRDQTQDKX					
g729	LDLLDAERISYAEGAALSAQLTRAENLADLYKALDGGGLKRDQTQGX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2467>:

a729.seq

```

1  ATGGATACTA CATTGAAAAC CACCTTGACT TCTGTTGCAG CAGCCTTCGC
51  ATTATCCGCC TGCACCATGA TTCCCAATA CGAGCAGCCC AAAGTCGAAG
101 TTGCCGAAAC GTTCAAAAAC GATACCGCCG ACAGCGGCAT CCGTGCGGTC
151 GATTGTGGTT GGCATGACTA TTTTGCCGAC CCGCGCCTGC AAAAGCTGAT
201 CGACATCGCA CTCGAGCGCA ATACCAGTTT GCGTACCGCC GTATTGAACA
251 GCGAAATCTA CCGCAAACAA TACATGATTG AGCGCAACAA CCTCCTGCCC
301 ACGCTTGCCG CCAATGCGAA CGACTCGCGC CAAGGCAGCT TGAGCGGCGG
351 CAATGTAAGC AGCAGCTACA AAGTCGGACT GGGTGCGGCA TCTTACGAAC
401 TCGATCTGTT CGGGCGTGTA CGCAGCAGCA GCGAGGCGGC ACTGCAAGGC
451 TATTTGCGCA GCACCGCCAA CCGCGATGCG GCACATTGTA GCCTGATTGC
501 CACCGTTGCC AAAGCCTATT TCAACGAACG TTATGCCGAA GAAGCGATGT
551 CTTTGGCGCA ACGTGTGTTG AAAACGCGCG AGGAAACCTA CAAGCTGTCC
601 GAATTACGTT ACAAGGCAGG CGTGATTTCG GCCGTCGCCC TACGTCAGCA
651 GGAAGCCCTA ATCGAATCTG CCAAAGCCGA TTATGCCCAT GCCGCGCGCA
701 GCGCGGAACA GCGCGCAAT GCCTGGCAA CCCTGATTAA CCAACCGATA
751 CCCGACGACC TGCCCGCCGG TTTGCCGTTG GACAAGCAGT TTTTGTGTTA
801 GAAGCTGCCG GCCGTTTGA GTTCCGAAGT ATTGCTCGAC CGTCCCGATA
851 TCCGTGCTGC CGAACACGCG CTCAAACAGG CAAACGCCAA TATCGGTGCG
901 GCACGCGCCG CCTTTTTCCT ATCCATCCGC CTGACCGGAA GCGTCGATAC
951 GCATTCTGCC GAATTGGGCG GGCTGTTCAA AAGCGGCACC GCGGTTTGGT
1001 TGTTGCGACC TTCCATTACC CTGCCGATTT TTACCTGGGG TACGAACAAG

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1180

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1051 GCGAACCTCG ATGTAGCCAA GCTGCGCCAA CAGGCACAAA TCGTTGCCTA
1101 TGAAGCCGCC GTCCAATCCG CATTTCAAGA CGTGGCAAAC GCATTGACCG
1151 CGCGCGAGCA GTTGATAAA GCCTATGACG CTTTAAGCAA ACAAGCCGC
1201 GCCTCTAAAG AAGCGTTGCG TTTGGTGGT CTGCGTTACA AACACGGCGT
1251 ATCCGGCGCG CTCGACTTGC TCGATGCGGA ACGCAGCAGC TATTCGGCGG
1301 AAGGTGCGGC TTTGTGCGCA CAACTGACCC GCGCCGAAAA CCTTGCCGAT
1351 TTGTACAAGG CACTCGGCGG CGGATTGAAA CGGGATACCC AAACCGACAA
1401 ATAA

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This corresponds to the amino acid sequence <SEQ ID 2468; ORF 729.a>:

a729.pep

```

1 MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV
51 DLGWHDFAD PRLQKLIDIA LERNTSLRTA VLNSEIYRKQ YMIERNLLP
101 TLAANANDSR QGSLSGGNVS SSYKVG LGAA SYELDLFGRV RSSSEALQG
151 YFASTANRDA AHLSLIATVA KAYFNERYAE EAMSLAQRVL KTREETYKLS
201 ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN ALATLINQPI
251 PDDLPA GLPL DKQFFVEKLP AGLSSEVLLD RPDIRAAEHA LKQANANIGA
301 ARAAFFPSIR LTGSVDTHSA ELGGLFKSGT GVWLFAPSIT LPIFTWGTNK
351 ANLDVAKLRQ QAQIVAYEAA VQSAFQDVAN ALTAREQLDK AYDALSKQSR
401 ASKEALRLVG LRYKHGVS GA LDLLDAERSS YSAEGAALSA QLTRAENLAD
451 LYKALGGGLK RDTQTDK*

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a729 / m729 98.1% identity in 467 aa overlap

a729.pep	10	20	30	40	50	60
	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
m729	MDTTLKTTLT SVAAAFALSA CTMIPQYEQP KVEVAETFKN DTADSGIRAV DLGWHDFAD					
	10	20	30	40	50	60
a729.pep	70	80	90	100	110	120
	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
m729	PRLQKLIDIALERNTSLRTAVLNSEIYRKQYMIERNLLPTLAANANDSRQGSLSGGNVS					
	70	80	90	100	110	120
a729.pep	130	140	150	160	170	180
	SSYKVG LGAA SYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
m729	SSYKVG LGAA SYELDLFGRVRSSEALQGYFASTANRDA AHLSLIATVAKAYFNERYAE					
	130	140	150	160	170	180
a729.pep	190	200	210	220	230	240
	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
m729	EAMSLAQRVLK TREETYKLS ELRYKAGVIS AVALRQOEAL IESAKADYAH AARSREQARN					
	190	200	210	220	230	240
a729.pep	250	260	270	280	290	300
	ALATLINQPI PDDLPA GLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
m729	ALATLINQPI PEDLPAGLPLDKQFFVEKLPAGLSSEVLLDRPDIRAAEHALKQANANIGA					
	250	260	270	280	290	300
a729.pep	310	320	330	340	350	360
	ARAAFFPSIR LTGSVDTHSA ELGGLFKSGTGVWLFAPSITLPIFTWGTNKANLDVAKLRQ					
m729	ARAAFFPSIR LTGTGTGS AELGGLFKSGTGVWSFAPSITLPIFTWGTNKANLDVAKLRQ					
	310	320	330	340	350	360
a729.pep	370	380	390	400	410	420
	QAQIVAYEAA VQSAFQDVANALTAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS GA					
m729	VQIVAYESAVQSAFQDVANALAREQLDKAYDALSKQSRASKEALRLVGLRYKHGVS GA					
	370	380	390	400	410	420

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g730.seq
1 GTGAAACCGC TGC GCAGACT GACAAACCTC CTTGCCGCCT GCGCGTAGC
51 GCGCGTCCGA CTCATACACC CCGCCCTCGC GCGGACTTG GCGCAAGACC
101 CGTTTCATTAC CGATAACACC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGcgacCC GCGCGGCAGC GTTTCGACG GCACCGCGAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGCGAAC CTGTCTATCC
251 AACAGGCGGC AATCCAAGGC AATCTTGGTT ACACCGTCCG CTTTTCGGGA
301 CACGGACACG AAGAACAACG CCCTTCGCAC AACCACGCCG CCGACAGCGC
351 AAGCGAAGAA AAAGGCAACG TTGACGACGG CTTTACCGTG TACCGGCTCA
401 ACTGGGAAGG ACAGCAACAT CATCCGCGCG ATGCCTACGA CGGCGCGAAG
451 GCGGCAATT ACCCCAACCC TACGGGCGCA CGAGACAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CAATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATTC GACAAC TACA ACAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TGTCACAAGG GTCGCGCGCG
701 GCGCGCTCAA CCCCCTTATC AGCGCGGCGG AAGCCTTGGG CATAGGCGCG
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCGA TGCGCAACAT
801 CGCCCCCTTA CCCGCGCGAGG GCAAATTGCG CGCCATCGGC GGCTTGGGCA
851 GCGCGGCGGG CTTTGAAAAA AATACGCGCG AAGCGGTGTA CCGGTGGATA
901 CAGGAAAAAC CCAATGCCGC CGAAACCGTC GAAGCCCTGG TCAACGTCCT
951 GCCGTTTGCC AAAGTCAAAA ACCTGACAAA GCGGCAAAAA CCGGGAAGG
1001 CTGCGGTTAG TGGGGATTTT TCTAAATCCT ACACCTGCTC CTTCCACGGC
1051 AGCACCTTGG TCAAAACGGC AGACGGCTAC AAAGCCATTG CCCATATTCA
1101 AGCCGGAGAC CGCGTCCTTT CCAAGGACGA GGCAGGCGGA GAAACGGGAT
1151 ACAAAACCGT TACCGCCCA TCGGCAATC CGTATCAAGA AACC GTTTAC
1201 ATTGAAGTTT CAGACGGCGA CCGCAACGAC CAACCCCTGA TTTCCAACCG
1251 CATCCACCGG TTTTATTCGG ACGGCAAATG GATTAAGGCG GAAGATTTAA
1301 AAGCGGGAAG CCGGCTGTTA TCCGAAAGCG GCAAAACCCA AACC GTCCG
1351 AACATCGTTG TCAAACCAA ACCGCTCAA GCCTACAATC TGACCGTTGC
1401 CGATTGGCAT ACCTACTTCG TCAAGGGTAA TCAGGCGGAA ACGGAAGGGG
1451 TTTGGGTTCA TAATGATTGT CCGCTTAAC CAAAACCAAC CAATCATGCC
1501 CAACAAAGAA AAGAAGAAGC TAAAAACGAT TCTCATCGAA GTGTGGGAGA
1551 TTCCAATCGT GTCGTTTCGCG AAGGAAAGCA ATATTTAGAT TCCGACACAG
1601 GAAACATGTT TTATGTAAAA GGAGATAAAG TGGTATTCTT AACTCCTGAT
1651 GAAAGACAGG TAACTCAATT TAAGAACTCG AAAGCCAATA CGTCAAAAG
1701 GGTAAAAAAT GAGGAAATGGA CACCAAAATA A

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g730.pep
1 VKPLRRLTNL LAACAAVAVA LIQPALAADL AQDPFITDNT QRQHYEPGGK
51 YHLFGDPRGS VSDRTGKINV IQDYTHOMGN LLIQAAAIQG NLGYTVRFSG
101 HGHEEHAPFD NHAADSASNE KQNVDDGFTV YRLNWEGEH HPADAYDGPK
151 GGNYPKPTGA RDEYTYHVNQ TARSIKLNPT DTRTSIRQIF DNYNNLGSNF
201 SDRADKANRK MFEHNAKLDR WGNSEMFVNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAAIG GLGSAAGFEK NTREAVDRWI
301 QENPNAAETV EALVNVLPFA RVKNLTKAAK PGKAAVSGDF SKSYTCFSHG
351 STLVKTTADGY KAIAHIQAGD KVLNKSDEASG ETGYKPVTAI YGNPYQETVY
401 IEVSDGIGNS QTLISNRIHP FYSKGKWIKA EDLKAGSRLI SESGKTQTVR
451 NIVVKPKPLK AYNLTVADWH TVFVKGNGQAE TEGVWVHNDG PPKPKPTNHA
501 QQRKEAKND SHRSVGDNRN VVREGKQYLD SDTGNHVVYK GDKVWILTPD
551 GRQVTQFKNS KANTSKRVKN GKWTFK*
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m730.seq  
1 GTGAAACCGC TGC GCAGACT GACAAACCTC CTTGCCGCCT GCGCCGTAGC  
51 GCGGCGCCGA CTCATACAGC CCGCCCTCGC GGCGGACTTG GCGCAAGACC

1182

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101 CGTTCATTAC CGATAACGCC CAACGGCAGC ACTACGAACC CGGCGGCAAA
151 TACCACCTCT TCGGCGACCC GCGCGGCAGC GTTTCGGACC GCACCGGCAA
201 AATCAACGTC ATCCAAGACT ATACCCACCA GATGGGCAAC CTGCTCATCC
251 AACAGGCAAA CATCAACGGC ACAATCGGCT ACCACACCCG CTTTCCGGA
301 CACGGACACG AAGAACACGC CCCCTTCGAC AACCACGCCG CCGACAGCGC
351 GAGCGAAGAA AAAGGCAACG TTGACGAAGG CTTTACCGTA TACCGGCTCA
401 ACTGGGAAGG ACACGAACAT CATCCCGCCG ATGCCTACGA CGGCCCGAAG
451 GGCGGCAATT ACCCCAAACC TACGGGCGCA CGAGACGAAT ACACCTATCA
501 CGTCAACGGC ACAGCCCGCA GTATCAAAC CTATCCGACC GACACCCGCA
551 GCATCCGGCA ACGCATATCC GACAATTACA GCAACCTCGG CAGCAATTTT
601 TCCGACCGCG CCGATGAAGC CAACAGAAAA ATGTTTCGAGC ACAATGCCAA
651 GCTCGACCGC TGGGGCAACA GCATGGAGTT TATCAACGGC GTCGCCGCCG
701 GCGCGCTCAA CCCCTTTATC AGCGCGGGCG AAGCCTTGGG CATAGGCGAC
751 ATACTGTACG GAACGCGCTA TGCCATAGAC AAAGCCGCAA TGCGCAACAT
801 CGCCCCCTTG CCGCCGAGG GCAAATTCGC CGTCATCGGC GGCTTGGGCA
851 GCGTGGCGGG CTTTGAAAAG AATACGCGCG AAGCCGTTGA CCGGTGGATA
901 CAGGAAAATC CCAATGCCGC CGAAACCGTC GAAGCCGCTT TCAACGTTGC
951 CGCAGCAGCC AAAGTCGCGA AGTTGGCAAA GGCGGCAAAA CCAGGGAAGG
1001 CTGCGGTTAG CGGGGATTTT GCTGATTCTT ATAAAAGAA ATTGGCTTTG
1051 TCTGATAGTG CGAGACAGTT ATATCAAAAT GCAAAGTATA GAGAAGCTCT
1101 AGATATACAT TATGAAGATT TAATTAGAAG AAAAAGTAT GGTTCATCAA
1151 AATTTATTAA CGGCAGAGAA ATTGACGCTG TTACGAATGA TGCTTTAATA
1201 CAAGCCAAAA GAACAATTTT AGCAATAGAT AAACCTAAAA ATTTCTTAAA
1251 TCAAAAAAAT AGAAAGCAAA TTAAAGCAAC CATCGAAGCA GCAAACCAAC
1301 AGGGAACACG TGCAGAATTT TGGTTTAAAT ACGGTGTTCA TTCACAAGTT
1351 AAGTCATATA TTGAATCAAA AGGCGGCATT GTTAAACAG GTTTAGGAGA
1401 TTA

```

This corresponds to the amino acid sequence <SEQ ID 2472; ORF 730>:

```

m730.pep
  1 VKPLRRLTNL LAACAVAAAA LIQPALAADL AQDPFITDNA QRQHYEPGGK
 51 YHLFGDPRGS VSDRTGKINV IQDYTHQMGN LLIQANING TIGYHTRFSG
101 HGHEEHAPFD NHAADSASEE KGNVDEGFTV YRLNWEGHEH HPADAYDGP
151 GGNYPKPTGA RDEYTYHVNG TARSIKLNPT DTRSIRQRIS DNYSNLGSNF
201 SDRADEANRK MFEHNAKLDR WGNMSMEFNG VAAGALNPFI SAGEALGIGD
251 ILYGTRYAID KAAMRNIAPL PAEGKFAVIG GLGSVAGFEK NTREAVDRWI
301 QENPNAAETV EAVFNVAAAA KVAKLAKAAK PGKAAVSGDF ADSYKKKLAL
351 SDSARQLYQN AKYREALDIH YEDLIRRKTD GSSKFINGRE IDAVTNDALI
401 QAKRTISAID KPNFLNQKN RKQIKATIEA ANQQKRAEF WFKYGVHSQV
451 KSYIESKGGI VKTGLGD*

```

g730 / m730 93.0% identity in 344 aa overlap

```

          10      20      30      40      50      60
g730.pep  VKPLRRLTNLLAACAVAAVALIQPALAADLAQDPFITDNTQRQHYEPGGKYHLFGDPRGS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VKPLRRLTNLLAACAVAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS
          10      20      30      40      50      60

          70      80      90      100     110     120
g730.pep  VSDRTGKINVIQDYTHQMGNLLIQAAIQGNLGYTVRFSGHGHEEHAPFDNHAADSASEE
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      VSDRTGKINVIQDYTHQMGNLLIQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE
          70      80      90      100     110     120

          130     140     150     160     170     180
g730.pep  KGNVDDGFTVYRLNWEGHEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGNNYPKPTGARDEYTYHVNGTARSIKLNPT
          130     140     150     160     170     180

          190     200     210     220     230     240
g730.pep  DTRSIRQRISDNYNNLGSNFSRADEANRKMFEHNAKLDRWGNMSMEFVNGVAAGALNPFI
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m730      DTRSIRQRISDNYNNLGSNFSRADEANRKMFEHNAKLDRWGNMSMEFVNGVAAGALNPFI
          190     200     210     220     230     240

```

1183

	250	260	270	280	290	300
g730.pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAAIGGLGSAAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSAAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
g730.pep	QENPNAAETVEALVNVLPFAKVNLTAKAPGKAAVSGDFSYSYCSFHGSLVKTADGY					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKAAVSGDFADSYKKKLALSDSARQLYQN					
	310	320	330	340	350	360
	370	380	390	400	410	420
g730.pep	KAIAHIQAGDRVLSKDEASGETGYKPVATARYGNPYQETVYIEVSDGIGNSQTLLISNRIHP					
m730	AKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNFNLQKN					
	370	380	390	400	410	420

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2473>:

a730.seq

1	GTGAAACCGC	TGCGAAGACT	CATCAAGCTC	CTTGCCGCCT	GTGCCGTAGC
51	GGCGGCCGCA	CTCATACAGC	CCGCCCTCGC	GGCGGACTTG	CGCAAGACCC
101	CGTTCATTAC	CGATAACGCC	CAACGGCAGC	ACTACGAACC	CGGAGGCAAA
151	TACCACCTCT	TGCGCGACCC	GCGCGGCAGC	GTCTCCGACC	GCACCGGTCA
201	AATCAACGTC	ATCCAAGACT	ATACCCACCG	GATGGGCAAC	CTGCTCATCC
251	AGCAGGCAAA	CATCAACGGC	ACAATCGGCT	ACCACACCCG	CTTTTCCGGA
301	CACGGATACG	AAGAACACGC	CCCCTTCGAC	AACCACGCCG	CCGACAGCGC
351	GAGCGAAGAA	AAAGGCAACG	TTGACGAAGG	CTTTACCGTA	TACCGGCTCA
401	ACTGGGAAGG	ACACGAACAT	CATCCGCGCG	ATGCCTACGA	CGGCCCGAAG
451	GGCGGCAATT	ACCCCAAACC	TACGGGTGCA	CGCGACGAAT	ACACCTATCA
501	CGTCAACGGC	ACAGCAGCA	GCATCAAAT	CAATCCGACC	GACACCGCA
551	GCATCCGGCA	ACGCATATCC	GACAATTACA	GCAACCTCGG	CAGCAATTTT
601	TCCGACCGCG	CCGATGAAGC	CAACAGAAAA	ATGTTTCGAGC	ACAATGCCAA
651	GCTCGACCGC	TGGGGCAACA	GCATGGAGTT	TATCAACGGC	GTCCGCCGCG
701	GGCGGCTCAA	CCCCTTTATC	AGCGCGGGCG	AAGCCTTGGG	CATAGGCGAC
751	ATACTGTACG	GAACCGGCTA	TGCCATAGAC	AAAGCCGCAA	TGCGCAACAT
801	CGCCCCCTTG	CCCGCCGAGG	GCAAATTCGC	CGTCATCGGC	GGCTTGGGCA
851	GCGTGGCGGG	CTTTGAAAAA	AATACGCGCG	AAGCCGTTGA	CCGGTGGATA
901	CAGGAAAACC	CCAATGCCGC	CGAAACCGTC	GAAGCCCTGG	TCAACGTCCT
951	GCGTTTGTCC	AAAGTCAAAA	ACCTGACAAA	GGCGGC AAAA	CCGGGGAAGG
1001	CTGCGGTTAG	CGGGGATTTT	TCTGCTGCAT	ACAATACAAG	AACAAC TAGA
1051	AAAGTTACTA	CAGAAACAGA	GGGGTTAAAT	AGAATCAGAC	AGAACCAGAA
1101	AAATAGTAAT	ATACATGAGA	AAAATTATGG	AAGAGATAAT	CCTAATCATA
1151	TTAATGTTTT	ATCTGGAAAT	TCTATACAAC	ATATACTGTA	TGGAGATGAA
1201	GCAGGAGGTG	GGCATCTTTT	TCCTGGCAAA	CCTGGTAAGA	CAACATTCCC
1251	CCAACATTGG	TCAGCCAGTA	AAATAACTCA	TGAAATTAGT	GATATCGTTA
1301	CATCCCCAAA	AACGCAATGG	TATGCACAGA	CTGGAACAGG	CGGCAAAATAT
1351	ATTGCTAAAG	GAAGACCAGC	TAGGTGGGTA	TCATATGAAA	CGAGAGATGG
1401	AATTCGTATC	AGAACAGTTT	ATGAACCTGC	AACAGGAAAA	GTGGTAAC TG
1451	CATTCCCCGA	TAGAACCTCT	AATCCCAAAT	ATAACCCTGT	AAAATAA

This corresponds to the amino acid sequence <SEQ ID 2474; ORF 730.a>:

a730.pep

1	VKPLRRLIKL	LAACAVAAAA	LIQPALAADL	AQDPFITDNA	QRQHYEPGGK
51	YHLFGDPRGS	VSDRTGQINV	IQDYTHRMGN	LLIQANING	TIGYHTRFSG
101	HGYEEHAPFD	NHAADSASEE	KGNVDEGFTV	YRLNWEGHEH	HPADAYDGPK
151	GGNYPKPTGA	RDEYTYHVNG	TARSIKLNPT	DTRSIRQRIS	DNYSNLGSNF
201	SDRADEANRK	MFEHNAKLDR	WGNMEEFING	VAAGALNPFI	SAGEALGIGD
251	ILYGTRYAID	KAMRNIAPL	PAEGKFAVIG	GLGSVAGFEK	NREAVDRWI
301	QENPNAAETV	EALVNVLPFA	KVNLTAKA	PGKAAVSGDF	SAAYNTRTTR
351	KVTTETEGLN	RIRQNQKNSN	IHEKNYGRDN	PNHINVLSGN	SIQHILYGDE
401	AGGGHLFPKG	PGKTTFPQHW	SASKITHEIS	DIVTSPKTQW	YAQTGTGGKY
451	IAKGRPARVW	SYETRDGIRI	RTVYEPATGK	VVTAFPDRTS	NPKNYPVK*



1184

a730 / m730 88.6% identity in 376 aa overlap

	10	20	30	40	50	60
a730 . pep	VKPLRRLIKLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	:					
m730	VKPLRRLTNLLAACAVAAAAALIQPALAADLAQDPFITDNAQRQHYEPGGKYHLFGDPRGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a730 . pep	VSDRTGQINVIQDYTHRMGNLLIQQANINGTIGYHTRFSGHGYEEHAPFDNHAADSASEE					
	:   :					
m730	VSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHGHEEHAPFDNHAADSASEE					
	70	80	90	100	110	120
	130	140	150	160	170	180
a730 . pep	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
m730	KGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGARDEYTYHVNGTARSIKLNPT					
	130	140	150	160	170	180
	190	200	210	220	230	240
a730 . pep	DTRSIRQIRISDNYSNLGSNFSRADEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
m730	DTRSIRQIRISDNYSNLGSNFSRADEANRKMFEHNAKLDRWGSMEFINGVAAGALNPFI					
	190	200	210	220	230	240
	250	260	270	280	290	300
a730 . pep	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
m730	SAGEALGIGDILYGTRYAIDKAAMRNIAPLPAEGKFAVIGGLGSVAGFEKNTREAVDRWI					
	250	260	270	280	290	300
	310	320	330	340	350	360
a730 . pep	QENPNAAETVEALVNVLPFAKVNLTAAKPGKAAVSGDFSAAYNTRTRKVTETETGLN					
	:     :     :     :     :     :     :     :     :     :     :					
m730	QENPNAAETVEAVFNVAATAAKVAKLAKAAGKPGKAAVSGDFADSY-----KKKLALSDSAR					
	310	320	330	340	350	
	370	380	390	400	410	420
a730 . pep	RIRQNKNSNIHEKNYGRDNPINHINVLSGNSIQHILYGDEAGGGHLFPKGKPGKTTFFQHW					
	::      : : :					
m730	QLYQNAKYREALDIHYEDLIRRKTDGSSKFINGREIDAVTNDALIQAKRTISAIKPKNF					
	360	370	380	390	400	410

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2475>:

```

g731 . seq
1   gatttttcgag cgttttcatG CGAGAACGGT TTGTCTGTGC GCGTCCGCAA
51  TTTGGACGGC GGCAAAATCG CGTTGCCGGT GGACGGCAGG CGTGCCGTCC
101 TCTCTTCCGA CGTTGCCGCA TCCGGCGAAC GCTATACCGC CGAACACGGT
151 TTGTTCGGAA ACGGAACCGA GTGGCACCAG AAAGGCGGCG AAGCCTTTT
201 CGGCTTTACC GATGCCTACG GCAATTCGGT CGAACTTCC TGCCGCGCCC
251 GTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2476; ORF 731.ng&gt;:

```

g731 . pep
1   DFRAFSCENG LSVVRNLDG GKIALRLDGR RAVLSSDVAA SGERYTAEHG
51  LFGNGTEWHQ KGGEAFFGFT DAYGNSVETS CRAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2477>:

```

m731 . seq
1   ATGAATATCA GGTTTTTTCGC GCTGACCGTA CCGGTTTTGT CTTTGGCGGC
51  CTGTGCCGTG CCGGAGGCGT ATGATGACGG CGGACGCGGG CATATGCCGC
101 CCGTTCAAAA CCAAGCCGGC ACGGACGATT TTCGGGCGTT TTCTGCGAG
151 AACGGTTTGT CTGTGCGCGT CCGCCATTG GACAGCGGCA AAGTCGCGTT
201 GCGGCTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG

```

1185

251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGC AACCGAGTGG  
 301 CACCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA  
 351 TTCGGTCGAA ACTTCCTGCC GCGCCCGTTA A

This corresponds to the amino acid sequence <SEQ ID 2478; ORF 731>:

m731.pep  
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TDDFRAFSCE  
 51 NGLSVRVRHL DSGKVALRLD GRRAVLSSDV AASGERYTAE HGLFGNATEW  
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR\*

g731/m731 95.2% identity in 84 aa overlap

g731.pep				10	20	30
				DFRAFSCE	NGLSVRVRNL	DGGKIALRLDGR
m731	LSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCE	NGLSVRVRHL	DSGKVALRLDGR			
	20	30	40	50	60	70

g731.pep	40	50	60	70	80
	RAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVETSCRARX				
m731	RAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVETSCRARX				
	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2479>:

a731.seq  
 1 ATGAATATCA GGTTCCTCGC GCTGACCGTA CCGGTTTGT CTTGGCGGC  
 51 CTGTGCCGTG CCGGAGCGCT ATGATGACGG CGGACGAGGG CATATGCCGC  
 101 CCGTTCAAAA CCAAGCCGGC ACGGCAGATT TTCGGGCATT TTCCTGCGAG  
 151 AACGGTTTGT CTGTGCACGT CCGCCGTTTG GACGGCGGCA GAATCGCGTT  
 201 GCGGTTGGAC GGCAGGCGTG CCGTCCTCTC TTCCGACGTT GCCGCATCCG  
 251 GCGAACGCTA TACCGCCGAA CACGGTTTGT TCGGAAACGG AACCGAGTGG  
 301 CATCAGAAAG GCGGCGAAGC CTTTTTCGGC TTTACCGATG CCTACGGCAA  
 351 TTCGGTCGAA ACCTCCTGCC GCGCCCGCTA A

This corresponds to the amino acid sequence <SEQ ID 2480; ORF 731.a>:

a731.pep  
 1 MNIRFFALTV PVLSLAACAV PEAYDDGGRG HMPPVQNQAG TADFRAFSCE  
 51 NGLSVHVRRL DGGRIALRLD GRRAVLSSDV AASGERYTAE HGLFGNGTEW  
 101 HQKGGEAFFG FTDAYGNSVE TSCRAR\*

a731/m731 94.4% identity in 126 aa overlap

a731.pep	10	20	30	40	50	60
	MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTADFRAFSCE	NGLSVHVRRL				
m731	MNIRFFALTVPVLSLAACAVPEAYDDGGRGHMPPVQNQAGTDDFRAFSCE	NGLSVRVRHL				
	10	20	30	40	50	60

a731.pep	70	80	90	100	110	120
	DGGRIALRLD	GRRAVLSSDVAASGERYTAEHGLFGNGTEWHQKGGEAFFGFTDAYGNSVE				
m731	DSGKVALRLD	GRRAVLSSDVAASGERYTAEHGLFGNATEWHQKGGEAFFGFTDAYGNSVE				
	70	80	90	100	110	120

a731.pep TSCRARX  
 |  
 m731 TSCRARX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2481>:

g732.seq  
 1 ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT  
 51 CAGCGGCGTG GCCGTAAGTC TGGCGGTGCA GGGTTTTGCC GCCGagaagg  
 101 ACGGgcgGGA TAACGAagtc CTGCCGGTGC AATCCATCCG TACGATGGCG

```

151 GAGGTTTACG GTCAGATTAA GGCAAACTAC TATCATGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGTTT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGAGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACGCGCGGT
451 ATGACGGTCA GCGAAGCGGT GAAAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACCTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACCGGCG CGGTCGGCGT GTCGGCGGCG TTTCTGCCGT CTGAAGCGGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCGTTCCCGA GGATTATGTG TACGGTATGG GCGGCGACCC TTTGGCGGGT
901 ATTCTCTCCG AGTTGAAAAC GATTCCGATG ACGgtattGG TcaaTTCCGG
951 TTCggcttCC GCGTCGGAGA TTGtcgCCGG CGCATTGCAG GACCACAAAC
1001 GCGCGGTACG CGTCGGTACG CAGAGCTTCG GTAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGTTGACGA CCGCCCTGTA
1101 TTACACGCCG AACGACCGTT CCATTACGGC ACAGGGGATT GTTCCCGATG
1151 TCgaagTAAA AGATAAGGAA CGTACTTTTG AAAGCCGCGA GGGCGACCTG
1201 GTCGGACACA TCGGCAATCC CTTgggcGGC GAGGATGTGA ACAGTGAAAC
1251 CCTtgcCGTA CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GCAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCGAAC
1351 CCTGCGAAAG ACGATCAGTT GCGTAAGGCT TTGGATTGG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GCGGAAAAAA CCGGTTTCAA
1451 ATAAAGATAA AAAAGATAAG AAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2482; ORF 732>:

g732.pep

```

1 MSKPVFKKIA LYLGAISGV AVSLAVQGFA AEKDRDNEV LPVQSIRTMA
51 EVYGOIKANY YHDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIEDTAE RAEVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVNLTIRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGGL
251 LTGAVGVSAF FLPSEAVVVS TKGRDGDGDM VLKAVPEDYV YMGGDPLAG
301 IPAELKTIPM TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFGRGSVQT
351 LIPLNNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RTFESREADL
401 VGHIGNPLGG EDVNSSETLAV PLEKADADKPA AKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKDKDK K*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2483>:

m732.seq

```

1 ATGTCGAAAC CTGTTTTTAA GAAAATCGCA CTTTATACTT TGGGTGCAAT
51 CAGCGGCGTG GCCGTCAGTC TGCGCGTGCA GGGTTTTGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGGTGC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCGC
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCCGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACCTTGTCGC GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCCGATT ACGGCTATAT CCGCGTGTCG CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAAGAGCT GGTAAAGGAA AATAAAGGAA
701 AACCGCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACGGCATG GTACTGAAAG
851 CCATTCTCTG AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCTCTCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCCGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTACG CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCCTT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA

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1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCGATG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTTG AAAGCCGCGA GGCGGATTTG
1201 GTCGGACACA TCGGCAATCC CTTGGGCGGC GAGGATGTGA ACGGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAAGGAC GAGGATTTGT CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAAG ACGACAGTT GCGGAAAGCT TTGGATTAG TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGCG GCGGAAAAAG CCGGTTTCAA
1451 ATAAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2484; ORF 732>:

m732.pep

```

1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EVYGOIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGGLGME IGQEDGFVKV VSPIDETPAE RAGVKSDFI VKIDNVSTRG
151 MTVSEAVKKM RGKPGTKITL TLRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDPGGL
251 LTGAVGVSA FLPSEAVVVS TKGRDGKDRM VLKAIPEDYV YGMGGDSLGA
301 IPAELKTIPT TVLVNNGSAS ASEIVAGALQ DHKRAVIVGT QSFSGKSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNGETLAV PLEKADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAACK FVSNKDKKDK KDKK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 732 shows 98.2% identity over a 491 aa overlap with a predicted ORF (ORF732.a) from *N. gonorrhoeae*:

m732/g732 98.2% identity in 491 aa overlap

m732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
g732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
m732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
g732	YHDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
m732.pep	130	140	150	160	170	180
	VSPIDETPAERAGVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
g732	VSPIDETPAERAEVKSDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
m732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
g732	IVVNLTRAIKVKSVRHHLIEPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
m732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS TKGRDGKDRMVLKAIPEDYVYGMGGDSLGA					
g732	LDLRDDPGGLLTGAVGVSAFLPSEAVVVS TKGRDGKDMVLKAVPEDYVYGMGGDPLAG					
	250	260	270	280	290	300
m732.pep	310	320	330	340	350	360
	IPAELKTIPTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
g732	IPAELKTIPTVLVNNGSASASEIVAGALQDHKRAVIVGTQSFSGKSVQTLIPLSNGSAV					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m732.pep	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNGETLAV					
	:					
g732	KLTTALYYTPNDRSIQAQGIVPDVEVKDKERTFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m732.pep	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	:					
g732	PLEKDADKPAAKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAAKK					
	430	440	450	460	470	480
	490					
m732.pep	PVSNDKKDKDKKX					
g732	PVSNDKKDKKX					
	490					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2485>:

```

a732.seq
1  ATGTCGAAAC CTGTTTTTAA GAAATCGCA CTTTATACTT TGGGTGCAAT
51  CAGCGGCGTG GCCGTCAGTC TGGCGGTGCA GGGTTTGGCC GCCGAGAAGG
101 ACAGGCGGGA TAACGAAGTC CTGCCGTGTC AATCCATCCG CACAATGGCG
151 GAGGTTTACG GTCAAATCAA GGCAACTAC TATCAGGACA AACCCGATGC
201 CGATTTGTTT GAAGGTGCGA TGAAGGGTAT GGTGGCCGGT TTGGATCCCG
251 ATTCCGAATA TATGGATAAA AAAGGTTATG CCGAGATAAA GGAGTCCACC
301 AGCGGCGAAT TTGGCGGCTT GGGGATGGAA ATCGGGCAGG AAGACGGATT
351 TGTCAAAGTG GTTTCGCCGA TTGAGGACAC GCCTGCGGAA CGGGCGGGGG
401 TGAAAAGCGG CGATTTTCATT GTGAAAATCG ATAATGTTTC GACACGCGGC
451 ATGACGGTCA GCGAAGCGGT GAAGAAAATG CGGGGCAAGC CGGGTACGAA
501 GATTACTTTG ACGCTGTCTG GCAAAAATGC CGACAAGCCG ATAGTCGTCA
551 ACCTGACCCG TGCCATTATT AAAGTGAAAA GCGTCCGCCA TCACCTGATC
601 GAACCGGATT ACGGCTATAT CCGCGTGTCT CAGTTCCAAG AGCGGACGGT
651 CGAAAGCGTC AATACCGCCG CAAAGAGCTT GGTAAAGGAA AATAAAGGAA
701 AACCCTCAA GGGGCTGGTG TTGGATTGTC GCGACGACCC CGGCGGGCTT
751 TTGACTGGCG CGGTCGGCGT GTCGGCGGCA TTTCTGCCGT CTGAAGCAGT
801 CGTCGTCAGC ACCAAGGGAC GCGACGGCAA AGACCGCATG GTACTGAAAG
851 CCGTTCCTGA AGATTATGTG TACGGGATGG GCGGCGATTG GTTGGCGGGC
901 ATTCCTGCCG AGTTGAAAAC CATACCGATG ACGGTATTGG TCAATTCGGG
951 TTCGGCTTCC GCGTCGGAGA TTGTCGCAGG TGCATTGCAG GATCATAAAC
1001 GCGCGGTCAT CGTCGGTACG CAGAGCTTCG GCAAAGGTTT GGTTCAGACT
1051 TTGATTCTCT TGTCCAACGG CAGCGCGGTC AAGCTGACAA CGGCACTGTA
1101 TTATACGCCG AACGACCGTT CTATTCAGGC GCAGGGGATT GTTCCCAGTG
1151 TCGAAGTAAA AGATAAGGAA CGCATTTTGT AAAGCCCGCA GCGGATTTTG
1201 GTCGGACACA TCGGCAATCC TTTGGGCGGC GAGGATGTGA ACAGTGAAAC
1251 CCTTGCCGTG CCGCTTGAAA AAGATGCGGA TAAGCCCGCT GTAAAAGAAA
1301 AAGGTAAAAA GAAAAGGAC GAGGATTGTG CTTCAAGGCG GATTCCCAAC
1351 CCTGCCAAG ACGACCAATT GCGGAAAGCT TTGGATTAGT TCAAGTCGCC
1401 CGAGCAGTGG CAGAAGTCTT TGGGGCTGGC GGCGAAAAAG CCGGTTTCAA
1451 AATAAGATAA GAAAGATAAA AAAGATAAGA AGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2486; ORF 732.a>:

```

a732.pep
1  MSKPVFKKIA LYTLGAISGV AVSLAVQGFA AEKDRRDNEV LPVQSIRTMA
51  EYVQGIKANY YQDKPDADLF EGAMKGMVAG LDPHSEYMDK KGYAEIKEST
101 SGEFGLGME IGQEDGFVKV VSPIEDTPAE RAGVKSGDFI VKIDNVSTRG
151 MTVSEAVKRM RGKPGTKITL TLSRKNADKP IVVNLTRAI KVKSVRHHLI
201 EPDYGIRVS QFQERTVESV NTAAKELVKE NKGKPLKGLV LDLRDDPGGL
251 LTGAUGVSAA FLPSEAVVVS TKGRDGKDRM VLKAVPEDYV YGMGGDSLAG
301 IPAELKTIPM TVLVNSGSAS ASEIVAGALQ DHKRAVIVGT QSFKGKSVQT
351 LIPLSNGSAV KLTTALYYTP NDRSIQAQGI VPDVEVKDKE RIFESREADL
401 VGHIGNPLGG EDVNSETLAV PLEKDADKPA VKEKGKKKKD EDLSSRRIPN
451 PAKDDQLRKA LDLVKSPEQW QKSLGLAAKK PVSNDKKDKD KDKK*

```

a732/m732 99.6% identity in 494 aa overlap

a732.pep	10	20	30	40	50	60
	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
m732	MSKPVFKKIALYTLGAISGVAVSLAVQGFAAEKDRRDNEVLPVQSIRTMAEVYGOIKANY					
	10	20	30	40	50	60
a732.pep	70	80	90	100	110	120
	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
m732	YQDKPDADLFEGAMKGMVAGLDPHSEYMDKKGYAEIKESTSGEFGGLGMEIGQEDGFVKV					
	70	80	90	100	110	120
a732.pep	130	140	150	160	170	180
	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
m732	VSPIEDTPAERAGVKSGDFIVKIDNVSTRGMTVSEAVKKMRGKPGTKITLTLSRKNADKP					
	130	140	150	160	170	180
a732.pep	190	200	210	220	230	240
	IVVNLTRAIKVKSVRHHLEIPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
m732	IVVNLTRAIKVKSVRHHLEIPDYGYIRVSQFQERTVESVNTAAKELVKENKGKPLKGLV					
	190	200	210	220	230	240
a732.pep	250	260	270	280	290	300
	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGDSLAG					
m732	LDLRDDPGGLLTGAVGVSAFLPSEAVVSTKGRDGKDRMVLKAVPEDYVYGMGDSLAG					
	250	260	270	280	290	300
a732.pep	310	320	330	340	350	360
	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFQKGSVQTLIPLSNGSAV					
m732	IPAELKTIPMTVLVNSGSASASEIVAGALQDHKRAVIVGTQSFQKGSVQTLIPLSNGSAV					
	310	320	330	340	350	360
a732.pep	370	380	390	400	410	420
	KLTTALYYTFNDRSIAQGGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
m732	KLTTALYYTFNDRSIAQGGIVPDVEVKDKERIFESREADLVGHIGNPLGGEDVNSETLAV					
	370	380	390	400	410	420
a732.pep	430	440	450	460	470	480
	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
m732	PLEKDADKPAVKEKGKKKKDEDLSSRRIPNPAKDDQLRKALDLVKSPEQWQKSLGLAACK					
	430	440	450	460	470	480
a732.pep	490					
	PVSNDKDKDKDKKX					
m732	PVSNDKDKDKDKKX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2487>:

g733.seq  
 1 ATGATGAATC CGAAAACCTT GGGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGCCG GCGGCGGGCA TAAAAACCTG TATTATTACG  
 101 GCGGTTATCC CGATACCGTC TATGAAGGTT TGA AAAACGc cGACACTTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGCGG AAGCCGCCAA  
 201 CAAAAAATG AATGCCGCCG CGGGTGC GCA CGCCATTTG GGACTGCTGC

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251 TT'TCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAATT TGAAGAAGAG  
 301 AA'AAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGtaaAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2488; ORF 733>:

g733.pep

1 MMNPKTLGRL SLCAAVLALT ACAGGGHKNL YYYGGYPDTV YEGLKNDTDS  
 51 LGKQTEKMEK YFAEAANKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEED  
 101 KR.LFPESGVF MDFLMKTGKG GKR\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2489>:

m733.seq

1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACTTCTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCACA CGCCCATCTG GGAAGTCTGC  
 251 TT'TCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AA'AAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2490; ORF 733>:

m733.pep

1 MMNPKTLSRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDTDS  
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEED  
 101 KR.LFPESGVF MDFLMKTGKG GKR\*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 733 shows 94.3% identity over a 123 aa overlap with a predicted ORF (ORF733.a) from *N. gonorrhoeae*:

m733/g733

	10	20	30	40	50	60
m733.pep	MMNPKTLSRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDTDSL	LGKQTEKMEK				
g733	MMNPKTLGRLSLCAAVLALTACAGGGHKNLYYYGGYPDTVYEGLKNDTDSL	LGKQTEKMEK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGA	FRQFEEDKRLFPESGVFMDFLMKTGKG				
g733	YFAEAANKMNAAPGAHAHLGLLLSRSGDKEGA	FRQFEEDKRLFPESGVFMDFLMKTGKG				
	70	80	90	100	110	120
m733.pep	GKRX					
g733	GKRX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2491>:

a733.seq

1 ATGATGAATC CGAAACCTT GAGCCGTTTG TCGCTGTGTG CGGCGGTCTT  
 51 GGCTCTGACC GCCTGCGGCG GCAACGGGCA AAAATCCCTG TATTATTACG  
 101 GCGGCTATCC CGATACCGTC TATGAAGGTT TGAAAAACGA CGACTTCTCG  
 151 TTGGGCAAGC AGACCGAAAA GATGGAAAAA TACTTTGTGG AAGCCGGCAA  
 201 CAAAAAATG AATGCCGCCC CGGGTGCACA CGCCCATCTG GGAAGTCTGC  
 251 TT'TCCCGTTC GGGAGACAAA GAGGGCGCGT TCCGCCAGTT TGAAGAAGAG  
 301 AA'AAGGCTGT TTCCCGAATC GGGCGTATTT ATGGACTTCC TGATGAAAAC  
 351 CGGTAAAGGA GGCAAGCGAT GA

This corresponds to the amino acid sequence <SEQ ID 2492; ORF 733.a>:

a733.pep

1191

1 MMNPKTSLRL SLCAAVLALT ACGGNGQKSL YYYGGYPDTV YEGLKNDDTS  
 51 LGKQTEKMEK YFVEAGNKKM NAAPGAHAHL GLLLSRSGDK EGAFRQFEEE  
 101 KRLFPESGVF MDFLMKTGKG GKR\*

a733/m733 100.0% identity in 123 aa overlap

	10	20	30	40	50	60
a733.pep	MMNPKTSLRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
m733	MMNPKTSLRLSLCAAVLALTACGGNGQKSLYYYGGYPDTVYEGLKNDDTSLGKQTEKMEK					
	10	20	30	40	50	60
	70	80	90	100	110	120
a733.pep	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPEESGVFMDFLMKTGKG					
m733	YFVEAGNKKMNAAPGAHAHLGLLLSRSGDKEGAFRQFEEERKLFPEESGVFMDFLMKTGKG					
	70	80	90	100	110	120
a733.pep	GKRX					
m733	GKRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2493>:

g734.seq

1 ATGATGAAAA AGATACTGGC AGTATCGGCA CTATGCCTGA TGACTGCGGC  
 51 GGCACAGGCT GCCGATACTT ACGGCTATCT CGCCGTTTGG CAGAATCCGC  
 101 AGGATGCAAA CGATGTTTTG CAGGTTAAAA CCACAAAAGA AGATTCCGGC  
 151 AAAAGCGAAG CGTTTGCCGA GTTGAAGCC TTTTGCAAAG GTCAGGACAC  
 201 GCTTGCGGGC ATTGCCGAAG ACGAGCCGAC CGGATGCCGG TCGGTCGTGT  
 251 CGCTGAACAA TACCTGTGTC TCGCTGGCAT ACCCGAAAGC CTGGGCGCG  
 301 ATGCGCGTTG AAAACGCCGT CGTGATTACT TCTCCGCGTT TTACGAGCGT  
 351 TCATCAGGTC GCACTCAACC AGTGCATAAA AAAATACGGC GCACAGGGAC  
 401 AATGCGGCTT GGAAACAGTG TATGCACGT CATCTTCTTA TTACGGCGGG  
 451 GCTGTTGCT CTTAATCCA ACACCTGAAA TAA

This corresponds to the amino acid sequence <SEQ ID 2494; ORF 734.ng>:

g734.pep

1 MMKILAVSA LCLMTAAQA ADTYGYLAVW QNPQDANDVL QVKTTKEDSA  
 51 KSEAFAELEA FCKGQDTLAG IAEDEPTGCR SVVSLNNTCV SLAYPKALGA  
 101 MRVENAVVIT SPRFTSVHGV ALNQCIKKYG AQGQCGLTV YCTSSSYGG  
 151 AVRSLIQHLK \*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2495>:

m734.seq (partial)

1 TCGGGCATTG CTGAAGACGA GCCGACCGGA TGCCGGTCGG TCGTGTGCT  
 51 GAACAATACC TGTGTCGCGC TGGCATACCC GAAAGCCTTG GGCGCGCTGC  
 101 GTGTCGACAA CGCCGTCGTG ATTACTTCTC CGCGTTTAC GAGCGTTCAT  
 151 CAGGTCGCAC TCAACCAAGT CATCAAAAAA TACGGCGTAC AGGGACAATG  
 201 CGGCTTGGAA ACAGTGTATT GCACATCTT TTCTTATTAC GGCGGAACGT  
 251 TGGCTCTTT GATTCAAAAT CTCAAATAA

This corresponds to the amino acid sequence <SEQ ID 2496; ORF 734>:

m734.pep (partial)

1 SGIAEDEPTG CRSVSLNNT CVALAYPKAL GALRVDNAV VITSPRFTSVH  
 51 QVALNQCIKK YGVQGCGLT TVYCTSSSY GGTVRSLIQN LK\*

m734/g734 92.4% identity in 92 aa overlap

	10	20	30
m734.pep	SGIAEDEPTGCRSVVSLNNTCVALAYPKAL		
g734	VLQVKTTKEDSAKSEAFAELEAFCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKAL		



		40	50	60	70	80	90
m734.pep		GALRVDNAVVITS	SPRFTSVH	QVALNQCIKKYGV	QGCGLET	VYCTSSSY	YGTVRSLIQN
g734		GAMRVENAVVITS	SPRFTSVH	QVALNQCIKKYGA	QGCGLET	VYCTSSSY	YGAVRSLIQH
		100	110	120	130	140	150
m734.pep	LKX						
g734	LKX						
	160						

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a734.seq
1 ATGATGAAAA AGATACTGGC CGTATCGGCA CTATGCCTGA TGACTGCGGC
51 GGCACGGGGCT GCCGATATCT ACGGCTATCT CGCCGTTTGG CAGAATCCGC
101 AGAATGCAAA CGATGTTTTC CAGGTTAAAA CCACAAAAGA AGATTGCGAC
151 AAAAGCGAAG CGTTTGGCCA GTTGGAAAGT TCTGCAAAAG GTCAGACAC
201 GCTTGCGGGC ATTGCCGAAG ACTGAGCCGAC CGGATGCCGG TCGGTCGTGT
251 CGCTGAACAA TACCTGTGTC GCGCTGGCAT ACCCGAAAGC CTTGGGCGCG
301 ATGCGCGTTG AAAACGCCGT TGTGATTACT TCTCCGCGTT TTACGAGCGT
351 TTATCAGGTC GCACTCAACC AGTGCATCAA AAAATACGGC GCACAGGGAC
401 AATGCGGCTT GGAAACAGTG TATTGCACGT CTTCTTCTTA TTACGGGGGA
451 ACTGTGCGCT CTTTGATTCA AAATCTCAA TAA
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a734.pep
  1  MMKKILAVSA LCLMTAAARA ADTYGYLAVW QNPQNANDVL QVKTTKEDST
 51  KSEAFAELEA FCKGQDTLAG IAEDPTGCR SVVSLNNTCV ALAYPKALGA
101 MRVENAVVIT SPRTSVYQV ALNQCIKKYG AQGCQGLETV YCTSSSYGG
151 TVRSLIOLNK *
```

	10	20	30	40	50	60
a734.pep	MMKKILAVSALCLMTAAARAADTYGYLAVWQNPQNANDVLQVKTTKEDSTKSEAFAELEA					
	:           :           :           :					
g734	MMKKILAVSALCLMTAAAQAADTYGYLAVWQNPQDANDVLQVKTTKEDSAKSEAFAELEA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a734.pep	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVALAYPKALGAMRVENAVVITSPRFTSVYQV					
	:           :           :           :					
g734	FCKGQDTLAGIAEDEPTGCRSVVSLNNTCVSLAYPKALGAMRVENAVVITSPRFTSVHQV					
	70	80	90	100	110	120
	130	140	150	160		
a734.pep	ALNQCIKKYGAGQGCGLETVYCTSSSYGGTVRSLIQNLKX					
	:           :           :					
g734	ALNQCIKKYGAGQGCGLETVYCTSSSYGGAVRSLIQHKLKX					
	130	140	150	160		

```
m735.seq
1  ATGAATCTCG  TGAAACTGCT  GGCGAATAAC  TGGCAACCGA  TTGCCATTAT
51  CGCGCTTTGC  GGCACGGGCT  TGGCTGTGTC  GCACCATCAA  GGCTACAAGT
101 CGGCATTTCG  GAAGCAGCAG  GCGGTCATCG  ACAAGATGGA  GCGCGACAAG
151 GCGCAAGCCC  TGCTGTTGTC  GGCTCAAAAC  TATGCGCGCG  AACTGGAACT
201 GGCACGCGCG  GAAGCTAAAA  AATATGAAGT  CAAGGCGCAG  GCTGTCGGCA
251 TGGCTTTGCG  GAAAAAACAG  CGGGAAGTCA  GCCGCTGTA  AACTGGAAAA
301 AAAAAGGAAA  TCGAAATGTG  CCTTACTCAA  GACGCTAAAA  ATGCAAGCGG
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1193

351 CGGTTGCATT GACGGCTTTG GCTCTCACGG CCTGCAGCTC TACAACCGCG  
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2500; ORF 735>:

m735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIDKMERDK  
 51 AQALLLSAQN YARELELARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN  
 101 KKEIENVLTQ DRKNASGGCI DFGSHGLQL YNRALGYGN\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2501>:

a735.seq

1 ATGAATCTCG TGAACTGCT GGCGAATAAC TGGCAACCGA TTGCCATCAT  
 51 CGCGCTTGTC GGCACGGGTT TGGCGGTGTC GCACCATCAA GGCTACAAGT  
 101 CGGCTTTTGC GAAGCAGCAG CGGCTCATTC AGAAAATGAA GCGCGACAAG  
 151 GCGCAAGCCC TGCTGTTGTC GGCTCAAAAC TACGCCCGCG AACTGGAACA  
 201 GGC GCGTGCG GAAGCTAAAA AATATGAAGT CAAGGCGCAC GCCGTCGGCA  
 251 TGGCTTTGGC GAAAAACAG GCGGAAGTCA GCCGTCTGAA AACGGAAAT  
 301 AAAAAGGAAA TCGAAAATGT CCTACTCAA GACCGTAAAA ATGCAGGCGG  
 351 CGGTTGTATT GACGGCTTTG GCCATCACGG CTTGCAGCTC TACAAGCGCG  
 401 CCCTCGGCTA CGGAAATTAA

This corresponds to the amino acid sequence <SEQ ID 2502; ORF 735.a>:

a735.pep

1 MNLVKLLANN WQPIAIIALV GTGLAVSHHQ GYKSAFAKQQ AVIEKMKRDK  
 51 AQALLLSAQN YARELEQARA EAKKYEVKAH AVGMALAKKQ AEVSRLKTEN  
 101 KKEIENVLTQ DRKNAGGGCI DFGHHGLQL YKRALGYGN\*

a735/m735 95.7% identity in 139 aa overlap

	10	20	30	40	50	60
a735.pep	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIEKMKRDKAQALLLSAQN					
m735	MNLVKLLANNWQPIAIIALVGTGLAVSHHQGYKSAFAKQQAVIDKMERDKAQALLLSAQN					
	10	20	30	40	50	60
	70	80	90	100	110	120
a735.pep	YARELEQARA EAKKYEVKAH AVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNAGGGCI					
m735	YARELELARA EAKKYEVKAH AVGMALAKKQAEVSRLKTENKKEIENVLTQDRKNASGGCI					
	70	80	90	100	110	120
	130	140				
a735.pep	DGFHHGLQLYKRALGYGNX					
m735	DFGSHGLQLYNRALGYGNX					
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2503>:

g736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC  
 51 CTTCGGCAGT ATCAGCTGT TTCTGCTGAA CATTGTCG AAATCCGGCA  
 101 CGGCTTTGCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC  
 151 GTGCTGTGCG TGCTGATTGT TGCCGTTTCG GGGCTGTCG TCGGTATGGT  
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAA TCCGCCGATA  
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TCGCGAACT GGGTCCCGTG  
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTGCGA TGACCAGCGA  
 351 AATCGGTTTG ATGAAAACGA CCGGACAGCT CGAAGCGATG AACGTGATGG  
 401 CGGTCAACCC CGTCGCGCGC GTGGTTGCCC CGCGTTTTCG GCGGGCGGTG  
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCGG GCATTTCGG  
 501 CGCGTATTTC GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT  
 551 GGCCGCAGAT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT

1194

601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA  
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA  
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA  
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2504; ORF 736>:

g736.pep

1 MNFIRSVGAK TLGLIQSFGS ITLFLNILA KSGTAFARPR LSVRQVYFAG  
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV  
 101 LAAILFASSA GGAMTSEIGL MKTTGQLEAM NVMVNPVAR VVAPRFWAGV  
 151 FSPMLLASIF NVAGIFGAYL VGVSWLGLDS GIFWPQMONN ITIHYDVI  
 201 LIKSAAFGVA VTLIAVHQQF HCIPTSEGIL RASTRTVVSS ALTILAVDFI  
 251 LTAWMFTD\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2505>:

m736.seq

1 ATGAATTTTA TCCGTTCCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC  
 51 CTTCGCGAGT ATCACGCTGT TTCTGCTGAA CATTTTGGCG AAATCCGGCA  
 101 CGGCTTTTCG CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC  
 151 GTGCTGTCCG TGCTGATTGT TGCCGTTTCG GGGCTGTCG TCGGTATGGT  
 201 TTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATCAAA TCCGCCGATA  
 251 TTTTGGGCTA TATGGTCGCG GCTTCTCTGT TGC CGCAACT GGGTCCCGTG  
 301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GCGGTCGCA TGACCAGCGA  
 351 AATCGGTTTG ATGAAAACGA CCGACAGCT CGAAGCGATG AACGTGATGG  
 401 CCGTCAACCC CGTCGCCCGC GTGGTTGCC CGCGTTTTCG GCGGGCGGTG  
 451 TTTTCTATGC CGCTTTTGGC TTCGATTTC AACGTCGCG GCATTTTCGG  
 501 CGCGTATTTG GTCGGCGTGA GCTGGCTGGG TTTGGACAGC GGTATTTTCT  
 551 GGCCGCGAGT GCAGAACAAC ATTACGATAC ATTACGATGT AATCAACGGT  
 601 TTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA  
 651 TCAGGGCTTC CACTGCATCC CGACTTCGGA AGGCATTTTG CGCGCCAGCA  
 701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA  
 751 TTGACCGCGT GGATGTTTAC AGATTGA

This corresponds to the amino acid sequence <SEQ ID 2506; ORF 736>:

m736.pep

1 MNFIRSVGAK TLGLIQSLGS ITLFLNILA KSGTAFVRPR LSVRQVYFAG  
 51 VLSVLIVAVS GLFVGMVLGL QGYTQLSKFK SADILGYMVA ASLLRELGPV  
 101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NVMVNPVAR VVAPRFWAGV  
 151 FSPMLLASIF NVAGIFGAYL VGVTWLGLDS GIFWSQMONN ITIHYDVI  
 201 LIKSAAFGVA VTLIAVHQQF HCVPTSEGIL RASTRTVVSS ALTILAVDFI  
 251 LTAWMFTD\*

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 736 shows 97.7% identity over a 258 aa overlap with a predicted ORF (ORF736.ng) from *N. gonorrhoeae*:

m736/g736

	10	20	30	40	50	60
m736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNILAKSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	:     :     :     :     :					
g736	MNFIRSVGAKTLGLIQSFGSITLFLNILAKSGTAFARPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m736.pep	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	:     :     :     :     :					
g736	GLFVGMVLGLQGYTQLSKFKSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m736.pep	MKTTEQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					
	:     :     :     :     :					
g736	MKTTGQLEAMNVMVNPVARVVAPRFWAGVFSMPLLASIFNVAGIFGAYLVGVSWLGLDS					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					
g736	GIFWPQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					
	190	200	210	220	230	240
	250	259				
m736.pep	ALTILAVDFILTAWMFTDX					
g736	ALTILAVDFILTAWMFTDX					
	250					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2507>:

a736.seq

```

1  ATGAATTTTA TCCGTTCGT CGGGGCGAAA ACCCTCGGCC TTATTCAATC
51  TCTCGGCAGT ATCACGCTGT TTCTGCTGAA TATTCTGGCG AAATCCGGTA
101 CGGCTTTCGT CCGTCCGCGC CTGAGCGTGC GCCAAGTGTA TTTTGCCGGC
151 GTGCTGTCGG TGTTGATTGT TGCCGTTTCA GGGCTGTTTG TCGGCATGGT
201 CTTGGGTTTG CAGGGCTATA CGCAGTTGTC GAAATTCAAA TCCGCCGATA
251 TTTTGGGCTA TATGGTCGCG GCTTCGCTGT TGC CGAACT GGGTCCGGTG
301 TTGGCGGCGA TTCTGTTTGC CAGCAGCGCG GGCCTGCGA TGACCAGCGA
351 AATCGGTTTG ATGAAAACGA CCGAACAGCT CGAAGCGATG AACGTGATGG
401 CGGTAAACCC CGTCGCCCGA GTGGTTGCGC CGCGCTTTTG GCGGGCGGTG
451 TTTTCCATGC CGCTTTTGGC TTCGATTTC AACGTGGCGG GTATTTTCGG
501 CGCGTATTTG GTCGGTGTA CCTGGCTGGG CTTGGACAGC GGTATTTTCT
551 GGTGCAAAAT GCAGAACAA ATCACGATAC ATTACGATGT AATCAACGCT
601 CTGATCAAAT CCGCCGCGTT CGGCGTGGCG GTAACGCTGA TTGCCGTGCA
651 TCAGGGCTTC CACTGCGTCC CGACCTCGA AGGCATTTTG CGGCCAGCA
701 CGCGCACGGT GGTTCGTCC GCCCTGACGA TTTTGGCGGT CGATTTTATA
751 TTGACCGCGT GGATGTTTAC AGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 2508; ORF 736.a>:

a736.pep

```

1  MNFIRSVGAK TLGLIQSLGS ITLFLNLA KSGTAFVRPR LSVRQVYFAG
51  VLSVLIVAVS GLFVGMVLGL QGYTQLSKEF SADILGYMVA ASLLRELGPV
101 LAAILFASSA GGAMTSEIGL MKTTEQLEAM NMAVNPVAR VVAPRFWAGV
151 FSPMLLASIF NVAGIFGAYL VGVTLWGLDS GIFWSQMNN ITIHYDVING
201 LIKSAAFGVA VTLIAVHQGF HCVPTSEGIL RASTRTVVSS ALTILAVDFI
251 LTAWMFTD*

```

a736/m736 100.0% identity in 258 aa overlap

	10	20	30	40	50	60
a736.pep	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
m736	MNFIRSVGAKTLGLIQSLGSITLFLNLA KSGTAFVRPRLSVRQVYFAGVLSVLIVAVS					
	10	20	30	40	50	60
	70	80	90	100	110	120
a736.pep	GLFVGMVLGLQGYTQLSKFSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
m736	GLFVGMVLGLQGYTQLSKFSADILGYMVAASLLRELGPVLAAILFASSAGGAMTSEIGL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a736.pep	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLWGLDS					
m736	MKTTEQLEAMNMAVNPVARVVAPRFWAGVFSMPMLLASIFNVAGIFGAYLVGVTLWGLDS					
	130	140	150	160	170	180
	190	200	210	220	230	240
a736.pep	GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRVVS					

1196

```

m736      GIFWSQMNNITIHYDVINGLIKSAAFGVAVTLIAVHQGFHCVPTSEGILRASTRTVVSS
           190      200      210      220      230      240

           250      259
a736.pep   ALTILAVDFILTAWMFTDX
           |||||
m736      ALTILAVDFILTAWMFTDX
           250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2509>:

```

g737.seq
1   atgaACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTTGGG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCGGC TTGGGCGCGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2510; ORF 737>:

```

g737.pep
1   MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDDGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2511>:

```

m737.seq..
1   ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAAT CATCAGCCGC
151 GCGCAAGCCG AAAAAGCAGC GTTGGGCGGT GTCGGCGGCA AAATCACCGA
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCC TACCGGCCGC
301 GTGATTTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2512; ORF 737>:

```

m737.pep
1   MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEY KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 737 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF737.a) from *N. gonorrhoeae*:

m737/g737

```

           10      20      30      40      50      60
m737.pep   MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRQAQEAALAR
           |||||
g737        MNIKHLLLTAAATALLGISAAPALAHHDGHGDDDHGHAHQHGKQDKIISRQAQEAALAR
           10      20      30      40      50      60

           70      80      90      100     109
m737.pep   VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           |||||
g737        VGGKITDIDLEHDDGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX
           70      80      90      100

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2513>:

1197

a737.seq

```

1 ATGAACTTCA AACGCCTTCT CTTGACCGCC GCCGCAACCG CACTGATGGG
51 CATTTCGCC CCCGCACTCG CCCACCAGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGCCGCG
301 GTGATTCCT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2514; ORF 737.a>:

a737.pep

```

1 MNFKRLLTA AATALMGISA PALAHHDGHG DDDHGHAHQ HSKQDKIISR
51 AQAEEAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQY KVVVDARTGR
101 VISSRRDD*

```

a737/m737 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a737.pep	MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAHQHSKQDKIISRAQAEEAALAR					
m737	MNIKHLTLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEEAALAR					
	10	20	30	40	50	60

	70	80	90	100	109
a737.pep	VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX				
m737	VGGKITDIDLEHDNGRPHYDVEIVKNGQYKVVVDARTGRVISSRRDDX				
	70	80	90	100	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2515>:

g738.seq

```

1 ATGTCCGCTG AAACGACCGT ATCCGGCGCG CGCCCCGCGG CCAAACTGCC
51 GATTATCATC CTGCCCTGCT TCCTTTGGAT AGGCATCATC CCCTTTACCT
101 TCGCACTCAG GCTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCGGCCGCGC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCCGCCA TCAGCTTCCT CCTGTTTGCA ATGGCGGCAT
251 TTTGGTGGCT TCAGGCACGC CTGATGAACC TGATTATACC CGGAATGAAC
301 GACATCGCCT CTTGGGTTTT CATCTTGCTC GCCGTCAGCG CGTGGGCCTG
351 CAAGAGTTTG GTCGCACACT ACGGACAAGA ACGCAtcgtT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTcgtCATC
451 CAGTTTGCCG GCTGGGAAAA CACCCCCCTG CTTCAAACA TCATCGTTCA
501 CAGAGGGCAA GGCCTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGCATA CTCGCCTCCG CCTACCTCAA CGGACAACGA
601 AAAATCCCCG CAGCCCTCGG CGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTGCG GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCCT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGACGG
751 ACGATGCTCG GCATAGCCCG AGCCGTATTC CTTACCGCGC TGTTCGAAT
801 TTCCATGAAC GCCATTCTGG AAACCTTTAC AGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACTTGCC GCGCCAAAGC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCGCA TATTCGGGCA
951 CGGCTGGAAC AGTTTGTGCC AACAAACCTT CCTGATCAAT GCCGAACAGC
1001 ACACCATACA CGACAACTTC CTCAGCACCT TGTTCAACCA TCCCACAAC
1051 ATCATCTTCC AACTCCTTGC AGAAATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCTCCCTGA
1151 CCCCCGCATC ACTTTTCCTG CTGTGCGCGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCTA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTGACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGACTG GACATACACC CGGCTGGTTA ACTCCTTTTC
1401 CCCC GCCGCT GACGACAGT CCAAAACCCT CAACCGGAAA ATCAACGAAC
1451 TGCGCTATAT TTCCGCAAAC AGCCCGATGC TGTCTTTTAA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCGGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAG CACTAAAATA CCGCCCTTAC TCCGCCACCT

```

```

1601 ACCGCATCGC CCTCTACTTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCAACACA GTCCTATTAC CCCTACCTGA TGCCCCGATA
1701 CGCCCGACGAA ATCCGCAAAC TGCCCGTATG GGCACCGCTG CTGCCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CTCCCGGCCA TCCGGAACAA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2516; ORF 738>:

g738.pap

```

1 MSAETTVSGA RPAAKLPYI LPCFLWIGII PFTFALRLKP SPDFYHDAAA
51 AAGLIVLLEF TAGKKLFDVK IPAISLLEFA MAAFWWLOAR LMNLIYPGMN
101 DIASWVFILL AVSAWACKSL VAHYGQERIV TLFAWSLLIG SLIQSCIVVI
151 QFAGWENTPL LQNIIVHRGQ GVIGHIGQRN NLGHYLMWGI LASAYLNGQR
201 KI PAALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPEW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN AILETFTGIR YETAVERVAN GGFTDLPRQS
301 EWNKALAAFO SAPIFGHGWN SFAQQTFLIN AEQHTIHDNF LSTLFTHSHN
351 IILQLLAEMG ISGTLVAAT LLTGIAGLLK RSLTPASLFL LCALAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAEASDG IAFKKAANLG ILTASAAIFA
451 GLLLHLDWYF RLVSFSPAA DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALPEY PETQTWAEAA TLKALKYRPY SATYRIALYL MRQKVAEAK
551 QWMRATQSYF PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPET
601 KPCK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2517>:

m738.seq

```

1 ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCGCGCG CCAAACGTGC
51 GATTTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TCGCGCTCAA ACTGAAACCG TCGCCCGACT TTTACCACGA TGCCGCGCGC
151 GCAGCCGGCC TGATTGTCCT GTTGTTCCTC ACGGCAGGAA AAAAAGTGT
201 TGATGTCAA ATCCCCGCCA TCAGCTTCCT TCTGTTTGA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTTACCC CGGTATGAAC
301 GACATCGTCT CTTGGATTTT CATCTTGCTC GCCGTACGCG CGTGGGCGTG
351 CCGGAGCTTG GTCGCACACT TCGGACAAGA ACGCATCGTG ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAAACA TCATCGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG GCAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CTAACCTCAA CGGACAACGA
601 AAAATCCCCG CCGCCCTCGG CGTAATCTGC CTGATTATGC AGACCGCGCT
651 TTTAGGTTTG GTCAACTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATGCTCG GCATAGCCGC AGCCGTATTC CTTACGCGCG TGTTCGAAT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC TGGCATCCGC TACGAAACTG
851 CCGTCGAACG CGTCGCCAAC GCGGTTTCA CAGACTTGCC GCGCAAATC
901 GAATGGAATA AAGCCCTTGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGGCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATATA CGACAACCTC CTCAGCAACT TGTTCAACCA TTCCACAAC
1051 ATCGTCCTCC AACTCCTTGC AGAGATGGGA ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGTGACGG GCATTGCCGG GCTGCTTAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCCTA ATCTGCACGC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCTTTCGG
1251 ACTGATGCTC TTCCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAAGCCG CAATCTCGGC ATACTGACCG CCTCCGCGCG CATATTGCA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGCTGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGT CCAAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAAT CACTAAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCgTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GCGCCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAAGCC TTCGCCGCCG CGCCCGGTCA TCCGGAAGCA
1801 AAACCCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2518; ORF 738>:

m738.pap

```

1 MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALKLKP SPDFYHDAAA

```

```

51  AAGLIVLLFL TAGKKLFDVK IPAISFLLEA MAAFWYLOAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHFGQERIV TLFWSLLIG SLLQSCIVVI
151 QFAGWEDTPL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR
201 KIPAAALGVIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR
251 TMLGIAAAVF LTALFQFSMN TILFTFTGIR YETAVERVAN GGFTDLPRQI
301 EWNKALAAFQ SAPIFGHWNS SFAQQTFLIN AEQHNIDNLL LSNLFTSHSN
351 IVLQLLAEMG ISGTLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH
401 SMLEYPLWYV YFLIPFGLML FLSPAASDGI IAFKKAANLG ILTASAAIFA
451 GLLHLDWYTY RLVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF
501 SLVNFALEPY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQGVAEAK
551 QWMRATQSY YPYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA
601 KPCK*

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 738 shows 95.0% identity over a 604 aa overlap with a predicted ORF (ORF738.a) from *N. gonorrhoeae*:

m738/g738

	10	20	30	40	50	60
m738.pep	MPAETTVSGAHPAAKLPYIILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
g738	MSAETTVSGARPAAKLPYIILPCFLWIGIIPFTFALRLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
m738.pep	70	80	90	100	110	120
	TAGKKLFDVKIPAISFLLEFMAAFWYLOARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
g738	TAGKKLFDVKIPAISFLLEFMAAFWYLOARLMNLIYPGMNDIASWVIFILLAVSAWACKSL					
	70	80	90	100	110	120
m738.pep	130	140	150	160	170	180
	VAHFGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
g738	VAHYGQERIVTLFAWSLLIGSLLQSCIVVIQFAGWENTPLLQNIIVHRGQGVIGHIGQRN					
	130	140	150	160	170	180
m738.pep	190	200	210	220	230	240
	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
g738	NLGHYLMWGI LAAAYLNGQRKIPAAALGVICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
m738.pep	250	260	270	280	290	300
	YFRSDKSNRR TMLGIAAAVFLTALFQFSMN TILFTFTGIR YETAVERVANGGFTDLPRQI					
g738	YFRSDKSNRR TMLGIAAAVFLTALFQFSMNAILFTFTGIR YETAVERVANGGFTDLPRQS					
	250	260	270	280	290	300
m738.pep	310	320	330	340	350	360
	EWNKALAAFQ SAPIFGHWNS SFAQQTFLINAEQHNIDNLLSNLFTSHSNIVLQLLAEMG					
g738	EWNKALAAFQ SAPIFGHWNS SFAQQTFLINAEQHTIHDNLFSLFTSHSNIIQLLAEMG					
	310	320	330	340	350	360
m738.pep	370	380	390	400	410	420
	ISGTLVAATLLTGIAGLLKRPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
g738	ISGTLVAATLLTGIAGLLKRSLTPASLFLICALAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
m738.pep	430	440	450	460	470	480
	FLSPAASDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNAFSPATDDSAKTLNRK					
g738	FLSPAASDGI IAFKKAANLGILTASAAIFAGLLHLDWYTYRLVNSFSPAADDSAKTLNRK					



1200

	430	440	450	460	470	480
	490	500	510	520	530	540
m738.pep	INELRYISANSPLMSFYADFSLVNFALPEYPETQTWAEELTKSLKYPHSATYRIALYL					
g738	INELRYISANSPLMSFYADFSLVNFALPEYPETQTWAEELTKALKYRPYSATYRIALYL					
	490	500	510	520	530	540
	550	560	570	580	590	600
m738.pep	MRQGVKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
g738	MRQGVKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPET					
	550	560	570	580	590	600
m738.pep	KPCKX					
g738	KPCKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2519>:

```

a738.seq
1  ATGCCCGCTG AAACGACCGT ATCCGGCGCG CACCCGCGCG CCAAAC TGCC
51  GATTACATC CTGCCCTGCT TCCTTTGGAT AGGCATCGTC CCCTTTACCT
101 TTGCGCTCAG GCTGCAACCG TCGCCGCGACT TTTACCACGA TGCCGCGCGC
151 GCAGCCGGCC TGATTGTCTT GTTGTCTCTC ACGGCAGGAA AAAAGCTGTT
201 TGATGTCAAA ATCCCACCTA TCAGCTTCCT TCTGTTTGCA ATGGCGGCGT
251 TTTGGTATCT TCAGGCACGC CTGATGAACC TGATTACCC CGGTATGAAC
301 GACATCGTCT CTGGGATTTT CATCTTACTC GCCGTCAGCG CGTGGGCGCTG
351 CCGGAGCTTG GTCGCACACT ACGGACAAGA ACGCATCGTT ACCCTGTTTG
401 CCTGGTCGCT GCTTATCGGC TCCCTGCTTC AATCCTGCAT CGTCGTCATC
451 CAGTTTGCCG GCTGGGAAGA CACCCCTCTG TTTCAAACA TCATTGTTTA
501 CAGCGGGCAA GCGTAATCG GACACATCGG ACAGCGCAAC AACCTCGGAC
551 ACTACCTCAT GTGGGGCATA CTCGCCGCGC CCTACCTCAA CGGACAACGA
601 AAAATCCCGC CCGCCTTGGG TGCAATCTGC CTGATTATGC AGACCGCCGT
651 TTTAGGTTTG GTCAATTCGC GCACCATCTT GACCTACATA GCCGCCATCG
701 CCCTCATCTT TCCCTTCTGG TATTTCCGTT CGGACAAATC CAACAGGCGG
751 ACGATACTCG GCATAGCCGC AGCCGTATTC CTTACCGCGC TGTTCCAATT
801 TTCCATGAAC ACCATTCTGG AAACCTTTAC CGGCATCCGC TACGAAACCG
851 CCGTCGAACG CGTCGCCAAC GGCGGTTTCA CAGACCTGCC GCGCCAAATC
901 GAATGGCGCA AAGCCCTCGC CGCCTTCCAG TCCGCCCCGA TATTCGGGCA
951 CGCCTGGAAC AGTTTGGCCC AACAAACCTT CCTCATCAAT GCCGAACAGC
1001 ACAACATACA CGACAACCTC CTCAGCAACT TGTTCAACCA TCCCAACAA
1051 ATCGTTCTCC AACTCCTTGC AGAGATGGGG ATCAGCGGCA CGCTTCTGGT
1101 TGCCGCAACC CTGCTGACGG GCATTGCCGG GCTGCTGAAA CGCCCCCTGA
1151 CCCCCGCATC GCTTTTCTCG ATCTGCACAC TTGCCGTCAG TATGTGCCAC
1201 AGTATGCTCG AATATCCTTT GTGGTATGTC TATTTCTCA TCCCCTTCGG
1251 ACTGATGCTC TTTCTGTCCC CCGCAGAGGC TTCAGACGGC ATCGCCTTCA
1301 AAAAAGCCGC CAATCTCGGC ATACTAACCG CCTCCGCCGC CATATTGCGA
1351 GGATTGCTGC ACTTGGACTG GACATACACC CGGATGGTTA ACGCCTTTTC
1401 CCCCGCCACT GACGACAGTG CCAAACCTT CAACCGGAAA ATCAACGAGT
1451 TGCGCTATAT TTCCGCAAAC AGTCCGATGC TGTCTTTTA TGCCGACTTC
1501 TCCCTCGTAA ACTTCGCCCT GCCGGAATAC CCCGAACCC AGACTTGGGC
1551 GGAAGAAGCA ACCCTCAAT CACTAAATA CCGCCCCAC TCCGCCACCT
1601 ACCGCATCGC CCTTACCTG ATGCGGCAAG GCAAAGTTGC AGAAGCAAAA
1651 CAATGGATGC GGGCGACACA GTCCTATTAC CCTACCTGA TGCCCCGATA
1701 CGCCGACGAA ATCCGCAAAC TGCCCGTATG GGCGCGCTG CTACCCGAAC
1751 TGCTCAAAGA CTGCAAGGCC TTCGCCGCGC CGCCCGGTCA TCCGGAAGCA
1801 AAACCTGCA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 2520; ORF 738.a>:

```

a738.pep
1  MPAETTVSGA HPAAKLPYI LPCFLWIGIV PFTFALRLQP SPDFYHDAAA
51  AAGLIVLLEF TAGKKLFDVK IPPISFLLEA MAAFWYLQAR LMNLIYPGMN
101 DIVSWIFILL AVSAWACRSL VAHYGQERIV TFAWSLLIG SLLQSCIVVI
151 QFAGWEDTFL FQNIIVYSGQ GVIGHIGQRN NLGHYLMWGI LAAAYLNGQR

```

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201 KIPPALGAIC LIMQTAVLGL VNSRTILTYI AAIALILPFW YFRSDKSNRR  
 251 TILGIAAAVF LTALFQFSMN TILEFTTGIR YETAVERVAN GGFTDLPRQI  
 301 EWRKALAAFO SAPIFGHWN SFAQOTFLIN AEQHNHNDNL LSNLFTSHSN  
 351 IVLQLLAEMG ISGTLLVAAT LLTGIAGLLK RPLTPASLFL ICTLAVSMCH  
 401 SMLEYPLWYV YFLIPFGLML FLSPAASDG IAFKKAANLG ILTASAAIFA  
 451 GLLHLDWYTYT RMVNAFSPAT DDSAKTLNRK INELRYISAN SPMLSFYADF  
 501 SILNFALPEY PETQTWAEAA TLKSLKYRPH SATYRIALYL MRQKVAEAK  
 551 QWMRATQSY PYLMPRYADE IRKLPVWAPL LPELLKDCKA FAAAPGHPEA  
 601 KPCK\*

a738/m738 98.3% identity in 604 aa overlap

	10	20	30	40	50	60
a738.pep	MPAETTVSGAHPAAKLPYILPCFLWIGIVPFTFALRLQPSPDFYHDAAGLIVLLFL					
m738	MPAETTVSGAHPAAKLPYILPCFLWIGIVPFTFALKLKPSPDFYHDAAGLIVLLFL					
	10	20	30	40	50	60
a738.pep	70	80	90	100	110	120
m738	TAGKKLFDVKIPPIISFLLFMAAFWYLQARLMNLIYPGMNDIVSWIFILLAVSAWACRSL					
	70	80	90	100	110	120
a738.pep	130	140	150	160	170	180
m738	VAHYGOERIVTLFAWSLLIGSLLQSCIVVIOFAGWEDTPLFQNIIVYSGQGVIGHIGQRN					
	130	140	150	160	170	180
a738.pep	190	200	210	220	230	240
m738	NLGHYLMWGILAAAYLNGQRKIPPALGAICLIMQTAVLGLVNSRTILTYIAAIALILPFW					
	190	200	210	220	230	240
a738.pep	250	260	270	280	290	300
m738	YFRSDKSNRRITILGIAAAVFLTALFQFSMNTILEFTTGIRYETAVERVANGGFTDLPRQI					
	250	260	270	280	290	300
a738.pep	310	320	330	340	350	360
m738	EWRKALAAFO SAPIFGHWN SFAQOTFLINAEQHNHNDNL LSNLFTSHSNIVLQLLAEMG					
	310	320	330	340	350	360
a738.pep	370	380	390	400	410	420
m738	ISGTLLVAATLLTGIAGLLKRPPLTPASLFLICTLAVSMCHSMLEYPLWYVYFLIPFGLML					
	370	380	390	400	410	420
a738.pep	430	440	450	460	470	480
m738	FLSPAASDGI AFKKAANLGILTASAAIFAGLLHLDWYTYTRMVNAFSPATDDSAKTLNRK					
	430	440	450	460	470	480
a738.pep	490	500	510	520	530	540
m738	INELRYISANSPMLSFYADFSLVNFALPEYPETQTWAEATLKSILKYRPHSATYRIALYL					
	490	500	510	520	530	540

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	550	560	570	580	590	600
a738 . pep	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
m738	MRQ GKVAEAKQWMRATQSYYPYLMRYADEIRKLPVWAPLLPELLKDCKAFAAAPGHPEA					
	550	560	570	580	590	600

a738 . pep	KPCKX
m738	KPCKX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2521>:

g739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCACC GC CATCGGCGCA TTGGCAGTAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT CCAAACCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGCCGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGAAG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTc AAACCGGCC CTTCGGATGC
351 GGCCCGGGCA GCCGATTCGT TAACCGGCAC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGCCCCCA TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CACCCAAAGA
501 AAAAGAAACG CCCAAAGAAA ACCATACCAA ACCGGACACC CCGAAAAACA
551 CGCCGGCCAA ACCCATATA GAGATTCTCG ACAACCTCTT TTGA

```

This corresponds to the amino acid sequence <SEQ ID 2522; ORF 739>:

g739 . pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICITAIGA LAVGIVSTFN PNGDKTLQTE
51  PQHTDSPRET EFWLPGAVG QDAAQPEHHH AASSEPAQPD GTEESGSGLP
101 SPAAPKKNRV KPRPSDARA ADSLTGTGTQ AENTLKETPV LPTNAPHEP
151 RKETPEKQQA PKETPKKET PKENHTKPD TPKNTPAKPHK EILDNLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2523>:

m739 . seq

```

1  ATGGCAAAAA AACCGAACAA ACCCTTCAGG CTGACCCCCA AACTCCTGAT
51  ACGCGCCGTA TTGCTCATCT GTATCGCCGC CATCGGCGCA TTGGCAATAG
101 GCATCGTCAG CACATTCAAC CCGAACGGCG ACAAACCCT TCAAGCCGAA
151 CCGCAACACA CCGACAGCCC CCGCGAAACC GAATTCTGGC TGCCAAACGG
201 CGTAGTCGGA CAAGATGCCG CCCAACCCGA ACACCACCAC GCCGCCTCAT
251 CCGAACCCGC ACAGCCGGAC GGCACAGACG AAAGCGGCAG CGGACTGCCG
301 TCCCCTGCCG CACCCAAGAA AAACCGGGTC AAACCGCAAC CTGCCGACAC
351 AGCTCAAACC GACAGGCAGC CGGACGACGC CGGAACACAA GCTGAAAACA
401 CACTCAAAGA AACCCCGTA CTGCCACAA ACGTCCCCCG TCCCGAACCC
451 CGAAAAGAAA CACCCGAAA ACAGGCGCAG CCCAAAGAAA CGCCAAAGA
501 AAACCATACC AAACCGGACA CCCCAGAAAA CACGCCGCC AAACCCATA
551 AAGAAATTCT CGACAACTC TTC

```

This corresponds to the amino acid sequence <SEQ ID 2524; ORF 739>:

m739 . pep

```

1  MAKKPNKPFR LTPKLLIRAV LLICIAAIGA LAIGIVSTFN PNGDKTLQAE
51  PQHTDSPRET EFWLPGVVG QDAAQPEHHH AASSEPAQPD GTDESGSGLP
101 SPAAPKKNRV KPQPADTAQT DRQPDAGTQ AENTLKETPV LPTNVRPEP
151 RKETPEKQQA PKETPKENHT KPDPKNTTP KPHKEILDKL F

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 739 shows 86.3% identity over a 197 aa overlap with a predicted ORF (ORF739.a) from *N. gonorrhoeae*:

m739/g739

1203

	10	20	30	40	50	60
m739.pep	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
g739	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAVGIVSTFNPNGDKTLQTEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
m739.pep	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
g739	EFWLPNGAVGQDAAQPEHHHAASSEPAQPDGTEESGSLPSPAAPKKNRVKPRPSDAARA					
	70	80	90	100	110	120
	130	140	150	160	170	
m739.pep	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKE-----NHTKPD					
g739	ADSLTGTGTAENTLKETPVLPTNAPHPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
	130	140	150	160	170	180
	180	190				
m739.pep	PKNTPPKPKHKEILDKLF					
g739	PKNTPAKPKHKEILDNLF					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2525>:

a739.seq

1	ATGGCAAAAA	AACCGAACAA	ACCCTTCAGG	CTGACCCCCA	AACTCCTGAT
51	ACGCGCCGTA	TTGCTCATCT	GTATCACCGC	CATCGGCGCA	TTGGCAATAG
101	GCATCGTCAG	CACATTCAAC	CCGAACGGCG	ACAAAACCTT	CCAAACCGAA
151	CCGCAACACA	CCGACAGCCC	CCGCGAAACC	GAATTCTGGC	TGCCAAACGG
201	CGTAGTCGGA	CAAGATGCCG	CCCAACCCGA	ACACCACCAC	GCCTCCTCAT
251	CCGCACCCGC	ACAGCCGGAC	GGCAGACAGC	AAAGCGGCAG	CGGACTGCCG
301	TCCCCTGCCG	CACCAAGAA	AAACCGGGTC	AAACCGCAAC	CTGCCGACAC
351	AGCTCAAACC	GACAGGCAGC	CGGACGACGC	CGGAGCACAA	GCTGAAAACA
401	CACTCAAAGA	AACCCCGTA	CTGCCACAA	ACGTCCCCCG	TCCCGAACCC
451	CGAAAAGAAA	CACCCGAAAA	ACAGGCACAG	CCCAAAGAAA	CACCCAAAGA
501	AAAAGAAACG	CCCAAAGAAA	ACCATACCAA	ACCGGACACC	CCGAAAACA
551	CGCCGCCTAA	ACCCCATAAA	GAAATTCTCG	ACAACCTCTT	CTGA

This corresponds to the amino acid sequence <SEQ ID 2526; ORF 739.a>:

a739.pep

1	MAKKPNKPFRLTPKLLIRAV	LLICITAIGA	LAIGIVSTFN	PNGDKTLQTE
51	POHTDSPRET	EFWLPNGVVG	QDAAQPEHHH	ASSSAPAQPD
101	SPAAPKKNRV	KPQPADTAQT	DRQPDAGAQ	AENTLKETPV
151	RKETPEKQAQ	PKETPKEKET	PKENHTKPD	PKNTPPKPKH
				EILDNLF*

a739/m739 93.9% identity in 197 aa overlap

	10	20	30	40	50	60
a739.pep	MAKKPNKPFRLTPKLLIRAVLLICITAIGALAIGIVSTFNPNGDKTLQTEPOHTDSPRET					
m739	MAKKPNKPFRLTPKLLIRAVLLICIAAIGALAIGIVSTFNPNGDKTLQAEPOHTDSPRET					
	10	20	30	40	50	60
	70	80	90	100	110	120
a739.pep	EFWLPNGVVGQDAAQPEHHHASSSAPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
m739	EFWLPNGVVGQDAAQPEHHHAASSEPAQPDGTDSESGSLPSPAAPKKNRVKQPADTAQT					
	70	80	90	100	110	120
	130	140	150	160	170	180
a739.pep	DRQPDAGAQQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPKEKETPKENHTKPD					
m739	DRQPDAGTQAENTLKETPVLPTNVPRPEPRKETPEKQAQPKETPK-----ENHTKPD					
	130	140	150	160	170	

1204

```

                190
a739.pep      PKNTPPKPHKEILDNLF
                |||||
m739          PKNTPPKPHKEILDKLF
                180   190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2527>:

```

g740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTC GCCGTCTGCC TCATCCCCTT
51 GgcgACGCTT GCCGTTTTCG CCGCCAATcc gcCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAa
151 ttcgtgctCT TTGAAACCAT CAAGCATCAT CTTAaacaag gGTTTGATT
201 GAAACgtcaa ACCATGTTTC TGTTTATTCC GATTGTTTTC CTGTTGTGT
251 ATTTGTTCCA CTATTTCCGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2528; ORF 740.ng>:

```

g740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQGFDLKRQ TMLLFIPIVL LVVYLFHYFG AF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2529>:

```

m740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GCCGTCTGCC TCATCCCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATCAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTTAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2530; ORF 740>:

```

m740.pep
1  MSRNLLVRWL AVCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

m740/g740 93.5% identity in 92 aa overlap

```

                10      20      30      40      50      60
m740.pep      MSRNLLVRWLA VCLIPLATL AVFAANPPED KLOHLINGII LACEATFLFK FVLFDTIKHH
                |||||
g740           MSRNLLVRWLA VCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK FVLFDTIKHH
                10      20      30      40      50      60

                70      80      90
m740.pep      LKQEFDLKRQ TMLLFIPILLIVYLFHYFGAFX
                |||
g740           LKQGFDLKRQ TMLLFIPIVLLVYLFHYFGAFX
                70      80      90

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2531>:

```

a740.seq
1  ATGTCCCGAA ACCTGCTTGT CCGCTGGCTT GTCGTCTGCC TGATACCCTT
51 GGCGACGCTT GCCGTTTTCG CCGCCAATCC GCCCGAAGAC AAACCCAGC
101 ATCTGATTAA CGGCATCATC CTTGCCTGCG AAGCGACGTT TTTGTTCAAA
151 TTCGTCCTTT TCGACACCAT CAAGCATCAT TTGAAACAAG AGTTTGATT
201 GAAACGTCAA ACTATGTTGC TGTTTATTCC GATTATTTTG CTGATTGTGT
251 ATTTGTTCCA CTATTTTGGC GCGTTTtag

```

This corresponds to the amino acid sequence <SEQ ID 2532; ORF 740.a>:

```

a740.pep
1  MSRNLLVRWL VVCLIPLATL AVFAANPPED KPOHLINGII LACEATFLFK
51 FVLFDTIKHH LKQEFDLKRQ TMLLFIPIL LIVYLFHYFG AF*

```

a740/m740 97.8% identity in 92 aa overlap

```

                10      20      30      40      50      60

```

1205

```

a740.pep  MSRNLLVRWLVVCLIPLATLAVFAANPPEDKPOHLINGIILACEATFLFKFVLFDTIKHH
|||||
m740      MSRNLLVRWLVVCLIPLATLAVFAANPPEDKLOHLINGIILACEATFLFKFVLFDTIKHH
              10      20      30      40      50      60

              70      80      90
a740.pep  LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
|||||
m740      LKQEFDLKRQTMLLFIPIILLIVLYLFHYFGAFX
              70      80      90

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2533>:

```

g741.seq
1  GTGAACCGAA CTACCTTCTG CTGCCTTTCT TTGACCGCCG GCCCTGATTC
51  TGACCGCCTG CAGCAGCGGA GGGGCGGAGG CGGTGGTGTG GCCGCCGACA
101 TCGGCACGGG GCTTGCCGAT GCATTAAACG CGCCGCTCGA CCATAAAGAC
151 AAAGGTTTGA AATCCCTAAC ATTGGAAGCC TCCATTCCCC AAAACGGAAC
201 ACTGACCCTG TCGGCACAAG GTGCGGAAAA AACTTTCAAA GCCGGCGGCA
251 AAGACAACAG CCTCAACACG GGCAAACTGA AGAACGACAA AATCAGCCGC
301 TTCGACTTCG TGCAAAAAAT CGAAGTGGAC GGACAAACCA TCACACTGGC
351 AAGCGGCGAA TTTCAAATAT ACAAACAGGA TCACTCCGcc gtcgtTgcCC
401 TacgGATTGA AAAAATCAAC AACCCCGACA AAATCGACAG CCTGATAAAC
451 CAACGCTCCT TCCTTGTCAG CGATTGCGGC GGAGAACATA CCGCCTTCAA
501 CCAACTGCCT GACGCGAAAG CCGAGTATCA CGGCAAAGCA TTCAGCTCCG
551 ACGATGCCGA CGGAAAACG ACCTATACCA TAGATTTCGC CGCCAAACAG
601 GGACACGGCA AAATCGAACA CCTGAAAACA CCCGAGCAGA ATGTTGAGCT
651 TGCCTCCGCC GAACGCAAG CAGATGAAAA ATCACACGCC GTCATTTTGG
701 GCGACACGCG CTACGGCGGC GAAGAGAAAG GCACCTACCG CCTCGCCCTT
751 TCGGCGGACC GCGCCCAAGA AATCGCTGGC TCGGCAACCG TGAAGATAGG
801 GGAAAAGGTT CACGAAATCG GCATCGCCGA CAAACAGTAG

```

This corresponds to the amino acid sequence <SEQ ID 2534; ORF 741.ng>:

```

g741.pep
1  VNRTTFCCLS LTAGPDSRL QRRGGGGGV AADIGTGLAD ALTAPLDHKD
51  KGLKSLTLEA SIPQNGTTL SAQGAETFK AGGKDNSLNT GKLKNDKISR
101 FDFVQKIEVD GQITLASGE FQIYQDHSA VVALRIEIN NPKIDSLIN
151 QRSFLVSDLG GEHTAFNQLP DGKAEYHGKA FSSDDADGKL TYTIDFAAQK
201 GHGKIEHLKT PEQNVELASA ELKADEKSHA VILGDTRYGG EEKGTYRLAL
251 FGDRAQEIAG SATVKIGEKV HEIGIADKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2535>:

```

m741.seq
1  GTGAATCGAA CTGCCTTCTG CTGCCTTTCT CTGACCACTG CCCTGATTCT
51  GACCGCCTGC AGCAGCGGAG GGGGTGGTGT CGCCGCGGAC ATCGGTGCGG
101 GGCTTGCCGA TGCACTAACC GCACCGCTCG ACCATAAAGA CAAAGGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT
201 GGCGGCACAA GGTGCGGAAA AAACCTATGG AAACGGTGAC AGCCTCAATA
251 CGGGCAAATT GAAGAACGAC AAGGTCAGCC GTTTCGACTT TATCCGCCAA
301 ATCGAAGTGG ACGGCGAGCT CATTACCTTG GAGAGTGGAG AGTTCCAAGT
351 ATACAAACAA AGCCATTCCG CTTAACC GCCTTCAGACC GAGCAAATAC
401 AAGATTCCGA GCATTCCGGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GGCGACATAG CGGCGAACA TACATCTTTT GACAAGCTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCGTTCGG TTCAGACGAT GCCGCGGAA
551 AACTGACCTA CACCATAGAT TTCGCCGCCA AGCAGGGAAA CGGCAAAATC
601 GAACATTTGA AATCGCCAGA ACTCAATGTC GACCTGGCCG CCGCGGATAT
651 CAAGCCGGAT GGAACCGCC ATGCCGTCAT CAGCGGTTCC GTCCTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCCCTCG GTATCTTTGG CGGAAAAGCC
751 CAGGAAGTTG CCGGCAGCGC GGAAGTGAAA ACCGTAAACG GCATACGCCA
801 TATCGGCCTT GCCGCCAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2536; ORF 741>:

```

m741.pep
1  VNRTAFCCLS LTTALILTAC SSGGGVVAAD IGAGLADALT APLDHKDKGL
51  QSLTLDSVR KNEKLKLAQ GAETKYNGD SLNTGKLKND KVSREFDFIRQ
101 IEVDGQLITL ESGEFQVYKQ SHSALTAFQT EQIQDSEHSG KMAKRFRI

```

151 GDIAGEHTSF DKLPEGGRAT YRGTAFGSDD AGGKLYTID FAAKQNGNKI  
201 EHLKSPELNV DLAADIKPD GKRHAVISGS VLYNQAEEKS YSLGIFGGKA  
251 QEVAGSAEVK TVNGIRHIGL AAKQ\*

[illegible]

```
a741.seq
1 GTGAACCGAA CTGCCTTCTG CTGCCTTCT TTGACCGCGG CCCTGATTCT
51 GACCGCTGCG AGCAGCGGAG GCGCCGGTGT CGCCCGCGGAC ATCGGCGCGG
101 TGCTTGCCGA TGCATAACG GCACCGCTCG ACACCAAGA CAAAAGTTTG
151 CAGTCTTTGA CGCTGGATCA GTCCGTCAGG AAAACGAGA AACTGAAGCT
201 GCGGCGACAA GGTGCGGAAA AAACCTATGG AAACGGCGAC AGCCTCAATA
251 CGGGCAAAAT GAAGAACGAC AAGGTCAGCC GCTTCGACTT TATCCGTCAA
301 ATCGAAGTGA AGCGGCAGCT CATTACCTTG GAGAGCGGAG AGTTCCAAGT
351 GTACAAACAA AGCCATTCCG CCTTAACCGC CCTTCAGACC GAGCAAGTAC
401 AAGATTCGGA GCATTCAAGG AAGATGGTTG CGAAACGCCA GTTCAGAATC
451 GCGATATATG CGGGTGAACA TACATCTTTT GACAGCTTTC CCGAAGGCGG
501 CAGGGCGACA TATCGCGGGA CGGCATTCCG TTCAGACGAT GCGAGTGGAA
551 AACTGAGTCA ACCATAGAT TTCGCGCCA AGCAGGGACA CGGCAAGATC
601 GAACATTGTA AATCGCCAGA ACTCAATGTT GACCTGGCCG CCTCCGATAT
651 CAAGCCGGAT AAAAAACGCC ATGCCGTCAT CAGCGGTTCC GTCTTTTACA
701 ACCAAGCCGA GAAAGGCAGT TACTCTCTAG GCATCTTTGG CGGGCAAGCC
751 CAGGAAGTTG CCGGCAGCGC AGAAGTGGAA ACCGCAAACG GCATACGCCA
801 TATCGGTCTT GCCGCAAGC AGTAA
```

```
a741.ppep
1  VNRTAFCCLS  LTAALILTAC  SSGGGGVAAD  IGAVLADALT  APLDHKDKSL
51  QSLTLDQSVR  KNEKLKLAQ  GAEKTYGND  SLNTGKLKND  KVSREDFIRQ
101 IEVDGQLITL  ESGEFQVYKQ  SHSALTALQT  EQQVDSEHS  KMVAKRQFRI
151 GDIAGEHTSF  DKLPEGGRAT  YRGTAFGSDD  ASGKLTYYTD  FAAKQGHGKI
201 EHLKSPELNV  DLAASDIKPD  KKRHAVISGS  VLYNQAEKGS  YSLGIFGGQA
251 QEVAGSAEVE  TANGIRHIGL  AAKO*
```

**a741/m741 95.6% identity in 274 aa overlap**

1207

	10	20	30	40	50	60
a741.pep	VNRTAFCCLSLTAALILTACSSGGGGVAADIGAVLADALTAPLDHKDKSLQSLTLDQSVR					
m741	VNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLDHKDKGLQSLTLDQSVR					
	10	20	30	40	50	60
	70	80	90	100	110	120
a741.pep	KNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVSRLFIRQIEVDGQLITLESGEFQVYKQ					
m741	KNEKLKLAQAQAEKTYGNGDSLNTGKLKNDKVSRLFIRQIEVDGQLITLESGEFQVYKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
a741.pep	SHSALTALQTEQVQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDD					
m741	SHSALTAFQTEQIQDSEHSGKMKVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAFGSDD					
	130	140	150	160	170	180
	190	200	210	220	230	240
a741.pep	ASGKLTYYTIDFAAQQGHGKIEHLKSPELNVDLAASDIKPKKRHAVISGSVLYNQAEKGS					
m741	AGGKLTYYTIDFAAQQGNKIEHLKSPELNVDLAAADIKPDGKRHAVISGSVLYNQAEKGS					
	190	200	210	220	230	240
	250	260	270			
a741.pep	YSLGIFGGQAQEVAGSAEVETANGIRHIGLAQKX					
m741	YSLGIFGGKAQEVAGSAEVTNNGIRHIGLAQKX					
	250	260	270			

g742.seq not found yet

g742.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2539>:

m742.seq

1	ATGGTTTACG	GCATTGCCGA	AGCCGATGCG	GGCGACAGCA	GTGTGCTTAC
51	TTTGGGCGGC	ATGTATCAGA	AGAGTAGGGA	GTTCTCTGAT	TTTTCGGGCA
101	TTATTTTGCC	CTGTGAAAT	CAGAAACTG	CCCCGTTTCA	TTCAACGCCT
151	GCCTGCAACC	GGCCTTTGCA	ACTGCCGCGC	AACACTTATT	TGGGGGAGGA
201	TTGGTCGCGG	TTAAGTGCCG	ACAAATACAA	CCTTTTCTCA	GGATTCAAAC
251	ATGTGTTTGA	CAACGGTTGG	CAGCTCAATG	CCGAAGTGTC	TTATACCAAG
301	AATGAATCCG	ATGCGAAGGT	GGGGCAGTTT	TTTCTGAAAA	ACGAATATGC
351	GGCGGGTTTG	TCGGGTGAGG	ATGCGGTAGG	CTTTTTGACT	GAAAAAACC
401	AAGTCATCCC	GTTTCGAGCCG	AAAGATAAGG	CATTGGAGAA	ACTGAAAGCA
451	TATCGTGATG	AAACCGCCAA	GGAATACCGG	GAGCGCAAAG	ACGATTTTGT
501	TAAAAACCGT	TTTGATAATA	CTGCTTTCGA	ACAGTATCGC	AGCCGCCGTG
551	CCGCAGAACG	CAAAGCCGGT	TTTGACAAGT	GTATGAGTGA	CCCTTTCGCG
601	CTGGACTTTA	TCTGTCAAGG	TTCTTGGGGG	GATCCGGGCG	TTGATGCCGA
651	CAAGGCGGAA	TTGTGCGATA	AAGCCCTTGC	GAAGGAGGGC	ATCTTTAATA
701	ATGCGGCACA	ACGTTTTTCCA	AACAGCCTGT	ATGACTCTTC	CTTTAATCGG
751	AAGGCTACCG	CCAACCGACG	ATACAGTTAT	ATGCCGTTGC	GGCATACCAA
801	AGACGACCGC	CAATGGGGAA	TTAAACTTGA	CCTGACCGGC	ACATATGGGC
851	TGTTCCGGCG	GGAGCATGAT	TTCTTTGTGCG	GCTATGCCTA	CGGTGATGAA
901	AAGATACGTT	CGGAATATCT	AGAAATCTAC	GAACGCCGCT	ACAGAGTACG
951	TCCGAATACG	GGGGCAACGC	ACGGCGTGTA	TGCGGGAAGT	TGTCAGGAGG
1001	AGCCGGACGG	CGATTTGTGCG	TCTCCTTTGG	TCAGGGGGCA	TAAAGAACCC
1051	GATTGGCAGG	CGTACGATGA	AAAAGGCAAC	CGTACCGTTT	ATGCCGAAGA
1101	ATGCAGGAAC	GCCAAGAAAA	TAAAAACCGA	GCCCAAGCTC	GATGCCGAAG
1151	GCAAGCAGGT	GTATTACTAT	GACGAATACA	GCGGCAGCCG	GACACCGGTA
1201	TATGTCGATG	TATATGAGCT	GGACGAAAAA	GGCAACAAGA	TTCAGGAGAC
1251	CAATCCCAGC	GGCAGCCCTG	CCTTTACCGG	TTTTTCCGGT	ACGGTGCCGG
1301	TTTGGAAAAA	CGTCAAAGTG	GCAGACGACC	ATGTTCTCTG	GCTGTATAAC
1351	TACGCCAAAT	ACCTCAACAC	CAACAAAACC	CATTGCTGTA	CTGCCAGCAC
1401	GCGTTTCAAC	GTAACCGGCC	GACTGCACCT	TTTGGGCGGG	CTGCACTACA



1208

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1451 CGCGCTATGA GACTTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAGGGCGG ATCAGGACCA
1551 TTACACGGCC AAGATGCAAG GTCATAAATT GACGCCCTAT GCAGGCATTA
1601 CCTATGACTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCGGC ACAAACTATG AGGTAGGCTG GAAAGGCGCG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTC GCATTGTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCT ATTTCCGCTA TGTTCCTGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCCAAACC GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTACAAAAC GCCGCCGAAG TCAACGCCGA
2001 ACGCCTTGCC AAAAATCCA GTGCAGACCC GTACAACTTC AGCAATTTC
2051 CACCCGTGCA CATATTCCTG TTCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGCGCG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCC AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAAACA
2301 CTTCTACGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2540; ORF 742>:

```

m742.pep
1  MVGIAEADA GDSSVLTGG MYQKSREVPD FSGIILPCEN OKTAPFS STP
51  ACNRPLQLPR NTYLGEDWSR LSADKYNLFS GFKHVFNGW QLNAEVS YTK
101 NESDAKVGQF FLKNEYAAGL SGEDAVGFLT EKNEVIPFEP KDKALEK LKA
151 YRDETAKEYR ERKDDFVKNR FDNTAFEQYR SRRAAERKAG FDKCMSD PFA
201 LDFICQGSWG DPGVDADKAE FVDKALAKEG IFNNAQRFP NSLYDSS FNR
251 KATANRRYSY MPLRHTKDDR QWGIKLDLTG TYGLFGREHD FVVGAYGDE
301 KIRSEYLEIY ERRYRVRPNT GATHGVYAGS CQEEPDGDL SPLVRGHKEP
351 DWQAYDEKGN RTVYAEECRN AKKIKTEPKL DAEGKQVYYY DEYSGSRTPV
401 YVDVYELDEK GNKIQETNPD GTPAFTGFSG TVPVWKTVKV ADDHVPALYN
451 YAKYLNNTKT HSLTASTREN VTGRLHLLGG LHYTRYETSQ TKDMPVR YGQ
501 PASDFQTASS IRADQDHYTA KMQGHKLTPY AGITYDLTPQ QSIYGSYTKI
551 FKQQDNVDVS AKTVLPPLVG TNYEVGWKGA FLQGRLNASF ALFYLEQKNR
601 TVVDFGYVPG AGGKQGSFQT VAKPIGKVV S RGAEFELSGE LNEDWKV FAG
651 YTYNKSRYKN AAEVNAERLA KNSSADPYNF SNFTPVHIFR FGTSFHI PNT
701 GLTVGGGVSA QSGTSSLYNI RQGGYGLIDG FVRYELGKHA KLSLIGTNLN
751 GRTYFENNYN RTRGANNFY G EPRTVSMKLD WQF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2541>:

```

a742.seq
1  ATGGTTTACG GCATTGCCGA AGCCGATGCG GCGGACAGCA GTGTGCTTAC
51  TTTGGGCGGC ATGTATCAGA AGAGTAGGGA GGTTCCTGAT TTTTCGGGCA
101 TTATTTTGTC CTGTGAAAT CAGAAACTG CCCCCTTCAG TTCAACGCC
151 GCCTGCAACC GGCCTTTGCA ACTGCCGCGC AACACTTATT TGGGGGAGGA
201 TTGGTCGCGG TTGAGTGCTG ACAATACAA CCTTTCTCA GGTTCATAAC
251 ATGTGTTTGA CAACGGTTGG CAGCTCAATG CCGAGTGTC TTATACCAAG
301 AATGAATCCG ATGCGAAGGT GGGGCAGTTT TTTCTGAAA ACGAACATGC
351 GCGGGGTTTG TCAGATGAGG ATGCGGTAGG CTTTTTGACC GAAAAAAGC
401 AAGTCATCCC GTTCGAGCCG AAAGATAAGG CATTGGAGAA ACTGAAAGCA
451 TATCGTGACG AAACCGCCAA GGAATACCGT GAGCGCAAAG ACGATTTTGT
501 TAAAAACCGT TTCGATAATA CTGCTTTCGA GCAGTACCGC AGCCGCCGTC
551 CCGCAGAACG CAAAGCCGCT TTTGACGAGT GTATGAGTGC CCCTTTTGCG
601 CTGGACTTTA TCTGTCAAGG TTCTTGGGGG GATCCGGGTG TTGATGCCGA
651 CAAGTCGGAA TTTGTCGATA AAGCCCTTGC GAAGGAAGGC ATCTTTAATA
701 ATGCGGCACA ACGTTTTCCA AACAGCCTGT ATGACTCTTC CTTTAATCGG
751 AAGGCTACCG CCAACCGACG ATACAGTTAT ATGCCGTGTC GGCATACCAA
801 AGACGACCGC CAATGGGGAA TTAACTTGA CCTGACCGGC ACATATGGGC
851 TGTTGCGGCG GGAGCATGAT TTCTTTGTCG GCTATGCCTA CGGCGATGAA
901 AAGATACGTT CCGAATATCT GGAAATCTAC GAACGCCGCC ACAGAGTACG
951 TCCGAATACA GGGCAACGC ACGGCGTGTA TGCGGGAAGT TGTCAGGGGG
1001 AGCCGGACGG TGATTTGTCT TCTCCTTGG TCAGGGGGCA TAAAGAACCC
1051 GATTGGCAGG CGTACGATGA AAAAGGCAAC CGTACCGTTT ATGCCGAAGA
1101 ATGCAGGAAT GCCAAGAAAA TAAAAACCGA GCCAAGCTC GATGCCGAAG
1151 GCAAGCAGGT GTATTACTAT GACGAATACA GCGGCAGCCG GACGCCAGTA

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1209

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1201 TATGTCGATG TATATGAACT GGATGAAAAA GGCAATAAGA TTCAGGAGAC
1251 CAATCCCGAC GGCACGCTG CCTTTACCGG TTTTTCGGT ACAGGTCGGG
1301 TTTGGAAAAC CGTCAAAGTG GCCGACGACC ATGTTCTGCTGC GCTGTATAAC
1351 TACGCCAAAT ACCTCAACAC CAACAAAACC CATTGCTGA CTGCCGGCAC
1401 GCGTTTCAAC GTAACCGGCC GACTGCATCT TTTGGGCGGG CTGCACTACA
1451 CGCGCTATGA AACCTCGCAA ACCAAAGATA TGCCTGTCCG CTATGGGCAG
1501 CCGGCAAGCG ATTTTCAGAC GGCATCGAGC ATTAAGGCGG ATCAGGACCA
1551 TTATACGGCC AAGATGCAAG GTCATAAAT GACGCCCTAT GCAGGCATTA
1601 CCTATGATTT GACACCGCAA CAGAGTATTT ACGGAAGTTA TACCAAAATC
1651 TTCAAACAGC AGGATAATGT CGATGTCAGT GCCAAAACCG TTTTACCGCC
1701 TTTGGTCCGG ACAAACATATG AGGTAGGCTG GAAAGCGCGG TTCTTGCAAG
1751 GACGGCTGAA TGCTTCGTTT GCATTGTTTT ACCTCGAACA GAAAAACCGC
1801 ACGGTCGTCG ATTTTGCTA TGTCCCGGA GCAGGCGGCA AGCAGGGGTC
1851 GTTCAAACCG GTTGCCAAAC CGATAGGCAA AGTGGTCAGC AGGGGTGCGG
1901 AATTCGAGTT GTCGGGTGAG TTGAACGAAG ATTGGAAAGT CTTTGCGGGT
1951 TACACCTACA ACAAGAGCCG CTCAAAAAC GCCGCGAAG TCAACGCCGA
2001 ACGCCTCGCC AAAACACAG GCGCAGACCC GTACAACTTC AGCAATTTCA
2051 CACCGTGCA CATATCCGT TCGGAACGA GCTTCCATAT ACCGAATACG
2101 GGGCTGACCG TCGGCGGCGG CGTGTCCGCA CAAAGCGGCA CAAGCAGTCT
2151 GTATAACATC AGGCAGGGCG GCTACGGGCT GATAGACGGT TTCGTCCGTT
2201 ACGAATTGGG CAAACACGCT AAATTGAGCC TCATCGGTAC GAACTTAAAC
2251 GGACGCACTT ATTTTGAGAA CAACTACAAC CGTACGCGCG GCGCAAACAA
2301 CTTCATGGA GAGCCGCGCA CTGTCAGCAT GAAACTGGAT TGGCAGTTTT
2351 AA

```

This corresponds to the amino acid sequence <SEQ ID 2542; ORF 742.a>:

```

a742.pep
1  M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N O K T A P F S S T P
51  A C N R P L Q L P R N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K
101 N E S D A K V G Q F F L K N E H A A G L S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A
151 Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R S R R A A E R K A G F D E C M S A P F A
201 L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P N S L Y D S S F N R
251 K A T A N R R Y S Y M P L R H T K D D R Q W G I K L D L T G T Y G L F G R E H D F F V G Y A Y G D E
301 K I R S E Y L E I Y E R R H R V R P N T G A T H G V Y A G S C Q G E P D G D L S S P L V R G H K E P
351 D W Q A Y D E K G N R T V Y A E E C R N A K K I K T E P K L D A E G K Q V Y Y Y D E Y S G S R T P V
401 Y V D V Y E L D E K G N K I Q E T N P D G T P A F T G F S G T V P V W K T V K V A D D H V P A L Y N
451 Y A K Y L N T N K T H S L T A G T R F N V T G R L H L L G G L H Y T R Y E T S Q T K D M P V R Y G Q
501 P A S D F Q T A S S I K A D Q D H Y T A K M Q G H K L T P Y A G I T Y D L T P Q Q S I Y G S Y T K I
551 F K Q O D N V D V S A K T V L P P L V G T N Y E V G W K G A F L Q G R L N A S F A L F Y L E Q K N R
601 T V V D F G Y V P G A G G K Q G S F Q T V A K P I G K V V S R G A E F E L S G E L N E D W K V F A G
651 Y T Y N K S R Y K N A A E V N A E R L A K N T G A D P Y N F S N F T P V H I F R F G T S F H I P N T
701 G L T V G G G V S A Q S G T S S L Y N I R Q G G Y G L I D G F V R Y E L G K H A K L S L I G T N L N
751 G R T Y F E N N Y N R T R G A N N F Y G E P R T V S M K L D W Q F *

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a742/m742 98.5% identity in 783 aa overlap

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a742.pep      10      20      30      40      50      60
M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L S C E N O K T A P F S S T P A C N R P L Q L P R
|||||
m742          10      20      30      40      50      60
M V Y G I A E A D A G D S S V L T L G G M Y Q K S R E V P D F S G I I L P C E N O K T A P F S S T P A C N R P L Q L P R

a742.pep      70      80      90      100     110     120
N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E H A A G L
|||||
m742          70      80      90      100     110     120
N T Y L G E D W S R L S A D K Y N L F S G F K H V F D N G W Q L N A E V S Y T K N E S D A K V G Q F F L K N E Y A A G L

a742.pep     130     140     150     160     170     180
S D E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R
| |||||
m742         130     140     150     160     170     180
S G E D A V G F L T E K N E V I P F E P K D K A L E K L K A Y R D E T A K E Y R E R K D D F V K N R F D N T A F E Q Y R

a742.pep     190     200     210     220     230     240
S R R A A E R K A G F D E C M S A P F A L D F I C Q G S W G D P G V D A D K S E F V D K A L A K E G I F N N A A Q R F P

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1210

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|||||:|||||:|||||
m742  SRRAERKAGFDKCMSDPFALDFICQGSWGDPGVDADKAEFVDKALAKEGIFNNAQRFP
      190      200      210      220      230      240

      250      260      270      280      290      300
a742.ppep NSLYDSSFNRKATANRRYSYMLRHTKDDRWGIGKLDLTGTGGLFGRHDFVGYAYGDE
      |||||:|||||:|||||
m742  NSLYDSSFNRKATANRRYSYMLRHTKDDRWGIGKLDLTGTGGLFGRHDFVGYAYGDE
      250      260      270      280      290      300

      310      320      330      340      350      360
a742.ppep KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPPDGLSSPLVRGHKEPDWQAYDEKGN
      |||||:|||||:|||||
m742  KIRSEYLEIYERRHRVRPNTGATHGVYAGSCQGEPPDGLSSPLVRGHKEPDWQAYDEKGN
      310      320      330      340      350      360

      370      380      390      400      410      420
a742.ppep RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD
      |||||:|||||:|||||
m742  RTVYAEECRNAKKIKTEPKLDAEGKQVYYYDEYSGSRTPVYVDVYELDEKGNKIQETNPD
      370      380      390      400      410      420

      430      440      450      460      470      480
a742.ppep GTPAFTGFSGTVPVWKTVKVADHDVHPALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGG
      |||||:|||||:|||||
m742  GTPAFTGFSGTVPVWKTVKVADHDVHPALYNYAKYLNTNKTSLTAGTRFNVTGRLHLLGG
      430      440      450      460      470      480

      490      500      510      520      530      540
a742.ppep LHYTRYETSQTKDMPVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTYPAGITYDLTPQ
      |||||:|||||:|||||
m742  LHYTRYETSQTKDMPVRYGQPASDFQTASSIRADQDHYTAKMQGHKLTYPAGITYDLTPQ
      490      500      510      520      530      540

      550      560      570      580      590      600
a742.ppep QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGLRLNASFALFYLEQKNR
      |||||:|||||:|||||
m742  QSIYGSYTKIFKQQDNVDVSAKTVLPPLVGTNYEVGWKGAFLOGLRLNASFALFYLEQKNR
      550      560      570      580      590      600

      610      620      630      640      650      660
a742.ppep TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
      |||||:|||||:|||||
m742  TVVDFGYVPGAGGKQGSFQTVAKPIGKVVSARGAEFELSGELNEDWKVFAGYTYNKSRYKN
      610      620      630      640      650      660

      670      680      690      700      710      720
a742.ppep AAEVNAERLAKNTGADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      |||||:|||||:|||||
m742  AAEVNAERLAKNSSADPYNFSNFTPVHIFRFGTSFHIPNTGLTVGGGVSAQSGTSSLYNI
      670      680      690      700      710      720

      730      740      750      760      770      780
a742.ppep RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
      |||||:|||||:|||||
m742  RQGGYGLIDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLD
      730      740      750      760      770      780

a742.ppep WQFX
      ||||
m742  WQFX

a742/ p25184
sp|P25184|PUPA_PSEPU FERRIC-PSEUDOBACTIN 358 RECEPTOR PRECURSOR
>gi|94923|pir||S15169
```

1211

ferric-pseudobactin receptor precursor - *Pseudomonas putida* >gi145723 (X56605)  
 pseudobactin uptake protein [*Pseudomonas putida*] Length = 819  
 Score = 152 bits (381), Expect = 6e-36  
 Identities = 110/356 (30%), Positives = 170/356 (46%), Gaps = 55/356 (15%)

Query: 436 KTVKVADHDV-PALYNYAKYLNTNKTSLTAGTRENVTGRLHLLGGLHYTRYETSQTKDM 494  
 +T K DD + P + +Y +N+ +RFN+T LHL+ G + Y

Sbjct: 511 QTPKPGDDEIIPGI-----QYNISNRQSGYFVASRNLTDLLHLILGARASNYRFDYAL-- 564

Query: 495 PVRYGQPASDFQTASSIKADQDHYTAKMQGHKLTYPYAGITYDLTPQQSIYGSYTKIFKQQ 554  
 R G + ++ ++ +TPYAGI YDLT +QS+Y SYT IFK Q

Sbjct: 565 -WRIGNEPAPYKM-----VERGVVTPYAGIVYDLTNEQSVYASYTDIFKQP 609

Query: 555 DNVDVSAKTVLPLVGTNYEVGWKGAFLOQRLNASFALFYLEQKNRTVVDFGYVPGAGGK 614  
 +NVD++ K L P VG NYE+GWKG FL+GRLNA+ AL+ +++ N VP +GG

Sbjct: 610 NNVDITGKP-LDPEVGKNYELGWKGEFLEGRNLNANIALYMKRDNLAESTNEVVPDSSGGL 668

Query: 615 QGSFQTVAKPIGKVVSRGAEEFELSGELNEDWKVFAGYTYNKSRYKNAAEVNAERLAKNTG 674  
 S + + ++G + ELSGE+ W VF GY++ ++

Sbjct: 669 IAS-----RAVDGAETKGVDELSEGLVPGWNVFTGYSHTRTE-----D 707

Query: 675 ADPYNFSNFTPVHIFRFGTSFHIPN--TGLTVGGGVSAQSGTS---SLYN--IRQGGYGL 727  
 AD + P+ FRF ++ +P LT+GGGV+ S ++ + YN + Q Y +

Sbjct: 708 ADGKRLTPQLPMDTFRFWNTYRLPGWEKLTGGGVNWNKSTLNFARYNSHVTQDDYFV 767

Query: 728 IDGFVRYELGKHAKLSLIGTNLNGRTYFENNYNRTRGANNFYGEPRTVSMKLDWQF 783  
 RY + + +L N+ + Y Y G+ YG PR ++ L + F

Sbjct: 768 TSLMARYRINESLAATLNVNINFDKKY----YAGMAGSYGHYGAPRNATVTLRYDF 819

g743.seq not found yet

g743.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2543>:

m743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TCTGGATACG GTCAATGTAC GCGGCTCTCA TGCTTTGTTG
151 GGCAAGACCG AAAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC
351 GCGGTTTGTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TGACCGTCAA TGTTCAGGCG CGTTCGGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGCGG GGTTCATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGAGGA ACCGTCAATT
551 TGATCCGTAA GTGA

```

This corresponds to the amino acid sequence <SEQ ID 2544; ORF 743>:

m743.pep

```

1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALL
51 GKTEKTRSYT IDRMSTATGM RIAGKDT PQS VSVITRSRLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGMTVNVAG RSGYTAKIDV
151 SPSTD LAVYD HIEVV RGATG LTQSNSEPGG TVNLIRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2545>:

a743.seq

```

1 ATGAATCAAA ATCATTTTTC ACTTAAATTT CTGACCGTTA TGCTGTTATC
51 GGCTTACGGT GGTTCCTTTG CAGACGGTGT TGTGCCTGTT TCAGACGGCA
101 ATACCGTCAG TTTGGATACG GTCAATGTAC GCGGCTCTCA TGCTCTGTCG
151 GGCAAGACCG AGAAGACCCG TTCTTATACG ATAGATCGGA TGTCACCCGC
201 CACAGGTATG AGGATTGCGG GCAAGGATAC GCCGCAGTCG GTCAGCGTCA
251 TCACGCGCAG CCGCCTTGAC GATAAGGCGG TGCATACGCT TGAAGAGGCA
301 ATGAAAAACA CGACGGGTGT CAACGTTGTG CGCGATTGAG GCTTGCAGAC

```

1212

```

351 GCGGTTTTTG TCACGCGGTT TCTATATTGA TCAGATTGGT GAAGACGGTA
401 TTACCGTCAA TGTTGCAGGC CGTTCCGGAT ATACGGCGAA AATCGACGTG
451 TCTCCGAGTA CCGATTGGGC GGTATTATGAC CATATTGAAG TTGTACGGGG
501 TGCAACGGGG TTGACCCAAT CCAATTCAGA GCCGGGTGGA ACCGTCAATT
551 TGATCCGTAA GCGA

```

This corresponds to the amino acid sequence <SEQ ID 2546; ORF 743.a>:

```

a743.pep
  1 MNQNHFSLKI LTVMLLSAYG GSFADGVVPV SDGNTVSLDT VNVRGSHALS
 51 GKTEKTRSYT IDRSTATGM RIAGKDPQS VSVITRSLD DKAVHTLEEA
101 MKNTTGVNVV RDSGLQTRFL SRGFYIDQIG EDGITVNVAG RSGYTAKIDV
151 SPSTDLAVYD HIEVVRGATG LTQSNSEPGG TVNLIRKR

```

a743/m743 98.9% identity in 187 aa overlap

```

a743.pep      10      20      30      40      50      60
MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALSGKTEKTRSYT
|||||
m743          10      20      30      40      50      60
MNQNHFSLKILTVMLLSAYGGSFADGVVPVSDGNTVSLDTVNVRGSHALLGKTEKTRSYT
|||||

a743.pep      70      80      90     100     110     120
IDRMSTATGMRIAGKDPQSVSVITRSLDDKAVHTLEAMKNTTGVNVVRDSSLQTRFL
|||||
m743          70      80      90     100     110     120
IDRMSTATGMRIAGKDPQSVSVITRSLDDKAVHTLEAMKNTTGVNVVRDSSLQTRFL
|||||

a743.pep      130     140     150     160     170     180
SRGFYIDQIGEDGITVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
|||||
m743          130     140     150     160     170     180
SRGFYIDQIGEDGMTVNVAGRSGYTAKIDVSPSTDLAVYDHIEVVRGATGLTQSNSEPGG
|||||

a743.pep      TVNLIRKR
|||||
m743          TVNLIRKX

```

g744.seq not found yet  
g744.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2547>:

```

m744.seq
  1 ATGAAACCGT TAAAAACATT AGAATTTGGA TTTGTGGATG CTGCAAACTA
 51 CAGAAGAAGA GAAAATAAAG ATTTATTTAA CCGAATATTT GTAAAAGGAG
101 AATATTGGGA TGAATTATGT GAACCAAATA TTTCGTTTTT AATCGGAGAA
151 AAGGGAAC TG AAGACAGC ATATGCTGTT TATTTAACTA ATAACCTCTA
201 TAAAAACATA CATGCCACTA CTAAGTTTGT TCGTGAAACC GATTATTCAA
251 AATTTATTCA GCTAAAGAAA GCAAGACACT TAACTGTTTC AGATTTTACA
301 AGTATTGGGA AAGTCATTTT ATATCTGTTG ATATCAAATC AAATCAAATG
351 TAAAGAAAAC GGAATATTAT CTTCAATATT TAATAAATTT AAAGCCTTAG
401 ATGAGGCTAT AATGAATAT TATTATGGCG CTTTGTATCC GGAAATTGTA
451 CAAGCAATTA CTTTAATAGA AAATTCAAAA GAAGCTGCGG AAATGATTTT
501 TGGAAATTT GTTAACTAG GTGAAGAGGA ATCCCAACAA ATAACTTTAA
551 CAGAAAGTAA ATTCCAAGCA AATTAGGTT TTATTGAAAG AAAATTTAAA
601 GATGCTTTAT CTCAGTTAAA GCTAAAAGAT AATCATATTT TGTTTATTGA
651 TGGGATAGAT ATTAGACCAT CACAGATTCC ATTTGATGAA TATCATGAGT
701 GTGTAAAAGG TCTTGCTAAC GCCATATGGA TGTTAAATAA TGATATCTTC
751 CCTTCCATTA AAGATAGTAA GGAAGGATG AGAGTTGTGT TATTGATTAG
801 ACCTGATATC TTTGATTCAT TAGGTTTACA AAATCAAAT ACCAACTTC
851 AAGATAATTC AGTATTTTAA GACTGGAGGA CGGATTATAA ATCTTATAGA
901 AGTTCAAAGA TTTTGGCGT TTTTGATCAT CTTTGAGAA CCCAGCAAGA
951 AAAACAAGAT AGTTTAGAAA AAGGCAACTC ATGGGATTAT TATTTCCAT
1001 GGAATGCTCC TAATTTACAT GATGAGTATA AAAATTTAAC TTCATTATT
1051 AGCTTCTTAA GAAAATCGTA TTATCGACCT CGCGATATTC TTCAGATGCT
1101 TACTTTGCTA CAAAAAATA AGAAAAGTAA GGAAGATTAT GTCGTAGCAG
1151 AAGATTTTGA TAATACTTCT TTTCAAAGAG AATACTCGAT ATATTACTT
1201 GGTGAAATCA AAGATCATCT TTTGTTTTAT TATAGTCAA GTGATTATCA
1251 AAATTTCTCG AAATTTTGTG AATTTTAAA CGGGAAGAT AGATTAAAT

```

1213

```

1301 ATAGTGATTT TTAAAGCA TTTGAACGTT TGAAGCA CTTACAAACA
1351 ACATCAGTGG AAATACCTAA ATTTATGAGT ACTGCTAATG AGTTTTTGCA
1401 ATTTTATTT GACTTGAATG TTATTGCTTA TTAGATAAC CCAGAAGATG
1451 AAACGAAACC ATATATCCAT TGGTGCTTA AAGATAGAAA TTATGCAAT
1501 ATTTCTCTA AAATAAAAC TGAAGCTGAA TATTTAATAT TTTCAGGATT
1551 ATCAAAAGCC CTGATGTTG GTACTCCATT TAAGAACAA CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2548; ORF 744>:

```

m744.pep
  1 MKPLKTLFEG FVDAANYRRR ENKDLFNRI VKGEYLDEL EPNISFLIGE
 51 KGTGKTAYAV YLTNNFYKNI HATTKFVRET DYSKFIQLK ARHLTVSDFT
101 SIWKVILYLL ISNQIKCKEN GILSSIENKF KALDEAINEY YYGAFDPEIV
151 QAITLIENSK EAAEMIFGKF VKLGEESQ ITFTESKFOA NLGFIERKFK
201 DALSQLKLD NHILFIDGID IRPSQIPFDE YHECVKGLAN AIWMLNNDIF
251 PSIKDSKGRM RVLLIRPDI FDSLGLQON TKLQDNSVEL DWRTDYKSYR
301 SSKIFGVFDH LLRTQQEKQD SLEKGNWDY YFPWNAPNLH DEYKNLTSFI
351 SFLKSYRYP RDILQMLTLL QKNKSKEDY VVAEDFDNTS FQREYSIYLL
401 GEIKDHLLEY YSQSDYQNFL KFFEFLNGKD RFKYSDFLKA FERLKKHLQT
451 TSVIIPKEMS TANEFLOFLF DLNVIAYLDN PEDETKPYIH WCFKDRNYAN
501 ISPKIKTETE YLIFSGLSKA LDVGTPEFKNK Q*

```

g745.seq not found yet

g745.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2549>:

```

m745.seq
  1 ATGTTTTGGC AACTGACCGT TGTTTCAGTA ACCGCCGTCA TTGCACTGCG
 51 GACAATATTC ATCAATAAGA AAACCTCAAA GCAAAGGCG ACATTAGATG
101 TTATTTTGAA TGATTACCAA GATGCACAAT TTGTAGAAGC CGACAATCAT
151 ATTTGCGCTT ATATTCGCGG CACGGCAGTT GACGACAACA ACGCGCGGAT
201 CGACCTGTAT GAAATTTATC AAAATAAGGG CGGACAATGG GAAAAGAGA
251 GAGGGCATT ACTTACCGTA ATCAATCGGC ACGAGTTTGA TGGGTGCGCA
301 ATCAACTCGG GAGTATTGGA TGAGGATTG TTTAAACGGC TGCATTGCAC
351 CAACTTCATA AAATTGTGGA ATGCAGTTT GCCTCTTGT ATGAAAATAC
401 GCGAAGAAGA ACGCAAAGAC ACAATATTTA GAGAGTTGGA AATTTGGTT
451 GCATTATGGA AAGCAAACCC CCTAAAGGCA TCTGATTGT GA

```

This corresponds to the amino acid sequence <SEQ ID 2550; ORF 745>:

```

m745.pep
  1 MFWQLTVVSV TAVIALGTIF INKKTSKOKA TLDVILNDYQ DAQFVEADNH
 51 ISPYIRGTAV DDNNARIDLY EIYQNKGGQW EKERGHLLTV INRHEFYACA
101 INSGVLDEDL FKRLHCTNFI KLWNAVSPV MKIREERKD TIFRELEILV
151 ALWKANPLKA SDL*

```

a745.seq not found yet

a745.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2551>:

```

g746.seq
  1 ATGTCCGAAA ACAACAAAA CGAAGTCCTG ACCGGTTACG AACAGCTGAA
 51 ACGGCGCAAC CGCGCGCGCC TCGTAACGGC AAGCTCCCTG GTTGCCGCCT
101 CCTGCATCCT GCTGGCAGCC GCACTCAGT CCGATCCTGC CGACAGCAAT
151 CCCGCACCGC AGGCCGCGCA AACCAGCGCA ACGGAAGCC AAACGGCAAA
201 CACGGCACAA ACCCTGCCT TGAATCCGC CGCCGAAAAC GGGGAAACCG
251 CCGCCGACAA ACCGCAGGAC TTGGCAGGCG AAGACAAGCC TTCTGCCGCC
301 GACAGCGAAA TCAGCGAGCC TGAAACGTA GCGCGCGCCG TGGTGCTGAT
351 TAACGACCGG CTCGAAGACA GCAACATCAA AGGTTTGAA GAATCCGAGA
401 AACTGCAACA GGCAGAAACC GCCAAAACCG AACCGAAGCA GGCAAAACAA
451 CGCGTGCCG AAAAAGTGTG GGCAACTGCC GACAGTACGG ATACGGTAGC
501 GGTGAAAAA CCGAAACGCA CTGCCGAACC CAAACCGCAA AAAGCGGAAC
551 GCACTGCCGA AGCCAAGCCC AAAGCCAAAG AAACCAAAAC CGCCGAAAAA
601 GTTGCCGACA AACCGAAAAC TGCTGCCGAA AAAACCAAAC CGGATACGGC
651 AAAATCCGAC AGCGCGGTAA AAGAACGAA AAAAGCCGAC AAGGCTGAAG
701 GCAAAAGAC AGCCGAAAAA GACCGTTCGG ACGGCAAAA ACACGAAACG

```

```
g746.pap
1 MS ENKQNEVL TGYEQLKRRN RRLVTASSL VAASCILLAA ALSSDPADSN
51 PA PQAGETGA TESQTANTAQ TPALKSAEN GETADKPDQ LAGEDKPSAA
101 DSEISEPENV GAPLVLINDR LEDSNIGLE ESEKLQQAET AKTEPKQAKQ
151 RAAEKVSATA DSTDTVAEKS PKRTAEPKPO KAERTAEAKP KAKETKTAEK
201 VADKPRTAAE KTKPDTAESD SAVKEAKKD KAEGKKTAEK DRSDGKKHET
251 AQTKDRADKT KTAPEKESGK AGKKAIIQAG YAEKERALS QRMKKAAGID
301 STITEIMTDN GKVYRVKSSN YKNARDAERD LNKLRVHGIA GQVTNE*
```

```
m746.seq
1      ATGTCCGAAA  ACAAAACAAA  CGAAGTCTGT  AGCGGTTACG  AACAACTCAA
51     ACGGCGCAAC  CGCCGCGCC  TCGTACCGC  AAGTTGCGCT  GTTGC CGCGCT
101    CCTGCTCCTT  GCTGGCAGC  GCCCTCAGTT  CCGGCCCTGC  CGAACAGACT
151    GCCGGCGAAA  CAAGCGGCGT  AGAAAAACAA  GCGGCAGGTT  CGCGCAACAA
201    CCTGCTCTTG  AAATCCGCG  CCGCAAAAC  GCAGGACTTG  GCAGGCGAAG
251    ACAAGAGCTT  TGCCGCCGAC  AGCGAAATCA  CGCAGCTCGA  AAACGTAGGC
301    GCGCCGCTGG  TGCTGATTAA  CGAGCGCCTC  GAAGACAGCA  ACATCAAAGG
351    TTTGGAGAGC  TCCGAGAAAC  GTCACAGGCG  AGAAACCGCG  AAAACCGCAG
401    AGTAGCAGGC  AAAACAACGC  GCGTCCGAAA  AAGTGCCGGC  AACTGCCGAC
451    AATACGGATA  CGGTAGCGGT  TGAAAAACCG  AAACGCACGT  CCGAAACAAA
501    ACCGCAAAAA  GCGGAACGCA  CTGCCAAAGC  CRAGCCCAAA  GCCAAAGAAA
551    CCAAAACCGC  GCAAAAAGTT  GCCGACAAAC  CGAAAATCTG  CGCCGAAAAA
601    ACCAAACCGG  ATACGGCAAA  ATCCGACAGC  GCGGTAAAG  AAGCGAAAAA
651    AGCCGACAAG  GCTGAAAGCA  AAAAAACAGC  CGAAAAAGAC  CGTTCCGGAG
701    GCAAAAAACA  CGAAACGGCA  CAAAAAACCG  ACAAAACGCG  CAAGACCAAA
751    ACCCGCGAGA  AGGAAAAATC  CGGTAAAAAA  GCGCGCATT  AGGCAGGTTA
801    TGC CGAAAAA  GAACGCGCCT  TAAGCCTCCA  GCGCAAAATG  AAGCGCGCGG
851    GTATCGATT  GACCATACC  GAAATTATGA  CCGCAACGCG  CAAAGTTTAT
901    GCGGTCAAAT  CAAGCAACTA  TAAAAACGCA  AGGGATCCGG  AACCGGTATC
951    GAACAAAATG  CGGCTACAGC  GTATCGCCGG  TCAGGTAACG  AATGAATAG
```

```
m746.pap
1  MSENKQNEVL SGYEQLKRRN RRLVLTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPDQL AGEDKPSAAD SEISEPENVG
101 APLVLINERL EDSTNIKLEA SEKIQQAEAT KTAPKQAKOR AAEPKVPATAD
151 STDTVAVEKP KRTAEKTPKQ AERTKAAPK AKETKAEKV ADKPFTAEEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QKTDKADTK
251 TAEKEKSGKK AAQIAGYAEK ERAISLQQRK KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYNKA RDAERDLNKL RVHGIAGQVT NE*
```

ORF 746 shows 89.9% identity over a 346 aa overlap with a predicted ORF (ORF 746) from *N. gonorrhoeae*:

	10	20	30	40	50
m746.pep	MSENKQNEVL	SGYEQLKRRNRRLVTASCLVAASCILLAAALSSGPAEQT	----	AGETSG	
g746	MSENKQNEVL	TGYEQLKRRNRRLVTASSLVAAACILLAAALSSDPADSNPAPQAGETGA			
	10	20	30	40	50
	60	70	80	90	100
m746.pep	VENKAAGAAQT	PALKSAA-----DKPQDLAGEDKPSAADSEISEPENVGAPLVLINER			
	:	:	:	:	:
g746	TESQTANTAQT	PALKSAAENGETAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDR			
	70	80	90	100	110
					120

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```

      110      120      130      140      150      160      169
m746.pep  LEDSNIKGLEASEKLQQAETAKTAPKQAKQRAAEKVPATADSTDTVAVEKPKRTAETKPQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g746      LEDSNIKGLEASEKLQQAETAKTEPKQAKQRAAEKVSATADSTDTVAVEKPKRTAEPKPQ
          130      140      150      160      170      180

      170      180      190      200      210      220      229
m746.pep  KAERTAKAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g746      KAERTAEAKPKAKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAEGKKTAEK
          190      200      210      220      230      240

      230      240      250      260      270      280
m746.pep  DRSDGKKHETAQKTDKADKTKTAEKEKSGK---KAAIQAGYAEKERALSQRKMKAAAGID
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g746      DRSDGKKHETAQKTDKADKTKTAEKEKSGKAGKAAIQAGYAEKERALSQRKMKAAAGID
          250      260      270      280      290      300

      290      300      310      320      330
m746.pep  STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g746      STITEIMTDNGKVYRVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX
          310      320      330      340

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2555>:

```

a746.seq
1   ATGTCCGAAA ACAAACAAA CGAAGTCCTG AGCGGTTACG AACAACTCAA
51  ACGGCGCAAC CGCCGCGGCC TCGTAACGGC AAGTTGCTCG GTTGCCCGCT
101 CCTGCATCCT GCTGGCAGCC GCCCTCAGTT CCGGCCCTGC CGAACAGACT
151 GCCGGCGAAA CAAGCGGCGT AGAAAACAAA GCGGCAGGTG CGGCACAAAC
201 CCCTGCCTTG AAATCCGCGC CGACAAACCC GCAGGACTTG GCAGGCGAAG
251 ACAAGCCTTC TGCCGCGGAC AGCGAAATCA GCGAGCCTGA AAACGTAGGC
301 GCGCCGCTGG TGCTGATTAA CGACCGCCTC GAAGACAGCA ACATCAAAGG
351 TT'TGGAAGCA TCCGAGAAAC TGCAACAGGC AGAAACCGCC AAAACCGCAC
401 CGAAGCAGGC AAAACAACGC GCTGCCGAAA AAGTGCCGGC AACTGCCGAC
451 AGTACGGATA CGGTAGCGGT TGAAAAACCG AAACGCACTG CCGAAACAAA
501 ACCGCAAAAA GCGGAACGCA CTGCCAAGC CAAGCCCAA GCCAAAGAAA
551 CCAAAACCGC CGAAAAAGTT GCCGACAAAC CGAAACTGC CGCCGAAAAA
601 ACCAAACCGG ATACGGCAAA ATCCGACAGC GCGGTAAGAG AAGCGAAAAA
651 AGCCGACAAG GCTGAAAGCA AAAAAACAGC CGAAAAAGAC CGTTCGGACG
701 GCAAAAAACA CGAAACGGCA CAAAAACCG ACAAGCGGA CAAGACCAAA
751 ACCGCGGAGA AGGAAAAATC CGGTAAAAA GCCGCCATT AGGCAGGTTA
801 TGCCGAAAAA GAACGCGCCT TAAGCCTCCA GCGCAAAATG AAGCGGCGCG
851 GTATCGATTG GACCATCACC GAAATTATGA CCGACAACGG CAAAGTTTAC
901 CGCGTCAATC CAAGCAACTA TAAAAACGCA AGGGATGCCG AACGCGATT
951 GAACAAATTG CGGTACACG GTATCGCCGG TCAGGTAACG AATGAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2556; ORF 746.a>:

```

a746.pep
1   MSENKQNEVL SGYEQLKRRN RRLVTASCL VAASCILLAA ALSSGPAEQT
51  AGETSGVENK AAGAAQTPAL KSAADKPQDL AGEDKPSAAD SEISEPENVG
101 APLVLINDRL EDSNIKGLEA SEKLQQAETA KTAPKQAKQR AAEKVPATAD
151 STDTVAVEKP KRTAETKPQR AERTAKAKPK AKETKTAEKV ADKPKTAAEK
201 TKPDTAKSDS AVKEAKKADK AESKKTAEKD RSDGKKHETA QRTDKADKTK
251 TAEKEKSGKK AAIQAGYAEK ERALSQRKM KAAGIDSTIT EIMTDNGKVY
301 RVKSSNYKNA RDAERDLNKL RVHGIAGQVT NE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 746 shows 99.7% identity over a 332 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a746/m746; 99.7% identity in 332 aa overlap

```

      10      20      30      40      50      60
a746.pep  MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m746      MSENKQNEVL SGYEQLKRRNRRRLVTASCLVAASCILLAAALSSGPAEQTAGETSGVENK
          10      20      30      40      50      60

```



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	70	80	90	100	110	120
a746.pep	AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINDRLEDSENIKGLEA					
m746	AAGAAQT PALKSAADKPQDLAGEDKPSAADSEISEPENVGAPLVLINERLEDSENIKGLEA					
	70	80	90	100	110	120
	130	140	150	160	170	180
a746.pep	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKAERTAKAKPK					
m746	SEKLQQAETAKTAPKQAKQRAAEKVPATADSTDVAVEKPKRTAETKPKAERTAKAKPK					
	130	140	150	160	170	180
	190	200	210	220	230	240
a746.pep	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
m746	AKETKTAEKVADKPKTAAEKTTPDTAKSDSAVKEAKKADKAESKKTAEKDRSDGKKHETA					
	190	200	210	220	230	240
	250	260	270	280	290	300
a746.pep	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY					
m746	QKTDKADKTKTAEKEKSGKKAIIQAGYAEKERALSQRKMKAAAGIDSTITEIMTDNGKVY					
	250	260	270	280	290	300
	310	320	330			
a746.pep	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
m746	RVKSSNYKNARDAERDLNKL RVHGIAGQVTNEX					
	310	320	330			

g747.seq not found yet

g747.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2557>:

```

n747.seq
1   CTGACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGGGTG CTTCCCGCGA TGTCAGCAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAACAA TCTACAAACC
201 CCGTGAGATT GTCTTGGACG GTGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAGCCGCAA CGTTCATAG TCAATTAAAA
301 TCAAAATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2558; ORF 747&gt;:

```

n747.pep
1   LTPWADAYAD LRKTKVMTT QMGASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPPYR HKTIIKPREI VLDGDKTKMG RSKSNEYGFR VAATFYSQLK
101 SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2559>:

```

a747.seq
1   CTAACCCCTT GGGCGGATGC ATATGCAGAT TTGCGCGGCA AAACCAAAGT
51  GATGACGACC CAGATGTGTG CTTCCCGCGA TGTCAGCAA AGCGCCAAAG
101 GTTGGAGTGT CGGTATCGGT CTGAATGTAG GCAAACAGTT GACCGACAGC
151 GTCGGTCTCG AGTTTGATCC ATACTACCGT CACAAACAA TCTGCAAAACC
201 CCGTGAGATT GTTTTGGACG GCGACAAAC CAAATGGGC CGCTCCAAAT
251 CCAACGAGTA CGGCTTCCGC GTAACCGCAA CGTTCATAG TCAATTAAAA
301 TCAAGTAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2560; ORF 747.a&gt;:

```

a747.pep
1   LTPWADAYAD LRKTKVMTT QMCASRDVSK SAKGWSVGIG LNVGKQLTDS
51  VGLEFDPPYR HKTICKPREI VLDGDKTKMG RSKSNEYGFR VTATFYSQLK
101 SK*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. meningitidis*

ORF 747 shows 97.1% identity over a 102 aa overlap with a predicted ORF (ORF 746) from *N. meningitidis*:

a747/m747 97.1% identity in 102 aa overlap

	10	20	30	40	50	60
a747.pep	LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKWSVGIGLNVGKQLTDSVGLFDPYYR					
m747	LTPWADAYADLRGKTKVMTTQMGASRDVSKSAKWSVGIGLNVGKQLTDSVGLFDPYYR					
	10	20	30	40	50	60
	70	80	90	100		
a747.pep	HKTICKPREIVLDGDKTKMGRSKSNEYGFRVTATFYSQLKSKX					
m747	HKTIIKPREIVLDGDKTKMGRSKSNEYGFRVAATFYSQLKSKX					
	70	80	90	100		

a747/m80195

gi|150271 (M80195) outer membrane protein [*Neisseria meningitidis*] Length = 272

Score = 59.3 bits (141), Expect = 6e-09

Identities = 29/99 (29%), Positives = 51/99 (51%), Gaps = 4/99 (4%)

Query: 1 LTPWADAYADLRGKTKVMTTQMCASRDVSKSAKWSVGIGLNVGKQLTDSVGLFDPYYR 60

+ PW++ DL + K+ T +D+++ GW G+G N+GK+L +S +E P+Y+

Sbjct: 174 INPWSEVKFDLNSRYKLNTGVNLLKDDINQKTNGWGFGLGANIGKKLGESASIEAGPFYK 233

Query: 61 HKTICKPREIVL---DGD-KTKMGRSKSNEYGFRVTATF 95

+T + E + GD + ++ EYG RV F

Sbjct: 234 QRTYKESGEFSVTTKSGDVSLTIPKTSIREYGLRVGIKF 272

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2561>:

g748.seq

1	ATGAGTCAAA	ACCAACCCGC	ACAACCGACC	AAACGCAATC	TGTTCAAAAC
51	CGCCCTTGCC	GTCGGCGCAA	TGCGGCGCAAT	CGGAGGTTAT	TTCGGCGGCA
101	AAAAACAGGG	CGAAACCGCC	GAACGCACCG	CCGAAAGCCA	ACACTCGCCC
151	CAAGCCATC	CCTGCTACGG	CGAACATCAG	GCAGGTATCG	TACGCGCGCG
201	GCAGCGGTTT	TCCATTATGT	GCGCCTTCGA	CGTAACCGCG	CAAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCACACTGA	CCGCCCGCAT	CGAGTTTCTC
301	ACCCAAGCG	GAGAATACCA	AGACGGCGAC	GACAAACTCC	CGTCAGCCGG
351	CAGCGGCATT	TTGGGTAAAG	CCTTCAACCC	CGACGGATTG	ACCGTTACCG
401	TGCGGGTGGG	CAGCAGCCTG	TTGACGGCC	GGTTCCGACT	CAAAGACAAA
451	AAACCGGTT	ATTTCAGGA	AATGCGCGAC	TCCCCAACG	ATAAGCTGCA
501	AAAAAGCTGG	TGCGACGGCG	ATTGAGCCT	GCAATCTCG	GCCTTCACCC
551	CCGAAACCTG	CCAAACCGCC	CTGCGCGACA	TCATCAACA	CACCGCCCAA
601	ACCGCCGTCA	TCCGCTGGAG	TATCGACGGG	TGGCAGCCTA	AATCCGAACC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCCGAGAC	GGCACGGGCA
701	ACCCAAGGT	TTCCGATCCC	AAAACCGCCG	ACGAGGTTTT	ATGGACGGGC
751	GTGGCCGCCA	ACAGCCTCGA	CGAACCAGG	TGGGCGAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCGCTTTGT	CGAGTTTGG	GACAGGACGC
851	CGCTTCAAGA	GCAAACCGAC	ATTTTCGGGC	GGCGAAAAATA	CAGCGGGGCG
901	CCGATGGACG	GCAAAAAGA	AGCCGACCAA	CCGATTTCG	CCAAAGACCC
951	CGAGGGTGAT	ATCAGCCCA	AAGACAGCCA	TATGCGCCTG	GCGAATCCGC
1001	GCGATCCCGA	ATTCTCTAAA	AAACACTGCC	TCTTCCGCG	CGCCTACAGC
1051	TATTCTCGCG	GACCCGCCTC	AAGCGGACAG	CTTGATGTCG	GGCTGGTGTT
1101	CGTCTGCTAT	CAGGCAATC	TTGCCGACGG	TTTCATCTTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCCTG	GAAGAATACA	TCAGCCCCCT	CGGCGGCGGC
1201	TATTCTCTCG	TCTTGGCCGG	CGTGGGAAAA	GGCGGATTCT	TGGGACAAGG
1251	GCTGCCGGGC	GTATAA			

This corresponds to the amino acid sequence <SEQ ID 2562; ORF 748.ng>:

g748.pep

1	MSQNQPAQPT	KRNLFKTALA	VGAIGAIGGY	FGGKKQGETA	ERTAESQHSP
51	QAYPCYGEHQ	AGIVTPROAF	SIMCAFDVTA	QSAKQLENLF	RTLTAIEFL
101	TQGGEYQDGD	DKLPSAGSGI	LGKAFNPDGL	TVTVGVGSSL	FDGRFGLKDK
151	KTVHLQEMRD	FPNDKLQKSW	CDGDLSLQIC	AFTPETCQTA	LRDIIKHTAQ
201	TAVIRWSIDG	WQPKSEPGAM	AARNLLGFRD	GTGNPKVSDP	KTADEVLTWG
251	VAANSLEDEP	WAKNGSYQAV	RLIRRFVEFW	DRPLQEQTD	IFGRRKYSGA
301	PMDGKKKADQ	PDFAKDPEGD	ITPKDSHMRL	ANPRDPEFLK	KHCLFRRAYS
351	YSRGPASSGQ	LDVGLVFVCY	QANLADGFIF	VQNLNGEPL	EYISPFGGG

748.809

1	ATGAGCAAAA	AACAACCCGC	ACAACCGACC	AGGCGCACTC	TTTTTAAAC
51	CGCGATCGCA	CGCGGAGCAG	TCGGCGCAAT	CGGAGGTTAT	CTCGGCGGGCA
101	AAAAACACGG	GCAAACCGCC	GAAACGACCG	CCGAAGATCA	ACACTCGCCC
151	CAAGCCTATC	CCTGCTACGG	CGAACATCAG	CGAGGCATCG	TTACGCGCGCA
201	GCAGGCGTTT	TCGATTATGT	GGCCCTTCGA	CGTAACCCGG	CRAAGTGCCA
251	AGCAGCTGGA	AAACCTGTTC	CGCAGCTGA	CCGCGCCGAT	CGAGTTTCTC
301	ACCCAAGGCG	CGGAAATACCA	AGACGGCGAC	GACAAACTTC	CGCCAGCCGG
351	CAGCGGCAAT	TTGGGCAAG	CCTTCAACCC	CGACCGGCTG	ACCGTTACCG
401	TGGGGTGGG	CAGCAGCCTG	TTTGACGGCC	GGTTCGGGACT	CAAGAAGCAAA
451	AAACCGATT	ATTTCGAGGA	ATATCGCGAC	TGTTCCAAAG	ATAAGCTGCA
501	AAAAGCTTGG	TGCGACGGCG	ATTTGAGCCT	GCAAACTCTGT	GCCTTCACCC
551	CCGAAACCTG	CCAAGCCGCG	CTGCGCGACA	TGCTCAAAAC	CACCTGCTCAA
601	ACGGCCGTTA	TCCGTTGGAG	TATCGACGGG	TGCAGGCCCA	ATATCCGAAC
651	CGGCGCGATG	GCGGCGCGCA	ACCTGTTGGG	CTTCAGGGAC	GGCACGGGCA
701	ACCCAAAGT	TTCCGATCCG	AAAATCTGCC	ACGAGGTTTT	GTGGACGGGG
751	GTGGCCGCCA	ACAGCTCCGA	CBAACCGGAG	TGGCGAAAA	ACGGCAGCTA
801	TCAGGCAGTC	CGCCTTATCC	GCCACTTTGT	CGAGTTTTTG	GACAGGACGC
851	CGCTTCAAGA	GCAAAACCGAC	ATTTTCGGGC	GGCGCAAAAT	CAGCGGTGCG
901	CCGATGGAGC	GCAAAAAGA	AGCCGACCAA	CCGGATTTTT	CCAAAGACCC
951	CGAGGGTGAT	ATCAGGCCCA	AAGACAGCCA	TATACGCGTG	CGGAATCCGC
1001	GCGATCCGCA	ATTCTCTCAA	AAACACCGCC	TCTTTCGCGC	CGCCTACAGT
1051	TATTCGCGCG	GACTCGCCTC	AAGCGGACAG	CTTGATGTCC	GGCTTGGTGTG
1101	CGTCTGCTAT	CAGGCAAAAC	TTGGCGACGG	ATTATCTTTC	GTGCAAAACC
1151	TCCTCAACGG	CGAACCCTGT	GAAGAATACA	TCAGCCCTTT	CGGCGGCGGC
1201	TATTTCTTCG	TCTTGCCCGG	CGTGAAAAA	GGCGGCTTTT	TGGGGCAAGG
1251	GCTGCTGGGC	GTATAA			

m748.pap

1	MSKKQPAQPT	RRTLFKTAIA	AGAVGAIGGY	LGGKKQGETA	ERTAESQHSP
51	QAYPYQEYGH	AGIVTPQOAF	SIMCAFNDTA	QSAKQENLNF	RTLTAIRIEFL
101	TQGGEYQBDQ	DKLPPAGSIG	LGKAFNPDGL	TVTVGVGSSL	FDTGFRGLKDL
151	KPIHLOQEMRD	FSNDKLQKSW	CDGDLSLQIC	AFTPETCQAA	LRDIIKHTVQ
201	TAIVRWSIDJ	WQPKSEPGAM	AARNLLGFED	G7GPNKVSOD	KTADAEVLMTG
251	VAANSIDDEE	WAKNGSYQAV	RLIRHFEWF	DRTPLEQBDT	IFGRRKYSGA
301	PMDGKKEADQ	PDFAKDFEGD	ITPKDISHIRL	ANPRDPEFLK	KHRLFRRAYS
351	YSRGLASSGQ	<u>LDVGLVFVCY</u>	<u>QANLADGFIF</u>	<u>VQNLNGEPL</u>	EEYISPFGGG
401	YFVFLPVGEK	GVGLGQGLLG	V*		

**ORF 748 shows 95.0% identity over a 421 aa overlap with a predicted ORF (ORF 748) from *N. gonorrhoeae***

m748/g748 95.0% identity in 421 aa overlap

	10	20	30	40	50	60
m748.pep	MSKKQPAQPT	RRTLFKTAIAAG	AVGAIGGYLG	GKKQGETAERT	AESQHSQ	QAYPCYGEHQ
	:	:	:	:	:	:
g748	MSQNQPAQPT	KRNLFKTAI	AVGAIGGYFG	GKKQGETAERT	AESQHSQ	QAYPCYGEHQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m748.pep	AGIVTPQQA	FSIMCAF	DVTAQSAKQ	LENLFRTL	TARIEFLT	QGGEYQD
g748	AGIVTPROA	FSIMCAF	DVTAQSAKQ	LENLFRTL	TARIEFLT	QGGEYQD
	70	80	90	100	110	120
	130	140	150	160	170	180
m748.pep	LGKAFNP	DGLTVTV	GVGSSL	FDGRFLG	KDKKPIH	LQEMRDFS
g748	LGKAFNP	DGLTVTV	GVGSSL	FDGRFLG	KDKKTVH	LQEMRDFP
	130	140	150	160	170	180
	190	200	210	220	230	240
m748.pep	AFTPETCQA	ALRDI	IKHTVQT	AVIRWSID	GWQPKSEP	GAMAARNLL
	190	200	210	220	230	240

```

a748.seq
1  ATGAGCAAAA ACCAACCCGC ACAACCGACC AGGCGCACTC TTTTAAAAAC
51  CCGCATCGCA GCTGGAGCAG TCGCGGCAAT CGGAGGTTAT CTGGCGGGCA
101 AAAAAAGCGGG CGAAACCGCC CCGAACGACCG CGGAAAGCCA ACACCTGCCC
151 CAAGCCTATC CTTGCTACGG CGAACATCAG GCAGGCATCG TTACGCCGCA
201 GCAGGCGGTT TCGATTATGT CGCGCTTCGA CGTAACCGCG CAAAGTGCCT
251 AGCAGCTGGA AAACCTGTTC CGACAGCTGA CCGCCGCGAT CGAGTTTCTC
301 ACCCAAGCGC GCGAATACCA AGACGGCGAC GACAAACTTC CGCCAGCCGG
351 CAGCGGCATT TTGGGCAAGC CTTTCAACCC CGACGGGGTG ACCGTTACCG
401 TGGGGGTGGG CAGCAGCTGT CTTACGGGCC GGTTCCGGAT CAAAGACAAA
451 AAACCGATTG ATTTGCAGGA AATGCGCGAC TTCTCAAACG ATTAGCTGCA
501 AAAAAAGCTG TCGGACGGCG ATTTGAGCCT GCAAATCTGT GCCTTCACCC
551 CCGAAACCTG CCAAGCCGCC CTCGCGGACA TCATCAAACA ACCCGTCCAA
601 ACCGCGGTTA TCCGCTGGAG TATGCACGGG TGGCAGCCTA AATCCGAACC
651 CGGCGCGGAT GCGGCGCGCA ACCTGTTGGG CTTCGCGGAC GGCACGGGCA
701 ACCCAAGAGT TTCCGACCCC AAAACTGCGC ACGAGGTTTT GTGGACGGGG
751 GTGGCGGCCA ACAGCCTFCGA CGAACCGGAG TGGGCGAAAA ACGGCAGCTA
801 TCAGGCAGTC CGCCTTATCC GCCACTTTGT TGAGTTTTGG GACAGGACGC
851 CGCTTCAAGA GCAAAACGCA ATTTTCGGGC GGCAGAAATA CAGCGGGGCA
901 CGATGGAGC GCAAAAAGA AGCGACCAA CCGGATTTTG CCAAAGACCC
951 CGAGGGGAAT ACCACGCCCA AGAGACGCA TATACGCTG CGGAATCCGC
1001 GCGATCCGCA GTTCCTTAAA AAACACCGCC TCTTCGCGCG CGCCTACAGC
1051 TATTCGCGCG GACTCGCCTC AAGCGGACAG CTTGATGTGC GGCTGGTGTG
1101 CGCTGCTGTA CAGGCAAAAC TTCCGACAGG ATTCATCTTC GTGCAAAACC
1151 TCCTCAACGC CGAAGCCGCT GAAGAATACA TCAGCCCTTT CGGCGGGCGC
1201 TATTTCTTCG TCTTGCCCGG CGTGGA AAAA GCGCGCTTTT TGGGGCAAGG
1251 GCTGCTGGGC GTATAA

```

```

a748.pap
1  MSKNQPAQPT RRTLFKTAIA AGAVGAIGGY LGGKRGETA ERTAESQHSP
51  QAYPCYGEHQ AGIVTPQQA F SIMCAFDVTA QSAQOLNLF RLTTLARIEFL
101 TQGGEQYQDGD DKLPAPAGSGI LGKAFNPDLG TVTVQGVSSL DFGREGLDKD
151 KPIHLOEMRD FSNDKLQKSW CDGDLSLQIC AFTPETCQAA LRDI IKHTVQ
201 TAVIRWSIDG WQKSPEGAM AARNLNLGFRD GTGNPKVSDP KTADEVLTWG
251 VAANSLDEPE WAKNGSYQAV RLIRHFVEFW DRTPLOEQDT IFGRRKYSGA
301 PMDGKKEADG PDFAKDPENG TTPKDSHRL ANPRDPEFLK KHRLFRFRAYS
351 YSRGLASSGQ LDVGLVFVCY QANLADGFIF VQNLNGEPL EEEYISPGGG
401 YEFVLPVEKE GGFLGOGLLG V*

```

**Computer analysis of this amino acid sequence gave the following results:**

**m748/m748** 99.0% identity in 421 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2567>:

```
g749.seq
1  ATGAGAAAAAT TCAATTGTGAC CGCATTGTCC GTGATGCTTG CCTTGGGTTT
51  AAGCCGCGTGC CAGCCGCGCG AGCGCGAGAA AGCCGCGCGC GCCGCGTCCG
101 GTGAGACCCA ATCCGCCAAC GAAGCGGTT CGGTGCGTAT CGCGCTCAAC
151 GACAATGCCT GCGAACCGAT GAATCTGACC GTGCGAGCGC GACAGGTTGT
201 GTTCAATATT AAAAACAACA CGCGCCGCAA GCTCGAATGG GAAATCTGTA
251 AGGCGGTGAT GTGGTGTGAC GAACCGGAAA ATATCGCCCC GGGGCTTTCC
301 GACAAATGA CCGTAACcct GCTGCCGGGC GAATACGAA TGCATGCGG
351 CCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAGCCGAC AGCGGCTTTA
401 AAGACACCGC CAACCAAGCG GATTGGAAAT AACTGCCCCA ACCGCTGCCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG CGGCGAAAC
501 CAAACCTTT ACCGAAGCCG TCRAAGCAGG CGACATTGAA AAGCGGAAAT
551 CCGTGTTCG CGCACCAGCG CTCATTACG AACGCATGAA ACCGATGCCC
601 GAGCTTTTCA GCGAACTCGA GTCGCTATC GATCGGTGTG AAGACGACTT
651 CAAAGACGTT GCGAAAGATG CCGGGTTTAC CGGCTTCCAC CGTATCGAAC
701 AGGCCCTTGT AGGTGAAAAA GACCTATCCG GCGTGAAGCA AACCCGCGGC
751 AAACGTATGA CCGATGTGCA AGCCGTGCAA AAAGAAATCG ACGCATGGG
```

```

801 GttccctCCG GGCAAAGTGG TCGCGCGCGC GTCCGAAGT ATTGAAGAAG
851 CGGCGGGCAG TAAATCAGC GCGGAGAAG ACCgttaCAG CCACACCGAT
901 TTGAGCGACT TCCAAGCTAA TCGGACGGA TCTAAAAAA TCGTCGATTT
951 GTTCCGTCCG TTGATTGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAATA CCGACCAAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGAGC GAAGCCGACC GCAAAGCATT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2568; ORF 749.ng>:

```

g749.pep
1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIQAVN
51 DNACEPMNLT VPSGQVVENI KNSGRKLEW EILKGVVVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPQPLA
151 DYKAYVQGEV KELAATKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKDTNFKQV NEILAKYRTK
351 DGFETYDKLS EADRKALQAP INALAEDLAQ LRILGLK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2569>:

```

m749.seq
1 ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTCAC
151 GACAATGCCT GCGAACCGAT GGAATGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAACAACA CCGCGCGCAA GCTCGAATGG GAAATCCTGA
251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAATA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
501 CAAAACTTTT ACCGAAGCCG TCAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCGCG GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTTTAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAACGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCCTCCG GGCAAGGTGG TCGCGCGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGGCAG TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAA TCGTCGATTT
951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCTCCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2570; ORF 749>:

```

m749.pep
1 MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQAVN
51 DNACEPMELT VPSGQVVENI KNSGRKLEW EILKGVVVVD ERENIAPGLS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKDTNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRILGLK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 749 shows 96.1% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. gonorrhoeae*

m749/g749 96.1% identity in 388 aa overlap

```

          10      20      30      40      50      60
m749.pep MRKFNLTALSVM LALGLTACQPPEAEKAAP AASGEAQTANEGGSVSIQAVNDNACEPMELT
          |||||
g749      MRKFNLTALSVM LALGLTACQPPEAEKAAP AASGETQSANEGGSVGIQAVNDNACEPMNLT
          10      20      30      40      50      60

```

1222

	70	80	90	100	110	120
m749.pep	VPSGQVVFNIKNNNGRKLWEILKGMVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
g749	VPSGQVVFNIKNNNGRKLWEILKGMVMVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m749.pep	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE					
g749	NPRGKLVVADSGFKDTANEADLEKLPQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m749.pep	KAKSLFADTRVHYERIEPIAELEFSELDPFVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
g749	KAKSLFAATRVHYERIEPIAELEFSELDPFVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
g749	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEAAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m749.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
g749	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS					
	310	320	330	340	350	360
	370	380	389			
m749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
g749	EADRKALQAPINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2571>:

a749.seq

```

1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCCGCTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGCGGTT CGGTCAGTAT CGCCGTC AAC
151 GACAATGCCT GCGAACC GAT GGAAGTACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACAACA CGCGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCTT GTTGCCGGGC GAATACGAAA TGACTTGGCG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTCA AGGCGAAGTC AAAGAGCTGG TGCGGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGTA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGATTGGC
801 GTTTCCTCCG GCGAAGGTGG TCGGCGGCGC GTCCGAAC TGATTGAAGAAG
851 TGCGCGGCGA TAAATCAGC GCGGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCAAAGCCAA TGTGGACGGA TCGAAAAAAA TCCTCGATTT
951 GTTCCGTCCG TTGATCGAGA CCAAAAACAA AGCCTTGT TG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGCGGAAATA CCGGACTAAA
1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTCGCGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2572; ORF 749.a>:

a749.pep

```

1  MRKFNLTALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIQVN
51  DNACEPMELT VPSGQVVFNI KNNNGRKLWE EILKGMVMVD ERENIAPLGS
101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEAD LEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD

```

301 LSDFQANVDG SKRIVDLFRP LIETKNKALL EKTDTNFKQV NEILAKYRTK  
 351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N meningitidis*

ORF 749 shows 99.7% identity over a 388 aa overlap with a predicted ORF (ORF 749) from *N. meningitidis*:

a749/m749 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
a749.pep	MRKFNLTSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
m749	MRKFNLTSVMLALGLTACQPPEAEKAAPAASGEAQTANEGGSVSIIVNDNACEPMELT					
	10	20	30	40	50	60
a749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
a749.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
m749	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT					
	70	80	90	100	110	120
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
	130	140	150	160	170	180
a749.pep	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
m749	NPRGKLVVTDSGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTTFTEAVKAGDIE					
	130	140	150	160	170	180
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
a749.pep	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
m749	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK					
	190	200	210	220	230	240
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
a749.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
m749	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
a749.pep	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
m749	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
	310	320	330	340	350	360
a749.pep	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
m749	LSDFQANVDGSKRIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG					
	310	320	330	340	350	360
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380	389			
a749.pep	EADRKALQASINALAEDLAQLRGILGLKX					
m749	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2573>:

g750.seq

1	GTGAAACCGC	GTTTTATTG	GGCAGcctGC	GCCGTCCTGC	CGGCCGCCTG
51	TTCCGCCGAA	CCTGCCGCCG	AAAAAACTGT	ATccgCCGCA	TCCCAAGCCG
101	CATCCACACC	TGTCGCCACG	CTGACCGTGC	CGACCGCGCG	GGCGGATGCC
151	GTTGTGCCGA	AGAATCCCGA	ACgcgtcgcc	gtgtAcgaCt	ggCGCGCGTt
201	ggaTACGCTG	ACCGAGCCGG	GCGTGAATGT	GGGCGCAACC	ACCGCGCCGG
251	TGCGCGTGGA	CTATTTGCAG	CCTGCATTG	ACAAGCGCGC	AACGGTGGGG
301	ACGCTGTTTG	AGCCCGATTG	CGAATCCCTG	CACCGCCACA	ATCCGCAGTT
351	TGTCATTACC	GGCGGGCCGG	GTGCGGAAGC	GTATGAACAG	TTGGCGAAAA
401	ACGCGACCAC	CATAGATTG	ACGGTGGACA	ACGGCAATAT	CCGCACCAGC
451	GGCGAGAAGC	AGATGGAGAC	CCTGTCGCGG	ATTTTCGGTA	AGGAAGCGCG
501	CGTGCGGAA	TTGAATGCGC	AGATTGACGC	GCTGTCGCC	CRAAAGCGCG
551	AAGCCGCCAA	AGGCAAAGGA	CGCGGGCTGG	TGCTGTCGGT	TACAGGCAAC
601	AAGGTGTCCG	CCTTCGGCAC	GCAATCGCGG	TTGGCAAGT	GGATACACGG
651	CGACATCGCG	CTGCCGCCCG	TGGACGAATC	TTACGCAAC	GAAGGGCAGC
701	GGCAGCCCGT	TTCCTTCGAA	TACATCAAAG	AGAAAAACCC	CGGCTGGATT
751	TTCATCATCG	ACCGCACCGC	CGCCATCGGG	CAGGAAGGGC	CGGCTGCCGT



q750.pap

1	VKP	RFYWAAC	AVLPAACSPE	PAAEKTVSAA	SQAASTPVAT	LTVP	TARGDA
51	VVP	KNPERVA	VYDWAALDTL	TEPGVNVAT	LAPNVRVDYL	PAFDKAA	ATVVG
101	TLE	EPDCESL	HRHNPKQFVIT	GGGPAEAYEQ	TAKNRTITDL	TVDNGN	IRTS
151	GEK	QMETLSR	IFGKEARVAE	LNAQIDALFA	QKREAAKGKG	RGLVLSVT	GN
201	KVS	AFGTQSR	LASWTHGDIG	LPVDESLSRN	EGHGQPVSE	YIKEKNPG	WGI
251	FTI	DRTAAG	QEGPAAEVIL	DNALVCGTNA	WKRKQIIVM	AANYIVAG	GA
301	RQL	IQAAEQ	KAQFAKEAPV	AAQ*			

750. 200

1	GTGAAACCGC	GTTTTATTG	GGCAGCCTGC	GCCGTCCTGC	TGACCGCCTG
51	TTCCGCCGAA	CCTGCCCGCA	AAAAACCTGT	ATCCGCGCGA	TCCGCATCTG
101	CCGCCCCAGT	GACCGTGCCG	ACCGCGCGGG	CGCATGCCGT	TATCGCCGAAG
151	AATCCCGAAC	GCCTCGCCGT	GTACAGCTGG	CGCGCGTTGG	GTACGCTGAC
201	CGAATTGGCG	GTGAATGTGG	CGCAACCCAC	CGCGCCCGTG	CGCGTGGATT
251	ATTTCGACCC	TGCATTTGAC	AAGCGGCGCA	CGGTGGGGAC	CGTGTTCGAG
301	CCCATTACG	AGGCCCTGCA	CGCCTACAAT	CTCCAGCTTG	TCTATTACCG
351	CGGCGCCGGC	CGGGAAGCTG	ATGAACAGTT	AGCGAAAAAC	CGCACCACCA
401	TAGATTCTGAC	GTGGGACAAC	GGCAATATCT	GCACCAACGG	CGAAAGACAG
451	ATGGAGACCT	TGGCGCGGAT	TTTTCGGCAAG	GAAGCGCGCG	CGGCGGAATT
501	GAAAGCGCAG	ATTGACGCGC	TGTTCGCCCA	AACCGCGCAA	GCCGCCAAAG
551	GCAAAGGACG	CGGGCTGGTG	TGCTCGGTTA	CGGGCAACAA	GGTGTCCGCC
601	TTCCGCCACG	AGTCGCGGTT	CGCAAGTTGG	ATACACGGCG	ACATCGGCCCT
651	ACCGCCTGTA	GACGAATCTT	TACGCAACGA	GGGGCACGGG	CAGCCTGTTT
701	CCTTCGAATA	CATCAAAGAG	AAAAACCCCG	ATTGGATTTC	CATCATCGAC
751	CGTACCGCCG	CCATCGGGCA	GGAAGGCCCG	CGCGCTGTCT	CAATATTGGA
801	TAAACGCGCT	GTACGCGGCA	CGAACGCTTG	GAAGCGCAAG	AGAATCATCG
851	TCATGCGCTG	CGCGAACTAC	ATTGTCCGGG	CGCGCGCGCG	GCAGTTGATT
901	CAGCGCGGCG	AGCAGTTGAA	GGCGGCGTTT	AAAAAGGCAG	AACCCGTTGC
951	GGCGGGGAAA	AAGTAG			

m750.pap

1	VPKRFYWAAC	AVLLTACSPE	PAAEKTVSAA	SASAATLTVP	TARGDAVVPK
51	NPERVAAYDW	AALDTLTTEL	VNVGATTAPV	RDVYDLQAFD	KAATVGTLFE
101	PDYEALHRYN	PQLVITGGPG	AEAYEQALKN	ATTIDLTVDV	GNRTSGEKQ
151	METLIARIFG	EARAELKAKI	IDALFAQTRE	AAKGKGRGLV	LSVTGNKVSA
201	FGTQSRLSA	IHGDIGLPPV	DESLRNEGHG	QPVSFYIYKE	KNPDWIFIID
251	RTAAIQGEQG	AAVEVLNDAI	VRGTNAWKRR	QIIVMPAANY	IVAGGARQLI
301	QAAEQLKAAF	KAAEPVAAGK	K*		

### Homology with a predicted ORF from *N. gonorrhoeae*

**m750/g750**      **93.8% identity in 322 aa overlap**

	10	20	30	40	50		
m750.pep	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASA----	ATLTVP	TARGDAVV	PKNP	PERVA	
		:					
g750	VKPRFYWAACAVLPAACS	EPAAEKTVSAASQAAS	TPVATLTVP	TARGDAVV	PKNP	PERVA	
		:					
	10	20	30	40	50	60	
	60	70	80	90	100	110	
m750.pep	VYDWAALDTLT	ELGVNGATTAP	VRVDYLQPA	FDKAATVGT	LFEPDYEAL	HRYPQLVIT	
g750	VYDWAALDTLT	EPGVNGATTAP	VRVDYLQPA	FDKAATVGT	LFEPDCESL	HRHNPQFVIT	
	70	80	90	100	110	120	
	120	130	140	150	160	170	
m750.pep	GGPGAEAYEQLAK	NATTIDLT	VDNGNI	RTSGEKQ	METLARI	FGKEARA	EALKAQIDALFA

```
g750      GGPGAEEAYEQLAKNATTIDLTVDNGNIRTSGEKOMETLSRIFGKEARVAELNAQIDALFA  
          130       140       150       160       170       180  
  
m750.pep   180       190       200       210       220       230  
QTREAAKKGKRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESILRNEGHGQPVSFE  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
g750      QKREAANKGKRGLVLSVTGNKVSAFGTQSRLASWIHGDIGLPPVDESILRNEGHGQPVSFE  
          190       200       210       220       230       240  
  
m750.pep   240       250       260       270       280       290  
YIKEKNPDWIFIIDRTAAGQGEPAAVEVLNALVRGTNAWKRRQIIVMPAANYIVAGGA  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
g750      YIKEKNPGWIFIIDRTAAGQGEPAAVEVLNALVCGTNAWKRRQIIVMPAANYIVAGGA  
          250       260       270       280       290       300  
  
m750.pep   300       310       320  
RQLIQAAEQLKAAFKAEPVAAGKKX  
| | | | | : | | | | |  
g750      RQLIQAAEQLKAFKAEPVAAQX  
          310       320
```

```
a750.seq
1      GTGAACCCGC GTTTTTATTG GGCAGCCTGC GCCGTCTCTGC TGACCCGCCTG
51     TTCGCCCAAG CCTGCCGCCG AAAAAACTGT ATCCGCCCGCA TCCGCATCTG
101    CGCGCAGCACT GACCGTCGCC GCGATCCCGT GCGATCCCGT TGGCCCGAAG
151    AATCCCGAACC GCGTCGCCGT GTACGACTGG GCGGCGTTGG ATACGCTGAC
201    CGAATTGGGT GTGAATGTGG GCGCAACCAC CGCGCGCGTG CGCGTGGATT
251    ATTTGCAGCG TGCATTTGAG AAGCGCGCAA CCGTGGGGAG CGTGTTCGAG
301    CCCGATTACG AAGCCCTGCA CCGCTACAAT CCTCAGCTTG TCATTACCGG
351    CGGGCCGGGG GCGGAAGCGT ATGAACAGTT GCGCAAAAAAC GCGACCACCA
401    TAGATCTGAC GGTGGACAAC GGCAATATCC GCACCGACGG CGAAAAGCAG
451    ATGGAGACCT TGGCGCGGAT TTTCGCGAAG GAAGCGCGCG CGCGCGGAAT
501    GAAGGCGCAG ATTGACGCGC TGTTCGCCCA AACCGCGCGA GCCGCCAAG
551    GCAAAAGGAG CCGGCTGGTG TGTTCGGTTA CCGGCAACAA GGTGTCGCCC
601    TTCGCCACGC AGTCGCGGTT GGCAAGTTGG ATACACGGCG ACATCGGCCT
651    ACCGCCTGTA GACGAATCTT TACGCAACGA GGGCGACGGG GACGCTTCTT
701    CCTTCGAATA CATCAAGAG AAAAACCCCG ATTGGATTCT CATCATCGAC
751    CGTATCCGCCG CCATCGGGCA GGAAGGGCCG GCGGCTGTTC AAGTATTGGA
801    TAACGCGCTG GTACGCGGCA CGAACGCTTG GAAGCGCAAG CAATCATCTG
851    TCATGCTCTG CGCGAACTAC ATTGTCCGGG GCGGCTCGCG GCAGTTGATT
901    CAGGCGCGCG AGCAATTGAA GGAGGCGTTT GAAAAGGCAG AACCCGTTGC
951    GGC GGCGAAG GAGTAG
```

```
a750.pep
1 VKPRFYWAAC AVLLTACSPE PAAEKTVSAA SASAATLTVP TARGDAVVPK
101 NPERVAVYDN AALDTLTGEL VNVGATTAPV RVDYDQPAFD KAATVGTLFE
151 PDYEALHYRN POLVITGGPG AEAYEQLAKN ATTIDLTVDN GNIRTSGEKQ
201 METLARIFGK EARAALKAQK IDALFAQTRE AAKGKGRGLV LSVTGNKVSQ
251 FGTQSRSLAS IHGDIGLPPV DESLRNEGHG QPVSFYIKE KNPDWIFIID
301 RTAAIGQEGP AAVEVLNDAL VRGTNAWKRK QIIVMPAANY IVAGGSRQLI
351 QAAEQLEKPEF EKAEFVAAGK E*
```

ORF 750 shows 98.8% identity over a 321 aa overlap with a predicted ORF (ORF 750) from *N. meningitidis*:

	10	20	30	40	50	60
a750.pep	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASAAT	LTVP	TARGDAVVPKNP	ERVA	VDW
m750	VKPRFYWAACAVLLTACSP	EPAAEKTVSAASASAAT	LTVP	TARGDAVVPKNP	ERVA	VDW
	10	20	30	40	50	60
	70	80	90	100	110	120
a750.pep	AALDTLT	ELG	VNVG	TATP	VRVD	YDLQ
m750	AALDTLT	ELG	VNVG	TATP	VRVD	YDLQ
	70	80	90	100	110	120

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	70	80	90	100	110	120
a750.pep	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNIIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
m750	130	140	150	160	170	180
	AEAYEQLAKNATTIDLTVDNGNIIRTSGEKQMETLARI FGKEARAAELKAQIDALFAQTRE					
a750.pep	190	200	210	220	230	240
	AAKGKGRGLVSVTGNKVS AFGTQSRLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
m750	190	200	210	220	230	240
	AAKGKGRGLVSVTGNKVS AFGTQSRLASWIHGDIGLPPVDES LRNEGHGQPVSFEYIKE					
a750.pep	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYIVAGGS RQLI					
m750	250	260	270	280	290	300
	KNPDWIFIIDRTAAIGQEGPAAVEVL DNALVRGTNAWK RKQIIVMPAANYIVAGGARQLI					
a750.pep	310	320				
	QA AEQLKEAF EKAEPVAAGKEX					
m750	310	320				
	QA AEQLKAAFK AEPVAAGKKX					

g751.seq not found yet

g751.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2579>:

m751.seq..

```

1  ATGGCTTGGA GTATGTTTGC CACAACCCAA GCCGATAGAG CGGTAAGGTC
51  TGCAACTGCA CCTAAAGAAA TGTGGTTCCA TAAGAAGATA ATAGATGAAA
101 AAACAGGTAA AGTATCCTTT GATACCAGAC AAAATTTGGTC ATTGAATGAT
151 TTAAGCAAGG AAGAACTGGC AAGCATTCAA GACACAAATG GCAAAGTTAT
201 TACTGTGTCT AATCCTGGTA TTTTCAATAA TCGAGAAGAT TCATTAAGCA
251 ACGCAGCAAA ACAAAATCGT AATAGTACAA ACGGTAGTGG TGTATTGCA
301 GTCATGAATC CTCCAACAGG GAAATATAAA TCTGATTCTA ATAACAAAAT
351 AAAAGATTTT TTATGGCTCG GTTCAAGTCT TGTTCCTGAA CTGATGTATG
401 TCGGTTACGA CCAATTAAAT AATAAAGTGT TCCAAGGCTA TTTACCCAAA
451 ACCAATTCAG AAAAACTGAA TCAAGATATT TATCGAGAGG TTCAAAAAAT
501 GGGTAACGGC TGGTCGGTTG ATACCAGTAA TCACAGTCGT GGGGGAATTA
551 CAGCAAGCGT TTCCTTAAAA GATTGGGTAA ACAATCAAAA ACAAAATGGC
601 ATTGCCCCAA TCAGAAAAGC ACGTTTCTAT GGTACAGCCA CAAATGTGCA
651 GAATGATTAC GCCGATGTTT TACAGAAAAA CGGCTATACC TATACGGGTG
701 CAGACGGCAA AACTTATAAC AGCGGATCCT ACTCAATCGT GCATGATAAA
751 GATTTTGTGG GGAACAAATG GATACCTTTC TTGCTAGGAA CCAATGACAC
801 CACACAAGGT ACATGTAAGG GGTGTGTGCTA TTCGCATAGC AGTTATTTTG
851 CCGAGGTGCC AAAAGCAGGT ACAAAAGAAT TTGATGACTA TGTA AAAATA
901 TGGGGTGAAG TTGAATATGA CGCTCAAGGT AAGCCAATTA ACAAACTCTA
951 ACCCATACTG GTAGAACCAA ACAAAACAAA AGATAATGAA AAATATGAAA
1001 AAGAAGCTTT CTA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2580; ORF 751&gt;:

m751.pep..

```

1  MAWSMFATTQ ADRAVRSATA PKEMWPHKKI IDEKTGKVSF DTRQIWSLND
51  LSKEELASIQ DTNGKVITVS NPGIFNNRED SLSNAAKQNR NSTNGSGVIA
101 VMNPPTGKYK SDSNNKIKDF LWLGSSLVSE LMVVG YDQLN NKVFQGYLPK
151 TNSEKLNQDI YREYQKMGNG WSVDTSNHSR GGITASVSLK DWVNNQKQNG
201 IAPIRKARFY GTATNVQNDY ADVLQKNGYT YTGADGKTYN SGSYSIVHDK
251 DFGVGNKWI PF LLGTNDTTQG TCKGLCYSHS SYFAEVPKAG TKEFDDYVKI
301 WGEVEYDAQG KPINKSKPIL VEPNKT KDNE KYEKEAF*

```

a751.seq not found yet

a751.pep not found yet

g752.seq not found yet

g752.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2581>:

m752.seq..

```

1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51 GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATTCCTT
1 01 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
1 51 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
2 01 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
2 51 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
3 01 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
3 51 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
4 01 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
4 51 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
5 01 AGTGGCCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
5 51 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
6 01 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC
6 51 TACCAGTAAC GCTATTGAAA ACAAGGCGA GCCCGGACAA TTCAGGCAGG
7 01 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
7 51 CCGCCGCACG GACAGGTTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
8 01 CAATAATACC TATGACGGCG TGGAAATCC GTTTATCCAT CCGGTGTGCC
8 51 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
9 01 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
9 51 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
10 01 CTCTCGCCA ATACGCCAAA TCCTATTGTG ATGCGGAAAC TGACGATTTA
10 51 GATTTAACCT ATTTATCTTA TTACCAATGC GATATTATCA AGCGGGCGGT
11 01 TGCCGATTTG GAGCACTACA TTTCCGACAA ACAAACACAC CAACAGGAAT
11 51 TCAAAGCAGC GATTGCCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
12 01 CGGCAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
12 51 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
13 01 GTAGCGATTG GAGTAAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
13 51 TCAGGAAATG CTTTAGAGTA TGTGCTCCT CAGGATTTAT TGGAAAGGTT
14 01 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2582; ORF 752>:

m752.pep

```

1 MKISRPPEFT LQOEYMOHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTESTRM KWRVAVKESRK KIQKPIDFPF
1 01 EHQWFECIPD SLQARLHLID KSCGSSIGTS SLGGFGRSEQ NRFLKSLIM
1 51 EEAITSAQLE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
2 01 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
2 51 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHPFGD
3 01 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
3 51 DLTYFIYYQC DIIKRAVADL EHYISDKQKH QQEFKAAIAQ YTEKIGKLNQ
4 01 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDLSKL GEYRFLVPFK
4 51 SGNALYVAP QDILLERLEKK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2583>:

m752-1.seq

```

1 ATGAAAATTT CCAGACCTCC GGAATTTACC CTGTTGCAAC AGGAATATAT
51 GCAGCATCTC ACTGAAAGAA TGACGCAAAAT TGCCAAGCTG CTGAATTCCTT
101 CCGCAAACAA TCCTGATATA GACATTCCCG ATTTTCTTAC TGAAATCAAA
151 GATTATTCAG AATTTTCCGT GACAGATGAA AATGGAACCT ACCTGCATTG
201 GGACAAATTC CGCCGGATTG ACACGGAAGA TACGCGGATG AAATGGCGCG
251 CCGTTAAGGA AAGCCGCAAA AAAATCCAAA AACCAATTGA TTTCCCGTTT
301 GAACATCAGT TTTGGTCTG CATTCCCGAC TCTTTCAGG CACGGCTTCA
351 TTTGATTGAC AAAAGCTGCG GCAGTTCTAT CGGCACGTCT AGCTTGGGTG
401 GCTTCGGCAG AAGCGAGCAA AACAGATTCT TGCTCAAGTC TCTGATTATG
451 GAAGAAGCGA TTACATCCGC CCAACTGGAA GGTGCGGCTA CCACGCGTAA
501 AGTGGCCCAAG GATATGCTCA AATCGCAGCG TAAACCCAAA ACAAAGACG
551 AAATCATGAT AGTGAACAAC TATCACTTGA TGAAAAAAGC GGTAGAATTG
601 AAAAATACGC CGTTAAGTGT TGAAATGATT TTGGATTTCG ACCGCATTGC

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651 TACCAGTAAC GCTATTGAAA ACAAGGCCGA GCCCGGACAA TTCAGGCAGG
701 ATGACGAAAT CTTTATCGCC GATATCAATG GTAACAGCCT GTATCAACCA
751 CCGCCGCACG GACAGGTCA TACGCTGATG GAAGAGGTGT GTGCGTTTGC
801 CAATAATACC TATGACGGCG TGGAAAATCC GTTTATCCAT CCGGTTGTCC
851 AAGCTATTAT CTTGCATTTC CTCATCGGCT ACATCCACCC ATTTGGTGAT
901 GGCAACGGGC GGACAGCGCG GGCTTTGTTC TATTGGTTTA TGCTCAAAAA
951 CGGCTACTGG CTATTTGAAT ACATATCCAT CAGCCGTCTT CTGAAAAACG
1001 CTCTGCCCCA ATACGCCAAA TCCTATTTGT ATGCGGAAAC TGACGATTTA
1051 GATTTAACCT ATTTATCTA TTACCAATGC GATATTATCA AGCGGGCGGT
1101 TGCCGATTG GAGCACTACA TTTCCGACAA AAAAAACAC CAACAGGAAT
1151 TCAAAAGCAGC GATTGCCAA TATACTGAAA AGATAGGAAA GTTGAACCAA
1201 CGGCAAAATTG GTATCCTGCA AAAAGCAGTG GAAGAAAGCG GAAAAATCTT
1251 TACTGCACAA GAAATTGCCA ACCAATACGG CATCTCCCTG AATACTGCCC
1301 GTAGCGATTG GAGTAACTG GGAGAATATA GATTCCTAGT GCCGTTCAAA
1351 TCAGGAAATG CTTTAGAGTA TGTTGCTCCT CAGGATTTAT TGGAAAGGTT
1401 AGAAAAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2584; ORF 752-1>:

m752-1.pep

```

1 MKISRPPEFT LLQEQYMQHL TERMTQIAKL LNSSANNPDI DIPDFLTEIK
51 DYSEFSVTDE NGTYLHWDKF RRIHTEDETRM KWRVAVKESRK KIQKPIDFPF
101 EHQFWFCIPD SLOARLHLID KSCGSSIGTS SLGGFGRSEQ NRELLKSLIM
151 EEAITSQALE GAATTRKVAK DMLKSQRKPK TKDEIMIVNN YHLMKKAVEL
201 KNTPLSVEMI LDHRIATSN AIENKAEPGQ FRQDDEIFIA DINGNSLYQP
251 PPHGQVHTLM EEVCAFANNT YDGVENPFH PVVQAILHF LIGYIHPFGD
301 GNGRTARALF YWFMLKNGYW LFEYISISRL LKNAPQYAK SYLYAETDDL
351 DLTYYFIYYQC DIIKRAVADL EHYISDKQKH QOEFKAAIAQ YTEKIGKLNQ
401 RQIGILQKAV EESGKIFTAQ EIANQYGISL NTARSDSLKL GEYRFLVPFK
451 SGNALYVAP QDLLELEKK *

```

a752.seq not found yet

a752.pep not found yet

g753.seq not found yet

g753.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2585>:

m753.seq

```

1 ATGCCCATCA CTCCACCCTT AAACATCATC TCTCCTAAAC TCTACCCCAA
51 TGAACAATGG AACGAAAGCG AAGCACTCGG TGCCATCACT TGGCTATGGT
101 ATCAGTCGCC TACGCATCGC CAAGTACCTA TTGTGGAGAT GATGACGTAT
151 ATATTGCCTG TGTAAAAAAA CGGGCAGTTC GCTTTGTTTT GCAAGGGTAC
201 CCAACCAATC GGTATATCT CATGGGCTTA TTTTGATGAA GTGGCGCAGG
251 CGCATTATTT AGAATCTGAC CGCCATTGTC GTGACAACAG CGATTGGAAC
301 TGTGGCGACA ATATTGGCT GATTCAATGG TTTGCGCCAT TGGGACACAG
351 TCATCAAATG CGCTCAGCTG TCGCCAGTT ATTCCTAGT ACGACAGTAC
401 GCGCCTTGTA TCATAAAGGG AGCGATAAGG GTTTGAGAAT TTTAACTTTT
451 AAAACTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2586; ORF 753>:

m753.pep

```

1 MPITPPLNII SPKLYPNEQW NESEALGAIW WLWYQSPTHR QVPFIVEMMTY
51 ILPVLKNGQF ALFCKGTQPI GYISWAYFDE VAQAHYLESR RHLRDNSDWN
101 CGDNIWLIQW FAPLGHSHQM RSAVRQLFPS TTVRALYHKG SDKGLRILTF
151 KT*

```

a753.seq not found yet

a753.pep not found yet

g754.seq not found yet

g754.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2587>:

```
m754.seq
1  ATGATGAAGT CTATCCTCAC CGTATCCGGA AATCGTATGC GTAAACCCAG
51  AATCACCTAT TTGGATGTTT GGGCAAACGA TGAAAGAATC GGTACTTTGG
101 AAAAGGGGGC CATGTATCGG TTCGCATACG ACAATCCCAA TTCTTCGTTG
151 CTGGGCCTGC ATTATCAAGA CAGAAGCAAG GTATATATCA GCAACAATAT
201 GCCGCATATC TTTGCACAGT ATTTTCCGGA AGGCTTTTGT GATGCACACA
251 TCACAAGCAA ATATGCTTTT CATGATGCGC CTTTGAAGA CAATGAGATG
301 CTGCGCTTGG CAATTCTGTG CAGAGAGACT TTGGGTCGGA TACATGTGCG
351 CTGTAATGAC CCGCTTTTTA ATGAATGGAT TGACGGGTTG GAGATGAAAA
401 ATCCAAGAAT ATTGACTGAA CGGGATTGTC TGGGCATAAA TGCCCGACAG
451 GTTTTTCAGC AATATATGGC AGAAATCTTC CATCACGGCC GTTTCGTCAG
501 TGTATCCGGG ATACAGCAGA AGATGTCCTT AGATGCCATC CGCAGAAATA
551 CCAAGCAAAC TGCCTCATAT ATTGCCAAAG GTTTTGATGC ATCCGAATAT
601 CCTTGCTTGG CTGCCAATGA ATTTTATGTC ATGCAGACCA TCAAACAAGC
651 CGGCATTGCC GTTGCACAGA CCAGCCTGTC GGAAGATTCA TCAGTCTTAT
701 TGGTACGTCG GTTGTATGTC AGTGAACAGG GTTATTTTTT AGGGATGGAA
751 GACTTTACCA GTCTGCGCCA GTATTCGTA GAAGATAAAT ATAAAGGCAG
801 TTATGCGGCT ATTGCACAGA TTATCCGACA GATATCCGGC AGACCAGATG
851 AAGATTTAAT CCATTTCTTT AATCAGCTTG CTGCCAGTTG CATATTGAAA
901 AACGGCGATG CACACCTCAA AAATTTTCA GTACTCTATC ATGACGAATA
951 CGATGTTCGT CTGACCTG TCTATGATGT ATTGGATACA TCAATATACA
1001 GGGTTGGAAC ACAAGGAATT TTTGATGCTT ATGACGATAC GCTGGCATT
1051 AACCTGACTA ACCACGGTAA GAAACATAT CCTTCCAAGA ATACATTGTT
1101 GGATTTTGCT GAGAAATATT GCGATTGGG AAGAGAAGAT GCATCCTTTA
1151 TGATAGATAC AATCGTTCAA GCTAAAGAAC AGGTTCTTGT TAAATACTCG
1201 GATGTATTGC GTGAGAATGA ATGGTTGGCG CAGAAGTGGC ATTTTATCCC
1251 GGATGAAAAT GAAGAAGGTC TACCGTTTAC ATTCCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 2588; ORF 754>:

```
m754.pep
1  MKKSILTVSG NRMKPRITY LDVWANDERI GTLEKGAMYR FAYDNPNSSL
51  LGLHYQDRSK VYISNNMPHI FAQYFPEGFL DAHITSKYAF HDAPFEDNEM
101 LRLAILCRET LGRIHVRCND PLFNEWIDGL EMKNPRILTE RDLLGINARQ
151 VFQQYMAEIF HHGRFVSUSG IQQKMSLDAI RRNTKQTASY IAKGFDASEY
201 PCLAANEFLC MQTIKQAGIA VAQTSLSSEDS SVLLVRRFDV SEQGYFLGME
251 DFTSLRQYSV EDKYKGSYAA IAQIIRQISG RPDEDLIHFF NQLAASCILK
301 NGDAHLKNFS VLYHDEYDVR LAPVYDVLDL SIYRVGTQGI FDAYDDTLAL
351 NLTNHGKITY PSKNTLLDFA EKYCDLGRED ASFMIDTIVQ AKEQVLVKYS
401 DVLRENEWLA QKWHFIPDEN EEGLPFTFR*
```

a754.seq not found yet

a754.pep not found yet

g755.seq not found yet

g755.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2589>:

```
m755.seq..
1  ATGAGCCGTT ACCTGATTAC CTTTGATATG GATACCAACT GCCTGAAAGA
51  CAATTACCAC GGAAATAACT ATACCAATGC CTAATCCGAT ATTAACCA
101 TCTTGCTAG ACATGGATTG GAGAACATTC AGGGCAGTGT TTATCTAGGC
151 CGTGAAGGCA TCAGTGAAGC ACACGGAACA ATAGCCATTC AGGAACTGAC
201 CGCTCGGTTT GATTGGTTT ACTCCTGTAT TTCAAACATT AAGTTTTACC
251 GCCTTGAAAG TGATTTGAAC GCACAATTTA TCGCTGATGG TGTGTATCAA
301 GCCAAACAGG CTTTCCTTCA ACGTGTGAA CAACTTCGTA TATCCCTAAC
351 AGAAGCTGGA TTGTCTGATG AGCAAATCAA TCAGGTTCTG GAAAAACAGA
401 AATTGAATT GGAAAGTCCT AACCTGAAAT TAAATTAA
```

1230

This corresponds to the amino acid sequence <SEQ ID 2590; ORF 755>:

m755.pep..

```

1 MSRYLITFDM DTNCLKDNYH GNNYTNAYSD IKTILARHGF ENIQGSVYLG
51 REGISEAHGT IAIQELTARE DWFYSCISNI KFYRLESDLN AQFIADGVYQ
101 AKQAFLLQVE QLRISLTEAG LSDEQINQVL EKQKFELESP NLKLN*

```

a755.seq not found yet

a755.pep not found yet

g756.seq not found yet

g756.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2591>:

m756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 CAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGTCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2592; ORF 756>:

m756.pep

```

1 MTANFAQTLV EIQDSLVRV SVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAEQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2593>:

a756.seq

```

1 ATGACCGCCA ACTTTGCACA GACGCTGGTC GAAATACAGG ACAGTCTGTA
51 NAGGGTTGTG TCAACCGTCC AATACGGGGA TGACAACCTC AAGCGGTTGA
101 CAGCGGACAA ACGGAAGCAG TATGAGTTGA ACTTCAAGAT TTCCGAGGGT
151 TCTACGCGTG TAGAGTCCGA CTTTAAAGAG ACTTTGGTTC GGTTCGGTAG
201 AGATATGCTT CAAGATATGC CCCCTAAAAT CCGTTCGGCA ACGCTGGTAG
251 CGTTGACGAC CCTGCTTGTC GGAGGGGCGT TGGGTTACGG TTATTGGAA
301 TACCTGAAGC AGGTTGCTTC GGAAGGGTAT CAGACCGAGC GTCTGTATAA
351 TGCCGTCGAC CGTCTGTCAG AATCCCAAGA ACGGATAACG TCCGCCATCC
401 TGAAGGGTGC TAGAGGTGCC GATTTCGTGC AAATCGGCAG ACGTTCCTAC
451 AGTAGGGAGG ATATATCGGA GGCAAATAGA CGTGCAGAGC GTGTCCCGTA
501 TGGCGCAGAG TTGGTTTCAG ACGGCAATTT TACCGCTGTT TTATCTGATA
551 TAGGGGATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2594; ORF 756.a>:

a756.pep

```

1 MTANFAQTLV EIQDSLVRV SVQYGGDNL KRLTADKRKQ YELNFKISEG
51 STRVESDFKE TLVRFGRDML QDMPPKIRSA TLVALTTLV GGALGYGYLE
101 YLKQVASEGY QTERLYNAVD RLAEQERIT SAILKGARGA DFVQIGRRSY
151 SREDISEANR RAERVYPYGA LVSDGNFTAV LSDIGD*

```

m756 / a756 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
m756.pep	MTANFAQTLVEIQDSLVRVSVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
a756	MTANFAQTLVEIQDSLVRVSVQYGGDNLKRLTADKRKQYELNFKISEGSTRVESDFKE					
	10	20	30	40	50	60

1231

	70	80	90	100	110	120
m756.pep	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
a756						
	70	80	90	100	110	120
	TLVRFGRDMLQDMPPKIRSATLVALTTLLVGGALGYGYLEYLKQVASEGYQTERLYNAVD					
	130	140	150	160	170	180
m756.pep	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVFPYGAELVSDGNFTAV					
a756						
	130	140	150	160	170	180
	RLAESQERITSAILKGARGADVFQIGRRSYSREDISEANRRAERVFPYGAELVSDGNFTAV					
m756.pep	LSDIGDX					
a756	LSDIGDX					

g757.seq not found yet

g757.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2595>:

m757.seq

```

1  ATGAAATAC TCGCTTTATT AATTGCCGCT ACCTGTGCTT TATCTGCGTG
51  TGGCAGCCAA TCTGAAGAAC AACCGGCATC TGCACAACCC CAAGAGCAGG
101 CACAATCCGA ATTAATAACC ATGCCGGTAA GCTATACCGA CTATCAATCA
151 GCAGCCAATA AAGGGCTGAA TGACCAAAA ACCGGTCTGA CCCTTCCTGA
201 ACATGTTGTC CCTATCGACA ATGCCGAAGG AAAGAATCTG CTGCATGACT
251 TTTCAGACGG CCTCACAATC TTAACCGTTG ATACCGATAA AGCCGACAAA
301 ATTACTGCTG TCCGAGTAGT CTGGAATACA GATGCAATGC CTCAAAAGC
351 GGAAAACTG TCCAAAGCTG CCGCAGCCTT GATTGCGGCA ACCGCTCCGG
401 AAGACCCGAC AATGCTGCGT GATACCGCGC ACCAAATCGA AATGCGGATT
451 GACAGCCATA ATGCGCAAAA AGAGCCAACC CGAGAATGGG CGCGTGGTGG
501 GATTGCTTAT AAAGTCACTG TTACCAATTT ACCGAGCGTG GTTTTGACGG
551 CAAAAGCTGA GTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2596; ORF 757&gt;:

m757.pep (lipoprotein)

```

1  MKILALLIAA TCALSACGSQ SEEQPASAQP QEQAQSELKT MPVSYTDYQS
51  AANKGLNDQK TGLTLEHVV PIDNAEGKNL LHDFSDGLTI LTVDTDRADK
101 ITAVRVVWNT DAMPKAEKL SKAAAALIAA TAPEDRTMLR DTGQDIEMAI
151 DSHNAQKEPT REWARGGIAY KVTVTNLPVS VLTAKAE*

```

a757.seq not found yet

a757.pep not found yet

g758.seq not found yet

g758.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2597>:

m758.seq

```

1  ATGAACAATC TGACCGTGTT TACCCGTTTC GATACCGATT TGGCGACGCT
51  TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAC TGTGGAATTT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CCGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGACAGAA GGATTGAGCC
501 ATGA

```



This corresponds to the amino acid sequence <SEQ ID 2598; ORF 758>:

```
m758.pep
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2599>:

```
a758.seq
  1 ATGAACAATC TGACCGTGTT CACCCGTTTC GATACCGATT TGGCGACGCT
 51 TGCCGATGAA TTGCAATATG TGTGGGAACA CACCGCCGTT ACAGACCATC
101 AGGGCAAAT GGTGGAAATT CCCGTCTGCT ACGGCGGCGA ATACGGCCCCG
151 GATTTGGCGG AAGTCGCTGC TTTCCATCAG ACGGTTATTT CCGAAATCGT
201 CCGCCGCCAT ACGGCGCAAA CTTATACCGT ATTTATGATG GGCTTCCAGC
251 CTGGTTTCCC TTATCTGGGC GGCTTGCCCG AAGCATTGCA CACGCCCCGC
301 CGTGCCGTGC CGAGAACGTC CGTTCCTGCC GGTTCGGTCG GTATCGGCGG
351 CAGTCAGACC GGTGTGTATC CGTTCGCTTC GCCCGGCGGC TGGCAGATTA
401 TCGGCAGAAC CGAATTACCC TTGTTCCGAG CCGATTGAA TCCGCCGACC
451 CTGCTGGCGG CGGGTGACCA AGTCCGCTTT GTTGCAGAAA GGATTGAGCC
501 ATGA
```

This corresponds to the amino acid sequence <SEQ ID 2600; ORF 758.a>:

```
a758.pep..
  1 MNNLTVFTRF DTDLATLADE LQYVWEHTAV TDHQGKLVEI PVCYGGGEYGP
 51 DLAEVAAFHQ TVISEIVRRH TAQTYTVFMM GFQPGFPYLG GLPEALHTPR
101 RAVPRTSVPA GSVGIGGSQT GVYPFASPGG WQIIGRTELP LFRADLNPPPT
151 LLAAGDQVRF VAERIEP*
```

m758 / a758 100.0% identity in 167 aa overlap

	10	20	30	40	50	60
m758.pep	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
a758	MNNLTVFTRFDTDLATLADELQYVWEHTAVTDHQGKLVEIPVCYGGGEYGPDLAEVAAFHQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m758.pep	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAAGSVGIGGSQT					
a758	TVISEIVRRHTAQTYTVFMMGFQPGFPYLGGLPEALHTPRRAVPRTSVPAAGSVGIGGSQT					
	70	80	90	100	110	120
	130	140	150	160		
m758.pep	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
a758	GVYPFASPGGWQIIGRTELP LFRADLNPPPTLLAAGDQVRFVAERIEPX					
	130	140	150	160		

g759.seq not found yet

g759.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2601>:

```
m759.seq
  1 ATGCGCTTCA CACACACCAC CCCATTTTGT TCCGTATTGT CCACCCTCGG
 51 TCTTTTGGCC GTTTCCTG CTTACTCATC CATTGTCCGC AACGATGTCG
101 ATTACCAATA TTTTCGCGAC TTTGCCGAAA ATAAAGGCGC GTTACCCGTA
151 GGTGCAAGCA ATATTTCCAT CCAAGACAAG CAAGGCAAAA TATTAGGCAG
201 GGTTCTCAAC GGCATCCCCA TGCCCGACTT CCGCGTCAGC AACCGCCAAA
251 CCGCCATCGC CACCTGGTT CACCCCAAT ACGTCAACAG TGTCAAACAC
301 AACGTCGGCT ACGGTTCCAT ACAATTGCGC AACGACACCC AAAATCCAGA
351 AGAACAAGCC TATACCTACC GCCTCGTATC ACGCAACCCG CACCCGGACT
401 ACGACTACCA CCTTCCCCGC CTCACAAAC TGGTTACCGA AATCTCACCT
```

451 ACCGCACTCA GCAGCGTACC CTTGCTTGGG AACGGCCAGC CAAAGGCCAA  
501 TGCCTACCTC GATACCGACC GCTTCCCCTA CTTGTACGA CTCGGCTCAG  
551 GCACGCAACA AGTCCGCAAA GCAGACGGCA CGCGTACACG AACCGCCCCG  
601 GCATACCAAT ACCTGACCGG CGGCACGCCG CTGAAAGTAT TGGGGTTCCA  
651 AAACCACGGC TTACTCGTCG GCGGCAGCCT GACCGACCAA CCCCTTAACA  
701 CCTACGCAAT CGCGGAGAC AGCGGTCCC CCCTGTTTGC CTTGACAAG  
751 CATGAAAACC GCTGGGTGCT TCGGGCGTA CTCAGCACCT ACGCCGGCTT  
801 CGATAATTTC TTCAACAAAT ACATCGTCAC GCAACCCGAA TTCATCCGTT  
851 CCACCATCCG CCAATACGAA ACCCGGCTGG ATGTCGGGCT GACCACCAAC  
901 GAACTCATAT GCGCGACAA CGGTAATGGC AACAGCACCC TGCAAGGGCT  
951 CAACGAACGC ATCACCCTGC CCATTGCAA CCCTTCGCTT GCCCCACAAA  
1001 ACGACAGCAG GCACATGCCG TCTGAAGATG CCGGCAAAAC GTCATCCTA  
1051 TCCAGCAGGT TCGACAACAA AACACTGATG CTGGCAGACA ATATCAACCA  
1101 AGGCGCAGGC GCATTGCACT TCGACAGCAA CTTACCCGTC GTCGGTAAAA  
1151 ACCACACATG GCAAGGTGCA GCGGTATCG TAGCCGACGG CAAACGCGTC  
1201 TTCTGGCAAG TCAGCAACCC CAAAGGCGAC CGGCTCTCCA AACTGGGCGC  
1251 AGGCACGCTT ATCGCCAACG GACAAGGCAT CAACCAGGGC GACATCAGCA  
1301 TCGGGGAAGG CACTGTGCTA CTCGCCCAA AAGCTGCTTC AGACGGCAGC  
1351 AAACAAGCAT TCAACCAAGT CCGCATCACC AGCGGCAGGG GCACGGCCGT  
1401 CCTCGCCGAC AGCCAGCAAA TCAAACCCGA AAACCTCTAT TTCGGCTTCA  
1451 GGGGCGGACG GCTCGACCTC AACGGCAACA ACCTTGCCCT TACCATATC  
1501 CGCCATCGCG ACGCGGCGC GCAAATCGTC AATCAACACC CTGACCAAGC  
1551 CGCGACACTG ACGCTGACCG GCAACCCCGT CCTCAGTCCC GAGCATGTCTG  
1601 AGTGGGTGCA ATGGGGCAAC CGTCCGCAAG GCAACGCGGC GGTTTACGAA  
1651 TACATCAACC CGCACCGCAA CCGTCGGACC GACTACTTCA TACTCAAACC  
1701 CGGCGGCAAC CCGCGCAAT TTTTCCGCTT AAATATGAAA AACTCAACAA  
1751 GCTGGCAATT TATCGGCAAC AACAGGCAAC AGGCGCCGA ACAAGTCGCC  
1801 CAAGCCGAAA ATGCCCGCCC CGACCTGATT ACCTTCGGCG GATACTTGGG  
1851 TGAAAACGCG CAAACGGGCA AAGCCGCGCC GAGTTACAGC AAAACCAATG  
1901 AAGCAGCCAT AGAAAAAACC CGCCATATCG CAAATGCCGC CGTATACGGC  
1951 CGGCCCGAAT ACCGTTACAA CGGCGCACTC AACCTGCACT ATCGTCCCAA  
2001 ACGCACCGAC AGCAGCTGT TGCTCAACGG CGGCATGAAC CTTAACGGGG  
2051 AAGTCTTGAT TGAGGGCGGC AATATGATTG TGTCAGGCAG GCCCGTACCC  
2101 CATGCTACG ACCACCAGGC CAAACGCGAA CCCGTTCTTG AAAACGAATG  
2151 GACCGACGGC AGCTTCAAGG CTGCACGGT CACCCTGCGA AACCATGCCC  
2201 GACTGACGGC AGGGCGCAAT ACCGCGCATC TGGACGGCGA CATAACCGCA  
2251 TACGATCTGT CCGGCATCGA CCTCGGCTT ACCCAAGGCA AAACACCGGA  
2301 ATGCTACCGC TCCTACCATA GCGGCAGCAC CCACTGCACA CCCAACGCGC  
2351 TTTTAAAAGC CGAAAACAT CAGTCACTAC CTGCAACGCA AGTACGCGGC  
2401 GACATTACCC TTAACGACCG TTCAGAGCTC CGCCTGGGCA AAGCACACCT  
2451 GTACGGCAGC ATCCGTGCCG GCAAAGACAC CGCAGTCCGC ATGGAAGCAG  
2501 ACAGCAACTG GACACTTTC CAGTCCAGCC ACACCGGCGC ACTGACGCTT  
2551 GACGGCGCAC AAATTACCCT GAACCCCGAT TTCGCCAATA ATACACACAA  
2601 CAACCGCTTC AACACACTGA CCGTCAACGG CACACTTGAC GGGTTTCGGA  
2651 CATTCCGATT CCTGACCGGC ATCGTCCGAA AACAAAATGC CCCCCCCTC  
2701 AAAGTGAAG GGGACAGCCG CGGCGCATTC CAAATCCAGC TCAAAAACAC  
2751 CCGACAAGAA CCTCAAACAA CCGAATCGCT TGCATTGTG AGCCTCAATC  
2801 CGAAACACAG CCACCAAGCC CGATTACCC TCCAAAACGG CTATGCCGAT  
2851 TTGGGTGCCT ACCGCTACAT CCTCCGCAA AACAAACAG GATACAGCCT  
2901 GTACAACCCG CTCAAAGAGG CCGAACTTCA AATTGAAGCC ACGCGTGCGG  
2951 AACATGAGCG CAACCAACAG GCATACAACC AATTACAGGC AACCGACATC  
3001 AGCAGACAGG TTCAACATGA CTCTGACGCG ACCAGGCAGG CACTACAGGC  
3051 CTGGCAGAAC AGTCAAACCG AACTTGCCCG CATCGACAGC CAAGTCCAAT  
3101 ATCTGTCCGC CCAATTGAAA CAGACAGACC CGCTGACCGG CATTCTGACG  
3151 CGTGCCCAA ACCTGTGTGC CGCACAAGGA TACAGTGCCG ATATCTGCCG  
3201 TCAGGTTGCC AAAGCCGCCG ACACGAACGA CCTGACACTC TTCGAAACCG  
3251 AACTGGATAC GTATATAGAA CGTGTAGAAA TGGCCGAATC CGAACTTGAC  
3301 AAAGCACGGC AAGGCGGCGA TGGCAAGGCC GTCGAAACAG CCGGCGACGC  
3351 CTACCTGAAC GCACTCAACC GTCTGTCCCG ACAAATCCAC AGTTTGAAAA  
3401 CCGGCGTTGC CGGCATCCGT ATGCCGAACC TGGCCGAATC GATCAGCCGG  
3451 TCGGCCAACA CCGCGTTTC CGAACAGGCC GCCTACAATA CCGGCGGCGA  
3501 ACAGGCGGGA CGCCGATCG ACCGCCACCT TACCGATCCG CAGCAGCAAA  
3551 ACATCTGGCT GGAAACCGGT ACGCAACAAA CCGACTACCA TAGCGGCACA  
3601 CACCGTCCCT ACCAACAAC TACCAACTAT GCACATATCG GCATCCAAC  
3651 CGGCATCACC GACCGTCTCA GTGTCGGTAC GATTTTAACC GATGAGCGCA  
3701 CAAACAACCG TTTTGATGAA GCGTATCCG CCCGAAACCG CAGCAACGGC

1234

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3751 GCACATCTGT TCGTCAAAGG GGAAACGGC GCACTCTTTG CCGCGGCAGA
3801 TTTAGGCTAC AGCAACAGCC GTACCCGATT TACCGATTAT GACGGGGCTG
3851 CCGTCCGCCG CCACGCATGG GATGCAGGCA TCAACACCGG CATCAAATC
3901 GATACCGGCA TCAACCTCAG ACCCTATGCC GGCATCCGTA TAAACCGCAG
3951 CAACGGCAAC CGGTACGTAC TCGACGGCGC AGAGATAAAC AGCCCGGCGC
4001 AAATCCAAAC CACATGGCAT GCCGGCATCC GTCTCGATAA AACCGTCGAA
4051 CTGGGTCAAG CCAAGCTGAC CCCCCTTC AGCAGCGATT ACTACCATAC
4101 CCGCCAAAAC AGCGGTTCG CCCTCAGCGT CAACGACCGT ACCTTACTGC
4151 AGCAAGCCGC CCACGGCACA CTGCATACCC TGCAAATCGA CGCCGGATAC
4201 AAAGGCTGGA ACGCCAACT TCATGCCGCT TACGGCAAAG ACAGCAACAC
4251 CGCCCGCCAC AAACAGGCAG GAATCAAAT AGGCTACAAC TGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2602; ORF 759>:

m759.pep

```

1 MRFTHTTFFC SVLSTLGLFA VSPAYSSIVR NDVDYQYFRD FAENKGAFTV
51 GASNISIQDK QGKILGRVLN GIPMPDFRVS NRQTAIATLV HPQYVNSVKH
101 NVGYGSIQFG NDTQNPEEQ A YTYRLVSRNP HPDYDYHLPR LNKLVTEISP
151 TALSSVPLLG NGQPKANAYL DTDFFPYFVR LSGGTQQVRK ADGTRTRTAP
201 AYQYLTGGTP LKVLGFQNHG LLVGGSLTDQ PLNTYAIAGD SGSPLEAFDK
251 HENRWLAGV LSTYAGFDNF FNKYIVTQPE FIRSTIROYE TRLDVGLTTN
301 ELIWRDNGNG NSTLQGLNER ITLPIANPSL APQNSDRHMP SEDAGKTLL
351 SSRFDNKTLM LADNINQAG ALQFDSNFTV VGKNHTWQGA GVIVADGKRV
401 FWQVSNPKGD RLSKLGAATL IANGQGINQG DISIGEGTVV LAQKAASDGS
451 KQAFNQVGIT SGRGTAVLAD SQQIKPENLY FGFRGRLDL NGNNLAFTHI
501 RHADGGAQIV NHPDQAATL TLTGNPVLSP EHVEWVQWGN RPQGNAAVYE
551 YINPHRNRT DYFILKPGGN PREFFPLNMK NSTSWQFIGN NRQQAEEQVA
601 QAENARPDLI TFGGYLGENA QTGKAAPSYS KTNEAAIEKT RHIANAAVYG
651 RPEYRYNGAL NLHYRPKRTD STLLNGGMN LGEVLEGG NMIVSGRPVP
701 HAYDHQAKRE PVLENWTDG SFKAARFTLR NHARLTAGRN TAHLDGDTA
751 YDLSGIDLGF TQKKTPECYR SYHSGSTHCT PNAVLKAENY RALPATQVRG
801 DITLNDREL RLGAHLYGS IRAGKDTAVR MEADSNWTL SSSHTGALT
851 DGAQITLNP FANNTNNRF NTLTVNGTLD GFGTFRELTG IVRKQNAAPL
901 KLEGDSRGAF QHVKNTGQE PQTTESLALV SLNPKHSHQA RFTLQNGYAD
951 LGAYRYILRK NNGYSLYNP LKEAELQIEA TRAEHERNQO AYNQLQATDI
1001 SRQVQHSDA TRQALQAWQN SQTELARIDS QVQYLSAQLK QTDPLTGILT
1051 RAQNLCAAQG YSADICRQVA KAADTNDLTL FETELDTYIE RVEMAESELD
1101 KARQGGDAQA VETARHAYLN ALNRLSRQIH SLKTGVAGIR MPNLAEISR
1151 SANTAVSEQA AYNTGRQQAG RRIDRHLTDP QQQNIWLETG TQTDYHSGT
1201 HRPYQQTNY AHIGIQTGIT DRLSVGTILT DERTNNRFE GVSARNRNG
1251 AHLFVKGENG ALFAAADLGY SNSRTRFTDY DGAAVRRHAW DAGINTGIKI
1301 DTGINLRPYA GIRINRNGN RYVLDGAEIN SPAQIQTTWH AGIRLDKTVE
1351 LGQAKLTAF SSYYHTRQN SGSALSVNDR TLLQQAAGHT LHTLQIDAGY
1401 KGWNAKLHAA YGKDSNTARH KQAGIKIGYN W*

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2603>:

g760.seq (partial)

```

1 AACAACCGCA ACACCCGTTA CGCCGCATTG GGCAAACGCG TGATGGAAGG
51 CGTTGAGACC GAAATCAGCG GTGCGATTAC ACCGAAATGG CAAATCCATG
101 CAGGTTACAG CTATCTGCAC AGCCAAATCA AAACCGCCGC CAATCCACGC
151 GACGACGGCA TCTTCCTGCT GGTGCCCAA CACAGCGCAA ACCTGTGGAC
201 GACTTACCAA GTTACGCCCC GGCTGACCGT CGGCGGCGGC GTGAACGCGA
251 TGAGCGGCAT TACTTCATCT GCAGGGATGC ATGCAGGCGG TTATGCCACG
301 TTCGATGCGA TGGCGGCATA CCGCTTCACG CCAAGCTGA AGCTGCAAAT
351 CAATGCCGAC AACATCTTCA ACCGCCATTA CTACGCCCGC GTCGGCGGCA
401 CGAACACCTT TAACATTCCT GGTTCGGAGC GCAGCCTGAC GGCAAACCTG
451 CGTTACAGTT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 2604; ORF 760.ng>:

g760.pep (partial)

```

1 NNRNTRYAAL GKRVMGVEV EISGAITPKW QIHAGYSYLH SIKTAANPR
51 DDGIFLLVPK HSANLWTTYQ VTPGLTVGGG VNAMSGITSS AGMHAGGYAT
101 FDAMAAYRFT PKLKLQINAD NIFNRHYAR VGGTNTFNIP GSERSLTANL
151 RYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2605>:

m760.seq

```

1 ATGGGACAGT TTATGTCAGT TTTCCGCATC AATATGACCG CCGCCACGGT
51 TTTGGCAGCA CTCTCGTCTT CGGTTTTTGC CGCACAAACG GAAGGTTTGG
101 AAACCGTCCA TATTAAGGGT CAGCGTTCTT ACAACGCGAT TGCCACCGAG
151 AAAAACGGCG ATTACAGCTC GTTTGCCGCC ACCGTCGGTA CAAAAATCCC
201 CGCTTCTTTG CGCGAAATTC CGCAATCCGT CAGCATCATT ACCAACCAGC
251 AGGTCAAAGA CCGCAATGTT GATACGTTTG ACCAGTTGGC ACGCAAAACG
301 CCGGCCTTGC GCGTGTGAG CAACGACGAC GGACGCTCTT CGGTTTACGC
351 GCGCGGTTAC GAATACAGCG AATACAACAT CGACGCGCTG CCGCGCAGA
401 TGCAGAGTAT CAACGGCAGC CTGCCCAACC TGTTCCGCTT CGACCGCGTG
451 GAAGTGATGC GCGGGCCGAG CGGACTGTTT GACAGCAGCG GCGAGATGGG
501 CGGCATCGTG AATCTGGTGC GCAAACGCCC GACCAAAGCG TTCCAAGGTC
551 ATGCGGCGGC AGGGTTCGGT ACGCACAAAC AATATAAAGC CGAGGCGGAC
601 GTATCGGGCA GCCTCAATTC AGACGGCAGC GTGCGCGGCC GCGTGATGGC
651 GCAGACCGTC GCGCGCTCTC CGCGTCCCGC CGAGAAAAAC AACCGGCGCG
701 AAACCTTCTA CGCGGCGGCG GATTGGGACA TCAACCCCGA TACGGTTTTG
751 GCGCGGGGCT ATCTTTACCA GCAACGCCGC CTCGCGCCGT ACAACGGCTT
801 GCCTGCCGAT GCCAATAACA AATTACCGTC CCTGCCGCAA CACGTATTTG
851 TCGGCGCGGA TTGGAACAAA TTAAAAATGC ACAGCCACGA CGTGTTCCGC
901 GATTTGAAAC ATTACTTCGG CAACGGCGGC TACGGCAAAG TCGGTATGCG
951 CTATTCGGAT CGGAAAGCCG ATTCCAATTA TACGTTTGCG GGCAGCAAAAC
1001 TCAACAATAC CGGACAAGCC GACGTAGCGG GTTTGGGTAC GGACATTAAA
1051 CAAAAGCCTT TTGCGGTTGA CGCAAGTTAC AGCCGTCGCT TTGCCTTGGG
1101 CAACACCGCC AACGAATTTG TGATTGGTGC AGACTACAAC CGCTTGCGCA
1151 GTACTAATGA ACAAGGGCGT TCGACTTTGT CAAAAGCGT CGCTTTAGAT
1201 GGTTCGCGG CTTTGCCTTA TAACGGCATA CTTCAGAACG CCCGCGCCGG
1251 AAACAAAGGT TTCAATCACT CCGTTACCGA AGAAAACCTC GACGAAACCG
1301 GTTTGTATGC CAAGACGGTG TTCCGTCCTC TGGAAAGGTT GTCGTTGATT
1351 GCAGGCGGAC GTGTAGGACA TCACAAAATC GAGTCGGGCG ACGGCAAAAC
1401 CCTGCATAAA GCTTCGAAAA CCAAATTTAC AAGCTACGCC GCGCGGTTT
1451 ACGATATAGA CGGCAGCAAC AGCCTGTACG CTTCCGCTC CCAACTCTAC
1501 ACACCGCAAA CCAGCATCGG CACCGACGGC AAGCTGCTCA AACCGCGCGA
1551 AGGCAACCAG TTTGAAATCG GCTACAAAGG CAGCTACATG GACGACCGCC
1601 TCAATACCGG GGTTCGTTT TACCGCATGA AGGATAAAAA CGCCGCCGCA
1651 CCGCTGGACT CAAACAACAA AAAAACCCTG TACGCCGCTT TGGGCAAAACG
1701 CGTGATGGAA GGTGTTGAGA CCGAAATCAG CGGCGCGATG ACACCGAAAT
1751 GGCAATCCA TGCAAGTTAC AGCTACCTGC ACAGCCAAAT CAAAACCGCC
1801 TCCAATTCGC GCGACGAAGG CATCTTCTCG CTGATGCCCA AACACAGCGC
1851 AAACCTGTGG ACGACTTACC AAGTTACGTC CGGGCTGACC ATCGGCGGCG
1901 GCGTGAACGC GATGAGCGGC ATTACTTCAT CTGCAGGGAT ACATGCAAGC
1951 GGTATGCCA CGTTCGATGC GATGGCGGCA TACCGCTTCA CGCCCAAAC
2001 GAAGCTGCAA ATCAACGCGC ACAACATCTT CAACCGCCAT TACTACGCC
2051 GCGTCGGCAG CGAGAGCACC TTTAACATTC CCGGTTCCGA GCGCAGCCTG
2101 ACGGCAAAAC TCGTTACAG TTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2606; ORF 760>:

m760.pep

```

1 MGQFMSVFRI NMTAATVLAA LSSSVFAAQT EGLETVHIKG QRSYNAIATE
51 KNGDYSSFAA TVGTKIPASL REIPQSVSII TNQVKDRNV DTFDQLARKT
101 PGLRVLSNDD GRSSVYARGY EYSEYNIDGL PAQMQSINGT LPNLFADFDRV
151 EVMRGPSGLF DSSGEMGGIV NLVRKRPTKA FQGHAAAGFG THKQYKAED
201 VSGSLNSDGS VRGRVMAQTV GASPRPAEKN NRRETFYAAA DWDINPDTVL
251 GAGYLYQRRR LAPYNGLPAD ANNKLPSLPQ HVFVGADWNK FRMHSADVFA
301 DLKHYFGNGG YGKVGMRYSR RKADSNTYFA GSKLNNTGQA DVAGLGTDIK
351 QKAFVADASY SRPFALGNTA NEFVIGADYN RLRSTNEQGR STLKSKVALD
401 GFRALPYNGI LQNRAGNKG FNHSVTEENL DETGLYAKTV FRPLEGLSLI
451 AGGRVGHKKI ESGDGKTLHK ASKTFTSYA GAVYDIDGSN SLYASASQLY
501 TPQTSIGTDG KLLKPREGNQ FEIGYKGSYM DDRLNTRVSF YRMKDKNAAA
551 PLDSNNKKTR YAALGKRVME GVETEISGAM TPKWQIHAGY SYLHSQIKTA
601 SNSRDEGIFL LMPKHSANLW TTYQVTSGLT IGGGVNAMSG ITSSAGIHAG
651 GYATFDAMAA YRFTPKLKLQ INADNIFNRH YYARVGSEST FNIPGSESL
701 TANLRYSF*

```

1236

m760 / g760 91.6% identity in 154 aa overlap

	530	540	550	560	570	580
m760 . pep	YKGSYMDRLNTRVSFYRMKDKNAAAPLDSNNKKTRYAALGKRVMEGVETEISGAMTPKW					
				:		
g760				NNRNTRYAALGKRVMEGVETEISGAITPKW		
				10	20	30
	590	600	610	620	630	640
m760 . pep	QIHAGYSYLHSQIKTASNSRDEGIFLLMPKHSANLWTTYQVTSGLTIGGGVNAMSGITSS					
g760	QIHAGYSYLHSQIKTAAANPRDDGIFLLVPKHSANLWTTYQVTPGLTVGGGVNAMSGITSS					
	40	50	60	70	80	90
	650	660	670	680	690	700
m760 . pep	AGIHAGGYATFDAMAAAYRFTPCLKLQINADNIFNRHYARVGSESTFNIPGSESLTANL					
g760	AGMHAGGYATFDAMAAAYRFTPCLKLQINADNIFNRHYARVGSTNTFNIPGSESLTANL					
	100	110	120	130	140	150
	709					
m760 . pep	RYSEFX					
g760	RYSEFX					

g761 . seq not found yet

g761 . pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2607>:

m761 . seq

1	ATGAAAATAT	CATTTCATTT	AGCTTTATTA	CCCACGCTGA	TTATTGCTTC
51	CTTCCCTGTT	GCTGCCGCCG	ATACGCAGGA	CAATGGTGAA	CATTACACCG
101	CCACTCTGCC	CACCGTTTCC	GTGGTCGGAC	AGTCOGACAC	CAGCGTACTC
151	AAAGGCTACA	TCACTACGA	CGAAGCCGCC	GTTACCCGCA	ACGGACAGCT
201	CATCAAAGAA	ACGCCGCAAA	CCATCGATAC	GCTCAATATC	CAGAAAAACA
251	AAAATTACGG	TACGAACGAT	TTGAGTTCCA	TCCTCGAAGG	CAATGCCGGC
301	ATCGACGCTG	CCTACGATAT	GCGCGGTGAA	AGCATTITTC	TGCGCGGTTT
351	TCAAGCCGAC	GCATCCGATA	TTTACCGCGA	CGCGGTGCCG	GAAAGCGGAC
401	AAGTGCGCCG	CAGTACTGCC	AACATCGAGC	GCGTGGAAT	CCTGAAAGGC
451	CCGTCTTCCG	TGCTTTACGG	CCGCACCAAC	GGCGGCGGCG	TCATCAACAT
501	GGTCAGCAAA	TACGCCAACT	TCAAACAAAG	CCGCAACATC	GGAGCGGTTT
551	ACGGCTCATG	GGCAAACCGC	AGCCTGAATA	TGGACATTAA	CGAAGTGCTG
601	AACAAAACG	TCGCCATCCG	TCTCACCAGC	GAAGTCGGGC	GCGCCAATTC
651	GTTCGCGAGC	GGCATAGACA	GCAAAAATGT	CATGGTTTCG	CCCAGCATT
701	CCGTCAAAC	CGACAACGGC	TTGAAGTGGA	CGGGGCAATA	CACCTACGAC
751	AATGTGGAGC	GCACGCCCGA	CCGCAGTCCG	ACCAAGTCCG	TGTACGACCG
801	CTTCGGAATG	CCTTACCGCA	TGGGGTTCCG	CCACCGGAAC	GATTTTGTCA
851	AAGACAAGCT	GCAAGTTTGG	CGTTCCGACC	TTGAATACGC	CTTCAACGAC
901	AAATGGCGTG	CCCAATGGCA	GCTCGCCAC	CGCACGGCGG	CGCAGGATTT
951	TGATCATTTT	TATGCAGGCA	GCGAAAATGG	CAACTTAATC	AAACGTAACT
1001	ACGCCTGGCA	GCAGACCGAC	AACAAAACCC	TGTCGTCCAA	CTTAACGCTC
1051	AACGGCGACT	ACACCATCGG	CCGTTTGTAA	AACCACCTGA	CCGTAGGCAT
1101	GGATTACAGC	CGCGAACACC	GCAACCCGAC	ATTGGGTTTC	AGCAGCGCCT
1151	TTTCCGCCTC	CATCAACCCC	TACGACCGCG	CAAGCTGGCC	GGCTTCGGGC
1201	AGATTGCAGC	CTATTCTGAC	CCAAAACCGC	CACAAAGCCG	ACTCCTACGG
1251	CATCTTTGTG	CAAAACATCT	TCTCCGCCAC	GCCCCGATTG	AAATTCGTCC
1301	TCGGCGGCCG	TTACGACAAA	TACACCTTTA	ATTCCGAAAA	CAAACTCACC
1351	GGCAGCAGCC	GCCAATACAG	CGGACACTCG	TTCAGCCCCA	ACATCGGCGC
1401	AGTGTGGAAC	ATCAATCCCG	TCCACACACT	TTACGCCTCG	TATAACAAAG
1451	GCTTCGCGCC	TTATGGCGGA	CGCGGCGGCT	ATTTGAGCAT	CGATACGTTG
1501	TCTTCCGCCG	TGTTCAACGC	CGACCCCGAG	TACACCCGCC	AATACGAAAC
1551	CGGCGTGAAA	AGCAGTTGGC	TGGACGACCG	CCTCAGCACT	ACGTTGTCTG
1601	CCTACCAAAT	CGAACGCTTC	AATATCCGCT	ACCGCCCCGA	TCCAAAAAAC
1651	AACCCCTATA	TTTATGCGGT	TAGCGGCAAA	CACCGTTCGC	GCGGCGTGGA

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1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT
1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAATACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACAACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 TGTTAACGTT ACCTTTGCCG CAGCCAATCT GCTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2608; ORF 761>:

```

m7 61 . pep
1 MKISFHLALL PTLIIASFV AAADTODNGE HYTATLPTVS VVGQSDTSVL
51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GAVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNMVVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDRFL PYRMGFAHRN DFKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAWQQT D NKTLSNLT
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSAFSASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KFLVLGGRYDK YTFNSENKLT
451 SSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 GSAVENADPE YTROQYETGVK SSWLDDRLST TLSAYQIERF NIRYRPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGLGVMQA KVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YNSRNKEVTT
651 LPGFARVDAM LGWNHKNVNV TFAAANLLNQ KYWRSDSMPG NPRGYTARVN
701 YRF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2609>:

```

a7 61 . seq
1 ATGAAAATAT CATTTTATTT AGCTTTATTA CCCACGCTGA TTATTGCTTC
51 CTTCCTGTGTT GCTGCCGCCG ATACGCAGGA CAATGGTGAA CATTACACCG
101 CCACTCTGCC CACCGTTTCC GTGGTCGGAC AGTCCGACAC CAGCGTACTC
151 AAAGGCTACA TCAACTACGA CGAAGCCGCC GTTACCCGCA ACGGACAGCT
201 CATCAAAGAA ACGCCGCAAA CCATCGATAC GCTCAATATC CAGAAAAACA
251 AAAATTACGG CACGAACGAT TTGAGTTCCA TCCTCGAAGG CAATGCCGGC
301 ATCGACGCCG CCTACGATAT GCGCGCGCAA AGCATTITTC TCGCGGGCTT
351 TCAAGCCGAC GCATCTGATA TTTACCGCGA CGGCGTACGC GAAAGCGGGC
401 AGGTGCGCCG TAGCACCGCC AACATCGAGC GCGTGGAAT CCTGAAAGGT
451 CCGTCCTCCG TGCTTTATGG GCGTACCAAC GCGCGCGGTG TCATCAACAT
501 GGTCAGCAAA TACGCCAACT TCAAACAAAG CCGTAATATC GGTACGGTTT
551 ATGGTTCGTG GGCACACCGC AGCCTGAATA TGGACATCAA CGAAGTGCTG
601 AACAAAAACG TCGCCATCCG TCTCACCAGC GAAGTCGGGC GCGCCAATTC
651 GTTCCGCAGC GGCATAGACA GCAAAAATGT CATGGTTTCG CCCAGCATTA
701 CCGTCAAACG CGACAACGGC TTGAAGTGA CGGGGCAATA CACCTACGAC
751 AATGTGGAGC GCACGCCCGA CCGCAGTCCG ACCAAGTCCG TGTACGACCG
801 CTTCGGACTG CCTTACCGCA TGGGGTTCGC CCACCGGAAC GATTTTGTCA
851 AAGACAAGCT GCAAGTTTGG CGTCCGACC TTGAATACGC CTTCAACGAC
901 AAATGGCGTG CCAATGGCA GCTCGCCAC CGCAGGCGG CGCAGGATT
951 TGATCATTTT TATGCAGGCA GCGAAAATGG CAACTTAATC AAACGTAAC
1001 ACGCCTGGCA GCAGACCGAC AACAAAACCC TGTCTGCTCA CTTAACGCTC
1051 AACGGCGACT ACACCATCGG CCGTTTTGAA AACCACCTGA CCGTAGGCAT
1101 GGATTACAGC CGCGAACACC GCAACCCGAC ATTGGGTTTC AGCAGCGCCT
1151 TTTCCGCCTC CATCAACCCC TACGACCGCG CAAGCTGGCC GGCTTCGGGC
1201 AGATTGCAGC CTATTCTGAC CCAAAACCGC CACAAAGCCG ACTCCTACCG
1251 CATCTTTGTG CAAAACATCT TCTCCGCCAC GCGCGATTTC AAATTCGTCC
1301 TCGGCGGCCG TTACGACAAA TACACCTTA ATTCCGAAAA CAAACTCACC
1351 GGCAGCAGCC GCCAATACAG CGGACACTCG TTCAGCCCCA ACATCGGCGC
1401 AGTGTGGAAC ATCAATCCG TCCACACACT TTACGCCTCG TATAACAAG
1451 GCTTCGCGCC TTATGCGGGA CGCGGCGGCT ATTGAGCAT CGATACGTTG
1501 TCTTCGCGCC TGTTCACGCG GACCCCGAG TACACCGGCC AATACGAAAC
1551 CCGCGTGAAA AGCAGTTGGC TGGACGACCG CCTCAGCACT ACGTTGTCTG
1601 CCTACCAAAT CGAACGCTTC AATATCCGCT ACCGCCCCGA TCCAAAAAAC
1651 AACCTTATA TTTATGCGGT TAGCGGCAAA CACCGTTCGC GCGGCGTGGA
1701 ATTGTCCGCC ATCGGGCAAA TCATCCCCAA AAAACTCTAT CTGCGCGGTT

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1238

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1751 CGTTGGGCGT GATGCAGGCG AAAGTCGTTG AAGACAAAGA AAATCCCGAC
1801 CGAGTGGGCA TCCATTTGAA TAACACCAGC AACGTTACCG GCAACCTGTT
1851 TTTCCGTTAT ACCCCGACCG AAAACCTCTA CGGCGAAATC GGCCTAACCG
1901 GTACAGGCAA ACGCTACGGT TACGACTCAA GAAATAAAGA AGTGACTACG
1951 CTTCCAGGCT TTGCCCCGAGT TGATGCCATG CTTGGCTGGA ACCATAAAAA
2001 GTTTAACGTT ACCTTTGCCG CAGCCAATCT GTTCAATCAA AAATATTGGC
2051 GTTCGGACTC TATGCCGGGT AATCCGCGCG GCTATACTGC CCGGGTAAAT
2101 TACCGTTTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2610; ORF 761.a>:

```

a761.pep
  1 MKISFHLALL PTLIIASFPV AAADTQDNGE HYTATLPTVS VVGQSDTSVL
 51 KGYINYDEAA VTRNGQLIKE TPQTIDTLNI QKNKNYGTND LSSILEGNAG
101 IDAAYDMRGE SIFLRGFQAD ASDIYRDGVR ESGQVRRSTA NIERVEILKG
151 PSSVLYGRTN GGGVINMVSK YANFKQSRNI GTVYGSWANR SLNMDINEVL
201 NKNVAIRLTG EVGRANSFRS GIDSKNVMVS PSITVKLDNG LKWTGQYTYD
251 NVERTPDRSP TKSVDYDFGL PYRMGFAHRN DFVKDKLQVW RSDLEYAFND
301 KWRAQWQLAH RTAAQDFDHF YAGSENGNLI KRNYAQQTND NKTLSNLTLL
351 NGDYTIGRFE NHLTVGMDYS REHRNPTLGF SSASFASINP YDRASWPASG
401 RLQPILTQNR HKADSYGIFV QNIFSATPDL KEVLGGRYDK YTFNSENKLT
451 GSSRQYSGHS FSPNIGAVWN INPVHTLYAS YNKGFPYGG RGGYLSIDTL
501 SSAVFNDPE YTRQYETGVK SSWLDDRLST TLSAYQIERF NIYRYPDPKN
551 NPYIYAVSGK HRSRGVELSA IGQIIPKKLY LRGS LGVMA QVVEDKENPD
601 RVGIHLNNTS NVTGNLFFRY TPTENLYGEI GVTGTGKRYG YDSRNKEVTT
651 LPGAARVDAM LGWNHKNVNV TFAANLENQ KYWRSDSMPG NPGYATARNV
701 YRF*

```

m761 / a761 99.6% identity in 703 aa overlap

	10	20	30	40	50	60
m761.pep	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
a761	MKISFHLALLPTLIIASFPVAAADTQDNGEHYTATLPTVSVVGQSDTSVLKGYINYDEAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m761.pep	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
a761	VTRNGQLIKETPQTIDTLNIQKNKNYGTNDLSSILEGNAGIDAAYDMRGESIFLRGFQAD					
	70	80	90	100	110	120
	130	140	150	160	170	180
m761.pep	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
a761	ASDIYRDGVRESGQVRRSTANIERVEILKGPSSVLYGRNNGGGVINMVSKYANFKQSRNI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m761.pep	GAVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
a761	GTVYGSWANRSLNMDINEVLNKNVAIRLTGEVGRANSFRSGIDSKNVMVSPSITVKLDNG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m761.pep	LKWTGQYTYDNVERTPDRSPKSVYDFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
a761	LKWTGQYTYDNVERTPDRSPKSVYDFGLPYRMGFAHRNDFVKDKLQVWRSLEYAFND					
	250	260	270	280	290	300
	310	320	330	340	350	360
m761.pep	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDNKTLSNLTNGDYTIGRFE					
a761	KWRAQWQLAHRTAAQDFDHFYAGSENGNLIKRNIAWQQTNDNKTLSNLTNGDYTIGRFE					
	310	320	330	340	350	360
	370	380	390	400	410	420

1239

```

m761.pep  NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
a761       NHLTVGMDYSREHRNPTLGFSSAFSASINPYDRASWPASGRLQPILTQNRHKADSYGIFV
           370      380      390      400      410      420

           430      440      450      460      470      480
m761.pep  QNIFSATPDLKFVLGGRYDKYTFENSENKLGTSSRQYSGHSFSPNIGAVWNINPVHTLYAS
a761       QNIFSATPDLKFVLGGRYDKYTFENSENKLGTSSRQYSGHSFSPNIGAVWNINPVHTLYAS
           430      440      450      460      470      480

           490      500      510      520      530      540
m761.pep  YNKGFPAPYGGRGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTLSAYQIERF
a761       YNKGFPAPYGGRGYLSIDTLSSAVFNADPEYTRQYETGVKSSWLDRLSTTLSAYQIERF
           490      500      510      520      530      540

           550      560      570      580      590      600
m761.pep  NIRYRPDPKNNPIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
a761       NIRYRPDPKNNPIYAVSGKHRSRGVELSAIGQIIPKKLYLRGSLGVMQAKVVEDKENPD
           550      560      570      580      590      600

           610      620      630      640      650      660
m761.pep  RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYSRNKEVTTLPGFARVDAM
a761       RVGIHLNNTSNVTGNLFFRYTPTENLYGEIGVTGTGKRYGYDSRNKEVTTLPGFARVDAM
           610      620      630      640      650      660

           670      680      690      700
m761.pep  LGWNHKNVNVTFAAANLLNQKYWRSDSMFGNPRGYTARVNYRFX
a761       LGWNHKNVNVTFAAANLFNQKYWRSDSMFGNPRGYTARVNYRFX
           670      680      690      700

```

g762.seq Not yet found

g762.pep Not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2611>:

```

m762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT
301 AGTTTATGGA ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA
351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTCTT
401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2612; ORF 762>:

```

m762.pep
1  MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT
51  LELLFIENFV TKSIMAIY PLYFFTIKK YYPYSRKVII LLSLALSIYF
101 SFMDFYFFSI YSDNLSYTE PLHLYIPIII NFFSLLVSNE ILSFINK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2613>:

```

a762.seq
1  ATGAAGTGGT TATTAAATAT GATAATGAGA CCTATTAAAT TTAGTATGGT
51  AAATACGTTA TTATTTATTG TTATATGTAG TTCATTTTTT GATCTGCTCG
101 TTCAATTATG TACAATTTTA TTTCATAGCC AAAAAATATA CTTTATTACA
151 TTATTTTAT TATTTATTTT TAATTTTGTT ACAAATCTA TCTATATGGC
201 AATTATTTAT CCTATTTTAT ATTTTITTTAC GATAAAAAAA TATTATCCTT
251 ACTCTAGGAA AGTGATAATT CTATTATCAT TAGCATTATC TATATATTTT

```



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301 AGTTTTATGG ACTTTTACTT TTTTCCATA TATTCAGATA ACCTTAGCTA  
 351 TGAAACGGAG CCTTTACATT TATACATCCC TATTATTATT AATTTTTTCT  
 401 CACTTTTAGT TTCTAATTTT ATTTTATCTT TTATCAACAA GTAA

This corresponds to the amino acid sequence <SEQ ID 2614; ORF 762.a>:

**a762 . pep**

1 MKWLLNMIMR PIKFSMVNTL LFIVICSSFF DLLVQLCTIL FHSQKIYFIT  
 51 LELLFIFNEV TKSIYMAIIY PILYFTIKK YYPYSRKVII LLSLALSIYF  
 101 SFMDFYFFSI YSDNLSYETE PLHLYIPIII NFFSLLVSNF ILSFINK\*

m762 / a762 100.0% identity in 147 aa overlap

	10	20	30	40	50	60
m762 . pep	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLELLFIFNEV					
a762	MKWLLNMIMRPIKFSMVNTLLFIVICSSFFDLLVQLCTILFHSQKIYFITLELLFIFNEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m762 . pep	TKSIYMAIIYPILYFTIKKYPYSRKVIIILSLALSIYFSFMDYFFFSIYSDNLSYETE					
a762	TKSIYMAIIYPILYFTIKKYPYSRKVIIILSLALSIYFSFMDYFFFSIYSDNLSYETE					
	70	80	90	100	110	120
	130	140				
m762 . pep	PLHLYIPIIIINFFSLLVSNFILSFINKX					
a762	PLHLYIPIIIINFFSLLVSNFILSFINKX					
	130	140				

g763 . seq not yet found

g763 . pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2615>:

**m763 . seq**

1 ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGGTA TTTCCGTTTG  
 51 CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT  
 101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA  
 151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCGTGAAG CATGGCGGGC  
 201 GGCGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG  
 251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCTT TCCCCATGTA  
 301 TCCGCCAATG CCAGCTACCA GCGCCAGCCG CCATCGATTT CTTCCACCCG  
 351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAACCTTA TTTGACGCTG  
 401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA  
 451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG  
 501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGGCGG  
 551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT  
 601 AAAGGTGCTG CCACCGCGCT GGATATTCAC GAAGCCAAAG CCGGTTACGA  
 651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG  
 701 AAAACCAAGT GAACGACTAC ACCGACCTGG ATAGCAAACA AATCGAGGCC  
 751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCCAAGC TGGAACGTTA  
 801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC  
 851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA  
 901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTGCGCT ATCAGAATAA  
 951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG  
 1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA  
 1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CCGCCGAAGC  
 1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCCGTA CGCCAGGCTT  
 1151 ATACCGAAAG CGGTGCGGCG CGTTACCAAA TCATGGCGCA AGAACGGGTT  
 1201 TTGGAAGCA GCCGTTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA  
 1251 CGGCATCCGC AACCGGCTGG AAGTAATACG GGCGCGGCAG GAAGTCGCCC  
 1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT  
 1351 TTGCGCTTGG TGAAAGAGAG CGGGTTAGGG TTGGAACCGG TATTTCGCGA  
 1401 ATAA

1241

This corresponds to the amino acid sequence <SEQ ID 2616; ORF 763>:

m763 . pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIIVLAEK QTYENQLNDY TDLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2617>:

a763 . seq

```

1  ATGACATTGC TCAATCTAAT GATAATGCAA GATTACGTA TTTCCGTTTG
51  CCTGACACTG ACGCCCTATT TGCAACATGA ACTATTTTCG GCTATGAAAT
101 CCTATTTTTC CAAATATATC CTACCCGTTT CACTTTTAC CTTGCCACTA
151 TCCCTTTCCC CATCCGTTTC GGCTTTTACG CTGCCTGAAG CATGGCGGGC
201 GGCGCAGCAA CATTGCGCTG ATTTTCAAGC GTCCCATAC CAGCGTGATG
251 CAGTGCAGCG ACGGCAACAA CAAGCCAAGG CCGCATTCCT TCCCATGTA
301 TCCGCCAATG CCAGCTACCA GCGCCAGCG CCATCGATT CTCCACCCG
351 CGAAACACAG GGATGGAGCG TGCAGGTGGG ACAAACCTTA TTTGACGCTG
401 CCAAATTTGC ACAATACCGC CAAAGCAGGT TCGATACGCA GGCTGCAGAA
451 CAGCGTTTCG ATGCGGCACG CGAAGAATTG CTGTTGAAAG TTGCCGAAAG
501 TTATTTCAAC GTTTTACTCA GCCGAGACAC CGTTGCCGCC CATGCGCGCG
551 AAAAAGAGGC TTATGCCAG CAGGTAAGGC AGGCGCAGGC TTTATTCAAT
601 AAAGGTGCTG CCACCGCGCT GGATATTAC GAAGCCAAAG CCGGTTACGA
651 CAATGCCCTG GCCCAAGAAA TCGCCGTATT GGCTGAGAAA CAAACCTATG
701 AAAACCAAGT GAACGACTAC ACCGCGCTGG ACAGCAAACA AATCGAGGCC
751 ATAGATACCG CCAACCTGTT GGCACGCTAT CTGCCAAGC TGGAACGTTA
801 CAGTCTGGAT GAATGGCAGC GCATTGCCTT ATCCAACAAT CATGAATACC
851 GGATGCAGCA GCTTGCCCTG CAAAGCAGCG GACAGGCGCT TCGGGCAGCA
901 CAGAACAGCC GCTATCCAC CGTTTCTGCC CATGTCGGCT ATCAGAATAA
951 CCTCTACACT TCATCTGCGC AGAATAATGA CTACCACTAT CGGGGCAAAG
1001 GGATGAGCGT CGGCGTACAG TTGAATTTGC CGCTTTATAC CGGCGGAGAA
1051 TTGTCGGGCA AAATCCATGA AGCCGAAGCG CAATACGGGG CTGCCGAAGC
1101 ACAGCTGACC GCAACCGAGC GGCACATCAA ACTCGCGTA CGCCAGGCTT
1151 ATACCGAAAG CGGTGCGGCG CGTTACCAA TCATGGCGCA AGAACGGGTT
1201 TTGGAAGCA GCCGTTGAA ACTGAAATCG ACCGAAACCG GCCAACAATA
1251 CGGCATCCGC AACCGGCTGG AAGTAATAC GGCGCGGAG GAAGTCGCCC
1301 AAGCAGAACA GAACTGGCT CAAGCACGGT ATAAATTCAT GCTGGCTTAT
1351 TTGCGCTTGG TGAAAGAGAG CGGTTAGGG TTGGAACGG TATTGCGGA
1401 ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2618; ORF 763.a>:

a763 . pep

```

1  MTLNLNLMIMQ DYGISVCLTL TPYLQHELFS AMKSYFSKYI LPVSLFTLPL
51  SLSPSVSAFT LPEAWRAAQ HSADFOASHY QDAVRARQQ QAKAAFLPHV
101 SANASYQRQP PSISSTRETQ GWSVQVGQTL FDAAKFAQYR QSRFDTQAAE
151 QRFDAAREEL LLKVAESYFN VLLSRDTVAA HAAEKEAYAQ QVRQAQALFN
201 KGAATALDIH EAKAGYDNAL AQEIIVLAEK QTYENQLNDY TGLDSKQIEA
251 IDTANLLARY LPKLERYSLD EWQRIALSNN HEYRMOQLAL QSSGQALRAA
301 QNSRYPTVSA HVGYNLYT SSAQNNDYHY RGKMSVGVQ LNLPLYTGGE
351 LSGKIHAEAE QYGAAEAQLT ATERHIKLA RQAYTESGAA RYQIMAQERV
401 LESSRLKLKS TETGQYQYR NRLEVIRARQ EVAQAEQKLA QARYKFMLAY
451 LRLVKESGLG LETVFAE*

```

m763 / a763 99.8% identity in 467 aa overlap

```

m763 . pep      10      20      30      40      50      60
MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
|||||
a763           MTLNLNLMIMQDYGISVCLTLTPYLQHELFSAMKSYFSKYILPVSLFTLPLSLSPSVSAFT
              10      20      30      40      50      60

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	70	80	90	100	110	120
m763.pep	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQPPSISSTRETQ					
a763	LPEAWRAAQHSADFQASHYQRDAVRARQQQAKAFLPHVSANASYQRQPPSISSTRETQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m763.pep	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
a763	GWSVQVGQTLFDAAKFAQYRQSRFDTQAAEQRFDAAREELLLKVAESYFNVLLSRDTVAA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m763.pep	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
a763	HAAEKEAYAQQVRQAQALFNKGAATALDIHEAKAGYDNALAQEI AVLAEKQTYENQLNDY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m763.pep	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
a763	TGLDSKQIEAIDTANLLARYLPKLERYSLDEWQRIALSNNHEYRMQQLALQSSGQALRAA					
	250	260	270	280	290	300
	310	320	330	340	350	360
m763.pep	QNSRYPTVSAHVGYNQNLTYSSAQNNDYHYRGKGM SVGVQLNPLTYTG GELSGKIHEAEA					
a763	QNSRYPTVSAHVGYNQNLTYSSAQNNDYHYRGKGM SVGVQLNPLTYTG GELSGKIHEAEA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m763.pep	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
a763	QYGAAEAQLTATERHIKLAVRQAYTESGAARYQIMAQERVLESSRLKLKSTETGQQYGIR					
	370	380	390	400	410	420
	430	440	450	460		
m763.pep	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
a763	NRLEVIRARQEVAAEQKLAQARYKFMLAYLRLVKESGLGLETVFAEX					
	430	440	450	460		

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g764.seq not found yet

g764.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2619>:

m764.seq

```

1 ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCTCGATACA TTAAGTATG
51 GCGCAATGTT TGGGCGGTGC GCGACAGTT GAAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTGGGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGCGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA
701 CAGCAGACTA CCGCGGTTTG CCGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CCGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCTACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGATTGC GCCCGATGAC GACAAAATGG ACGTGGAAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGTG GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGCTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAAGCAGT GAATCTGACG GCGGGCATGA ATGTCACGGC GGAGATTAA
1351 ACGGGTAAAC GCGGGTGTCT GGATTATCTG TTAAGCCCGC TGCAAACCAA
1401 ATTGGACGAA AGCTTTAGGG AGCGATAG

```

This corresponds to the amino acid sequence &lt;SEQ ID 2620; ORF 764&gt;:

m764.pep

```

1 MFFSALKSFL SRYITVWRNV WAVRDQLKPP KRTAEEOAFL PAHLELTDTP
51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETAVVKAVHV RDGQHVQKQE TLAELEAVGT DSDVVSQSEA LQAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSAALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLESTRG QMRQIAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVIAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGKAVNLT AGMNVTAIEK
451 TGKRRVLDYL LSPLQTKLDE SFRER*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2621>:

a764.seq (partial)

```

1 ATGTTTTTCT CCGCCCTGAA ATCCTTTCTT TCCCGCTACA TTACCGTATG
51 GCGCAATGTT TGGGCGGTGC GCGACAGTT GGAACCGCCC AAACGCACGG
101 CGGAAGAACA GCGGTTTTTG CCCGCGCATT TGGAACTGAC CGATACGCCG
151 GTCTCTGCCG CTCCGAAATG GCGGCGCGCT TTTATTATGG CGTTTGCGCT
201 TTTGGCTTTG TTGTGGTCCT GGTTCGGCAA AATCGATATT GTGGCGGCGG
251 CTTGGGGCAA AACGGTGTCT GCGGGGCGCA GCAAACCAT CCAGCCGCTG
301 GAAACGGTGG TGGTTAAGGC GGTACATGTG CCGGACGGGC AGCATGTGAA
351 ACAGGGAGAA ACGCTGGCGG AACTGGAGGC TGTGGGAACA GACAGCGATG
401 TGGTGCAGTC GGAGCAGGCT TTGCAGGCTG CCCAATTGTC CAAACTGCGT
451 TATGAAGCGG TATTGGCGGC ATTGGAAAGC CGTACCGTGC CGCATATCGA
501 TATGGCGCAA GCACGGTCTT TAGGTCTCTC CGATGCCGAT GTGCAATCGG
551 CGCAGGTGTT GCGCGAGCAC CAGTATCAGG CATGGGCGGC GCAGGATGCG
601 CAATTGCAGT CCGCTTTGCG CGGCCATCAG GCGGAATTGC AGTCGGCCAA
651 GCGCAGGAG CAGAAGCTGG TTTCGGTGGG GCGGATCGAG CAGCAGAAAA

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701 CAGCAGACTA CCGCCGTTTG CGGGCCGACA ATTTTATTTT GGAACATGCG
751 TTTTGGAGC AGCAGAGCAA ATCGGTCAGC AATTGGAACG ATTTGGAAG
801 TACGCGCGGT CAGATGAGGC AGATTCAGGC GGCCATTGCA CAGGCGGAGC
851 AGAATCGGGT GCTGAATACG CAGAACCTGA AACGCGATAC GCTGGATGCG
901 CTGCGCCAGG CAAACGAACA GATTGACCAA TACCGCGGCC AAACGGATAA
951 GGCAAAGCAG CGGCAGCAGC TGATGACAAT ACAGTCGCCT GCGGACGGCA
1001 CGGTGCAGGA ATTGGCCACC TATACGGTGG GCGGTGTGGT GCAGGCTGCC
1051 CAAAAAATGA TGGTGGTTGC GCCCGATGAC GACAAAATGG ACGTGGAAGT
1101 TTTGGTATTG AACAAAGACA TCGGTTTGT GGAACAGGGA CAGGATGCGG
1151 TGGTGAAGAT TGAGAGTTTT CCCTATACGC GCTACGGTTA TCTGACGGGC
1201 AAGGTGAAAA GTGTCAGCCA TGATGCGGTA AGCCACGAAC AGTTGGGCTT
1251 GGTTTATACG GCGGTGGTGT CGCTGGACAA ACATACCTTG AATATTGACG
1301 GCAAA

```

This corresponds to the amino acid sequence <SEQ ID 2622; ORF 764.a>:

```

a764.pep (partial)
  1 MFFSALKSFL SRYITVWRNV WAVRDQLEPP KRTAEQAF LPAHLELTDTP
 51 VSAAPKWAAR FIMAFALLAL LWSWFGKIDI VAAASGKTVS GGRSKTIQPL
101 ETVVVKAVHV RDGQHVKGQE TLAELEAVGT DSDVVQSEQA LQAAQLSKLR
151 YEAVLAALES RTVPHIDMAQ ARSLGLSDAD VQSAQVLAQH QYQAWAAQDA
201 QLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL RADNFISEHA
251 FLEQQSKSVS NWNLDLESTRG QMRQIQAAIA QAEQNRVLNT QNLKRDTLDA
301 LRQANEQIDQ YRGQTDKAKQ RQQLMTIQSP ADGTVQELAT YTVGGVVQAA
351 QKMMVAPDD DKMDVEVLVL NKDIGFVEQG QDAVVKIESF PYTRYGYLTG
401 KVKSVDHDAV SHEQLGLVYT AVVSLDKHTL NIDGK

```

m764 / a764 99.3% identity in 435 aa overlap

	10	20	30	40	50	60
m764.pep	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
a764	MFFSALKSFLSRYITVWRNVAVRDQLEPPKRTAEQAF LPAHLELTDTPVSAAPKWAAR					
	10	20	30	40	50	60
m764.pep	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
a764	FIMAFALLALLWSWFGKIDIVAAASGKTVSGGRSKTIQPLETAVVKAVHVRDQHVKGQE					
	70	80	90	100	110	120
m764.pep	TLAELEAVGTDSDDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARSIGLSAD					
a764	TLAELEAVGTDSDDVVQSEQA LQAAQLSKLRYEAVLAALESRTVPHIDMAQARSIGLSAD					
	130	140	150	160	170	180
m764.pep	VQSAQVLAQH QYQAWAAQDAQLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL					
a764	VQSAQVLAQH QYQAWAAQDAQLQSALRGHQ AELQSAKAQE QKLVSVAIE QOKTADYRRL					
	190	200	210	220	230	240
m764.pep	RADNFISEHAFLEQQSKSVSNWNLDLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
a764	RADNFISEHAFLEQQSKSVSNWNLDLESTRGQMRQIQAAIAQAEQNRVLNTQNLKRDTLDA					
	250	260	270	280	290	300
m764.pep	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
a764	LRQANEQIDQYRGQTDKAKQRQQLMTIQSPADGTVQELATYTVGGVVQAAQKMMVAPDD					
	310	320	330	340	350	360
m764.pep	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					
a764	DKMDVEVLVLNKDIGFVEQGQDAVVKIESFPYTRYGYLTGKVKSVDHDAVSHEQLGLVYT					
	370	380	390	400	410	420
m764.pep						
a764						

1245

```

|||||
a764      DKMDVEVLVLNKDIGFVEQGDVVKIESFPYTRYGYLTGKVKSVSHDAVSHEQLGLVYT
           370      380      390      400      410      420

           430      440      450      460      470
m764 . pep AVVSLDKHTLNIDGKAVNLTAGMNVTAIEIKTGKRRVLDYLLSPLQTKLDESFRERX
           |||||
a764      AVVSLDKHTLNIDGK
           430

```

g765.seq not yet found

g765.pep not yet found

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2623>:

```

m765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTGCG CAGTAATCTC GGTATTGGGG
151 GCTTGTGCGG TCGTTGCTGA TGTTTACGGT CATGATTCCG CCACAATGAA
201 CGCTGCGGCT GCCAAGATT ATATGAAAC GGTGAGTTA AACAGTCTG
251 CCGCAATGT CGATACCACA TCCAGAACAG CCCGCAGGGT GCAGGCAGTA
301 TTTTCGACGTA TGCTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACCGGTGGG
401 CAATGCCCGG TGGAAAAATG GCGTTTTATA CGGGGATAGT CGACAACTC
451 AAGCTGACCG ATGACGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 CGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGCAA ATCTTGACCA
551 ATACGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAT
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGACGTACGG
651 TCTTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCGGC CGCTGTACGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAACCGGCT TTATTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCAAAGTGT CAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2624; ORF 765&gt;:

```

m765.pep
1  MLRCRPSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG
51  ACVVADVYG HDSATMNAHA AKDYMKTVEL NKSAGNVDTT SRTARRVQAV
101 FRRMLPYADA ANNTSHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLTDEIAAI MGHENTHALH EHGKKNVGOQ ILTNTAAQIG TQIILDKKPD
201 TNPELVGLGM DILGTYGLTL PYSRSLIEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT S THPTNNARIE NLKRLLPV M PVYEQSVRNK
301 GRVNNKRRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2625>:

```

a765.seq
1  ATGTTAAGAT GCCGTCCGAA ATCCGTTTGG GATTGAGACG GCATTTTTTT
51  GAAATTTAAT TTTTAAAGGA GTAAACCTAA ATATGAAATT TCCTTCCTTC
101 CTTCCTTTAA ACGGATACTC TGCCTGTGCG CAGTAATCTC GGTATTGGGG
151 GCTTGTACGG TCGTTGCTGA TGTTTACGGT CAGGATTCCG CCACAATGAA
201 TGCTGCGGCT GCCAAGATT ATATGAAAC GGTGAGTTG AACAGTCTG
251 CCGCAATGT CGATACTACA TCCAAACAG CCCGTAGGGT GCAGGCAGTA
301 TTTTCGACGTA TGTTGCCTTA TGCCGATGCG GCAAATAATA CCAGCCATAA
351 GTTTGACTGG AAAATGACGG TTTTCAAAA CGATGAGCTG AACCGGTGGG
401 CAATGCCCGG CGGAAAAATG GCGTTTTATA CGGGGATAGT CGATAAATT
451 AAGCTGACCG ATGGCGAAAT TGCCGCCATT ATGGGGCATG AAATGACGCA
501 TGCCCTGCAT GAACACGGTA AAAATAAGGT CGGGCAGAAA ATCTTGACTA
551 ATATGGCGGC GCAGATAGGC ACGCAGATTA TATTAGACAA AAAACCGGAC
601 ACTAATCCGG AATTGGTCGG ATTGGGTATG GATATTTTGG GGATGTACGG
651 CATTACCTTG CCTTATAGCC GCAGCTTGGG AGAAGAAGCC GATGAGGGGG
701 GAATGATGTT GATGGCGCAG GCAGGCTATC ATCCGGCAGC CGCTGTACGG
751 GTTTGGGAAA AAATGAATCA GGAAAACGAC CAAACCGGCT TTATTATGC
801 TATTACCTCT ACTCATCCGA CAAACAATGC CCGTATAGAA AATCTAAAC
851 GGTGTGTGCC GACCGTTATG CCGGTTTATG AGCACAGTGT TAGAAATAAG
901 GGGCGCGTTA ATAAAAACG TCGGCGTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2626; ORF 765.a&gt;:

```

a765.pep
1  MLRCRPSVL DSDGIFLKFN FLRSKPKEYI SFLPSFKRIL CLSAVISVLG

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```

51  ACTVVADVYG QDSATMNAAA AEDYMKTVEL NKSAGNVDTT SKTARRVQAV
101 FFRMLPYADA ANNTGHKFDW KMTVFKNDEL NAWAMPGGKM AFYTGIVDKL
151 KLT DGEIAAI MGHEMTHALH EHGKKNVGQK ILTNMAAQIG TQIILDKKPD
201 TNPELVGLGM DILGMYGITL PYSRSL EEEA DEGGMMLMAQ AGYHPAAAVR
251 VWEKMNQEND QNGFIYAIT S THPTNNARIE NLKRLLEPTVM PVYEH SVRNK
301 GRVNKNRRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 765 shows 96.18% identity over a 309 aa overlap with a predicted ORF (ORF 765) from *N. meningitidis*:

m765 / a765 96.1% identity in 309 aa overlap

	10	20	30	40	50	60
m765.pep	MLRCRPKSVLDS	GI FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACAVVADVYG		
a765	MLRCRPKSVLDS	GI FLKFNFLRSKPKYEIS	FLPSFKRILCLSAVIS	VLGACTTVADVYG		
	10	20	30	40	50	60
	70	80	90	100	110	120
m765.pep	HDSATMNAAA	KDYMKTVELNKSAGNVD	TTSRTARRVQAVFRML	PYADAANNTSHKFDW		
a765	QDSATMNAAA	AEDYMKTVELNKSAGNVD	TTSRTARRVQAVFRML	PYADAANNTGHKFDW		
	70	80	90	100	110	120
	130	140	150	160	170	180
m765.pep	KMTVFKNDEL	NAWAMPGGKMAFYTG	IVDKLKLTDDEIAAIM	GHMTHALHEHGKKNVG	QQ	
a765	KMTVFKNDEL	NAWAMPGGKMAFYTG	IVDKLKLTDGEIAAIM	GHMTHALHEHGKKNVG	QK	
	130	140	150	160	170	180
	190	200	210	220	230	240
m765.pep	ILTNMAAQIG	TQIILDKKPD	TNPPELVGLGMDIL	GTGTLPLPYSRSL	EEEADEGGMMLMAQ	
a765	ILTNMAAQIG	TQIILDKKPD	TNPPELVGLGMDIL	GMYGITLPLPYSRSL	EEEADEGGMMLMAQ	
	190	200	210	220	230	240
	250	260	270	280	290	300
m765.pep	AGYHPAAAVR	VWEKMNQENDQNGFI	YAITSTHPTNNARIEN	LKRLLEPTVMPVYE	QSVRNK	
a765	AGYHPAAAVR	VWEKMNQENDQNGFI	YAITSTHPTNNARIEN	LKRLLEPTVMPVYE	H SVRNK	
	250	260	270	280	290	300
	310					
m765.pep	GRVNKKRRRX					
a765	GRVNKNRRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2627>:

```

g767.seq
1  ATGAAGTTTA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC
51  GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC
101 CCATTCTCTCA AGAACAGCCG GGAAAAATTG AGGTTTGTGA ATTTTTCGGC
151 TATTTTTCGCG TACATTGCCA TCATTTCGAT CCTTTGTAT TGAACCTGGG
201 CAAGGCATTG CCGTCTGATA CTTATCTGCG GACGGAGCAC GTGGTCTGGC
251 GGCTTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCTG
301 GGTTTGAAAT ATCAGGCAAA CTCTGCTGTG TTAAAGCAG TTACGAAACA
351 AAAAATCCGT TTGGAAAACA GGGCTGTTGC CGGAAATGG GCTTATCTC
401 AAAAAGGTTT TGACGGCAAA AAAGTGATGC GCGCCTATGA TTCCCCCGAA
451 GCTGCCGCCG TCGCATTAAA AATGCAGAAA CTGACGGAAC AATACGGTAT
501 TGACAGCAGC CCGACCGTTA TTGTCGGCGG AAAATACCGG GTTATCTTCA
551 ATAATGGCTT TGATGGCGGC GTTCATACGA TTAAAGAATT GGTGCCCAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2628; ORF 767.ng>:

```

g767.pep
1  MKFKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPQEQP GKIEVLEFFG
51  YFCVHCHHFD PLLKLKGLAL PSDTYLRTEH VVWRPEMLGL ARMAAAVKLS

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101 GLKYQANSV FRAVYEQKIR LENRAVAGKW ALSQKGF DGK KLMRAYDSPE  
 151 AAVALKMQK LTEQYGDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK  
 201 VREERKRQTP AVQK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2629>:

m767.seq  
 1 A TGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC  
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC  
 101 CCATTCTCTCA AGAACAGTCG GGTAAAATTG AGGTTTGTGA ATTTTTCGGC  
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAACTGGG  
 201 CAAGGCATTG CCGTCTGATG CCTATTTGAG GACGGAGCAC GTGGTCTGGC  
 251 AGCCTGAAAT GCTCGGTTTG GCTAGGATGG CGGCTGCCGT CAATTTGTCTG  
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCTGTG TTTAAAGCAG TTTACGAACA  
 351 AAAAAATCCG TTGAAAACA GGTGGTTGCG CGGAAAATGG GCTTTGTCTC  
 401 AAAAAAGGCTT TGACGGCAAA AAAGTGATGC GCGCTATGA TTCCCCGAA  
 451 GCTGCCGCGG CCGCATTAAT AATGCAGAAA CTGACGGAAC AATACCGCAT  
 501 CGACAGCACG CCGACCGTTA TTGTCGGCGG AAAATACCGG GTTATCTTCA  
 551 ATAACGGCTT TGACGGCGGC GTTCATACGA TTAAAGAATT GGTGCAAAA  
 601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

This corresponds to the amino acid sequence <SEQ ID 2630; ORF 767>:

m767.pep  
 1 MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPOEQS GKIEVLEFFG  
 51 YFCVHCHHFD PLLKLKGKAL PSDAYLRTEH VVWQPEMLGL ARMAAANLNS  
 101 GLKYQANPAV FRAVYEQKIR LENRSVAGKW ALSQKGF DGK KLMRAYDSPE  
 151 AAAAAALMQK LTEQYRIDST PTVIVGGKYR VIFNNGFDGG VHTIKELVAK  
 201 VREERKRQTP AVQK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 767 shows 95.8% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. gonorrhoeae*

m767/g767 95.8% identity in 214 aa overlap

	10	20	30	40	50	60
g767.pep	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPOEQS	GKIEVLEFFG	YFCVHCHHFD
m767	MKFKHLLPLL	LSAVLSAQAY	ALTEGEDYLV	LDKPIPOEQS	GKIEVLEFFG	YFCVHCHHFD
	70	80	90	100	110	120
g767.pep	PLLLKLGKAL	PSDYLRT	EHVVRPEMLGL	ARMMAAVKLS	GLKYQANSV	FRAVYEQKIR
m767	PLLLKLGKAL	PSDYLRT	EHVVRPEMLGL	ARMMAAVKLS	GLKYQANPAV	FRAVYEQKIR
	130	140	150	160	170	180
g767.pep	LENRAVAGKW	ALSQKGF DGK	KLMRAYDS	PEAAVALKMQ	KLTEQYRIDST	PTVIVGGKYR
m767	LENRSVAGKW	ALSQKGF DGK	KLMRAYDS	PEAAAAALKMQ	KLTEQYRIDST	PTVIVGGKYR
	190	200	210			
g767.pep	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
m767	VIFNNGFDGG	VHTIKELVAK	VREERKRQTP	AVQKX		
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2631>:

a767.seq  
 1 A TGAAGCTCA AACATCTGTT GCCGCTGCTG CTGTCGGCAG TGTGTCCGC  
 51 GCAGGCATAT GCCCTGACGG AAGGGGAAGA CTATCTTGTG TTGGATAAAC  
 101 CCATTCTCTCA AAAACAGTCG GGCAAAATTG AGGTTTGTGA ATTTTTCGGC  
 151 TATTTCTGCG TACATTGCCA TCATTTCGAT CCTTTGTTAT TGAAATTGGG  
 201 CAAGGCATTG CCGTCTGATG CCTATTTAAG GACGGAGCAC GTGGTCTGGC  
 251 AGCCTGAAAT GCTCGGTCTG GCAAGAATGG CTGCTGCGGT CAAGCTGTCA  
 301 GGTTTGAAAT ATCAGGCAAA CCCTGCCGTG TTTAAAGCAG TTTACGAACA  
 351 AAAAAATCCG TTGAAAACA GGTGGTTGCG CGAAAATGG GCTTTGTCTC  
 401 AAAAAAGGCTT TGACGGCAAA AAAGTGATGC GCGCTACGA CTCTCCTGCG



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451 GCAGCGGCTG CTGCATCAAA AATGCAGCAA TTGACGGAAC AGTACCGCAT
501 CGACAGTACG CCGACCGTTG TCGTCGGCGG AAAATACCGC GTTATCTTCA
551 ATAAATGGCTT TGACGGCGGT GTTCATACGA TTAAAGAATT GGTGCCAAA
601 GTCAGGGAAG AACGCAAGCG TCAGACCCCT GCTGTACAGA AATAG

```

This corresponds to the amino acid sequence <SEQ ID 2632; ORF 767.a>:

```

a767.pep
1  MKLKHLLPLL LSAVLSAQAY ALTEGEDYLV LDKPIPKQKS GKIEVLEFFG
51  YFCVHCHHFD PLLKLKGLAL PSDAYLRTEH VVWQPEMLGL ARMAAAVKLS
101 GLKYQANPAV FKAUYEQKIR LENRSVAEKW ALSQKGFDPK KLMRAYDSPA
151 AAAAAASKMQQ LTEQYRIDST PTVVVGKRYR VIFNNGFDGG VHTIKELVAK
201 VREERKRQTP AVQK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 767 shows 96.7% identity over a 214 aa overlap with a predicted ORF (ORF 767) from *N. meningitidis*:

m767/a767 96.7% identity in 214 aa overlap

	10	20	30	40	50	60
a767.pep	MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQKSGKIEVLEFFGYFCVHCHHFD					
m767	MKLKHLLPLL LSAVLSAQAYALTEGEDYLVLDKPIPKQKSGKIEVLEFFGYFCVHCHHFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
a767.pep	PLLLKLGLKALPSDAYLRTEHVWQPEMLGLARMAAAVKLSGLKYQANPAVFKAVYEKQIR					
m767	PLLLKLGLKALPSDAYLRTEHVWQPEMLGLARMAAAVNLSGLKYQANPAVFKAVYEKQIR					
	70	80	90	100	110	120
	130	140	150	160	170	180
a767.pep	LENRSVAEKWALSQKGFDPKLMRAYDSPAAAAASKMQQLTEQYRIDSTPTVVVGKRYR					
m767	LENRSVAGKWALSQKGFDPKLMRAYDSPEAAAAALKMQKLTQYRIDSTPTVIVVGKRYR					
	130	140	150	160	170	180
	190	200	210			
a767.pep	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
m767	VIFNNGFDGGVHTIKELVAKVREERKRQTPAVQKX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2633>:

```

g768.seq
1  ATGAATATCA AACAAATGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCACGCAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATTACAG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGTCAATTTG ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATATACGAA GCCCGGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC
251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT
301 TATACAAATG TTGCCAATCA CGCGGTTAT GAAGACCTGC TCAAAAAGG
351 GATGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2634; ORF 768.ng>:

```

g768.pep
1  MNIKQLITAA LIASAAFATQ AAPQKPVSA QTAQHSVWI DVRSEQEFSE
51  GHLHNAVNI PVDQIVRRIE AAPDKDTPVN LYCRSGRRAE AALQELKKAG
101 YTNVANHGGY EDLLKKGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2635>:

```

m768.seq
1  ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT
51  TGCCCGCGAG GCAGCCCGCG AAAAACCCTG ATCCGCCGCC CAAACCGCGC
101 AACATCCGCG CGTTTGGATC GATGTCCGTT CCGAACAGGA ATTTAGCGAA
151 GGGCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAA TCGTCCGCCG
201 CATACACGAA GCCCGGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC

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251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAGCTGAA AAAAGCAGGT  
 301 TATACAAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2636; ORF 768>:

m768.pep  
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNI PVDQIVRRIE AAPDKTPVN LYCRSGRRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKGMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 768 shows 96.6% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. gonorrhoeae*

m768/g768 96.6% identity in 119 aa overlap

	10	20	30	40	50	60
g768.pep	MNIKQLITAALIASAAFATQAAPQKPVSAQAQHSVWIDVRSEQEFSEGLHNAVNI P					
m768	MNIKHLITAA LIASAAFAAQ AAPQKPVSAQAQHPAVWIDVRSEQEFSEGLHNAVNI P					
	10	20	30	40	50	60
	70	80	90	100	110	120
g768.pep	V DQIVRRIE AAPDKTPVNL YCRSGRRAE AALQELKKAG YTNVANHGGY EDLLKGMKX					
m768	V DQIVRRIE AAPDKTPVNL YCRSGRRAE AALQELKKAG YTNVANHGGY EDLLKGMKX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2637>:

a768.seq  
 1 ATGAATATCA AACACCTGAT TACCGCCGCA CTCATTGCCT CAGCCGCCTT  
 51 TGCCGCGCAG GCAGCCCGCG AAAAACCCTG ATCCGCGCGC CAAACCGCGC  
 101 AACATTACG CATTGGATC GATGTCGCA GCGAACAGGA ATTTAGCGAA  
 151 GGTCATTTGC ACAACGCGGT CAACATCCCC GTCGACCAAA TCGTCCGCGC  
 201 CATACACGAA GCCGCGCCCG ACAAGACAC GCCGGTCAAC CTCTACTGCC  
 251 GCAGCGGACG GCGTGCCGAA GCCGCCCTTC AAGAACTGAA AAAAGCAGGC  
 301 TATACGAATG TTGCCAATCA CGGCGGTAT GAAGACCTGC TCAAAAAGG  
 351 GATGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2638; ORF 768.a>:

a768.pep  
 1 MNIKHLITAA LIASAAFAAQ AAPQKPVSA QTAQHSAVWI DVRSEQEFSE  
 51 GHLHNAVNI PVDQIVRRIE AAPDKTPVN LYCRSGRRAE AALQELKKAG  
 101 YTNVANHGGY EDLLKGMK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 768 shows 99.2% identity over a 119 aa overlap with a predicted ORF (ORF 768) from *N. meningitidis*:

m768/a768 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
a768.pep	MNIKHLITAA LIASAAFAAQ AAPQKPVSAQAQHSVWIDVRSEQEFSEGLHNAVNI P					
m768	MNIKHLITAA LIASAAFAAQ AAPQKPVSAQAQHPAVWIDVRSEQEFSEGLHNAVNI P					
	10	20	30	40	50	60
	70	80	90	100	110	120
a768.pep	V DQIVRRIE AAPDKTPVNL YCRSGRRAE AALQELKKAG YTNVANHGGY EDLLKGMKX					
m768	V DQIVRRIE AAPDKTPVNL YCRSGRRAE AALQELKKAG YTNVANHGGY EDLLKGMKX					
	70	80	90	100	110	120

1250

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2639>:

g769.seq

```

1  T TGATAATGG TTATTTT TTTTATTTT TGTGGGAAGA CATTATGCC
51  T GCACGAAAC AGATGGATGC TGCTGCCTTT ATTGGCAAGC GCGGCATACG
101 C CGAAGaAAC ACCgtgCGAA CCGGATTGA GAAGCCGTCC CGAGTTCAGG
151 C TTTCATGAAG CGGAGGTCAA ACCGATCGAC AGGGAGAAGG TACCGGGGCA
201 G GTGCGGGAA AAAGGAAAAG TTTTGCAGGT TGACGgcGAA ACCCTGCTGA
251 A AAATCCCGA ATTGTTGTCG CGTGCCATGT ATTCGCGAGT GGTCTCAAAC
301 A ATATTGCCG GTATCCGCGT GATTTTGCCG ATTTACCTAC AACAGGCGCG
351 G CAGGATAAG ATGTTGGCAC TTTATGCACA AGGGATTTTG GCGCAGGCAG
401 A GGGCAGGGT GAAGGAGGCG GTTTCCTTAT ACCGGAATT GATTGCCGCC
451 C AACCAGGAG CGCCCGCCGT CCGTATGCGT TTGGCGGCGG CATTGTTTGA
501 A GACAGCGAG AACGAGGCGG CGGCAGACCA GTTCGACCGC CTGAAAACAG
551 A AGATCTGCC GCGCAGCTT ATGGAGCAGG TCGAGCTGTA CCGCAAGGCA
601 T TGCGCGAAC GCGATGCGTG GAAGGTAAAC GCGGTTTCA GCGTTACCCG
651 C GAACACAAT ATCAACCAAG CCCGAAACA GCAGCAGTAC GGCAATTGGA
701 C TTTCCCGAA ACAGGTGGAC GGCACGGCAG TCAATTACCG GTTCGGCGCG
751 G AGAAAAAAT GGTGCTGAA AAACGGCTGG TACACGACGG CCGGCGGCGA
801 C GTGTCGCGG AGGTTTATC CGGGGAATA GAAATTAAC GATATGACGG
851 C AGGTGTTTC CGGCGGCATC GGTTTTGGCG ACCGGCGTAA AGATGTCGGG
901 C TGGCAGTGT TCCACGAACG CCGCACCTAC GGCAACGACG CTTATTCTTA
951 C GCCCAACGGC GCACGCCTTT ATTTCAACCG TTGGCAAACC CCGAGATGGC
1001 A AACGCTGTC TTCGGCGGAG TGGGGCGGTT TGAAGAATAC GCGCCGGGCG
1051 C GTTCCGACA ATACCCATTT GCAAATTTCC AATTGCTGG TGTTTTACCG
1101 G AATGCGCGC CAATATTGGA CCGGCGGTTT GGATTTTAC CCGCAGCGCA
1151 A CCCCCGCCA CCGTGGCGAC AATTCAACC GTTACGGCCT GCGCTTTGCC
1201 T GGGGGCAGG AATGGGGCGG CAGCGGCTG TCTTCGCTGT TCCGCTCGG
1251 C GTGGCGAAA CGGCATTATG AAAAACCCGG CTTCTCAGC AGTTTTAAAG
1301 G GGAAGGCGC CAGGGATAAA GAATCGGACA CATCCTTAG CTTTGGCAC
1351 C CGGCATTGC ATTTCAAAGG CATCACGCGC CGCCTGACG TGTCGCACCG
1401 C GAAACGTGG AGCAACGATG TGTTTAACA ATACGAGAAA AACAGGCGCT
1451 T TGTGAGT TAACAAAACG TTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2640; ORF 769.ng>:

g769.pep

```

1  L IMVIFYFYF CGKTEMPARN RWMLLELLAS AAYAEETPCE PDLRSRPEFR
51  L HEAEVKPID REKVPQVRE KGKVLQVDGE TLLKNPELLS RAMYSAVVSN
101 N IAGIRVILP IYLOQARQDK MLALYAQIL AQAEGRVKEA VSHYRELIAA
151 Q PDAPAVRMR LAAALFEDRQ NEAADQFDR LKTEDLPQL MEQVELYRKA
201 L RERDAWKVN GGFSVTREHN INQAPKQQY GNWTFPKQVD GTAVNYRFGA
251 E KKWSLKNW YTTAGDVSF RVYPGNKKFN DMTAGVSGGI GFADRRKDVG
301 L AVFHERRY GNDAYSANG ARLYFNWQT PRWQTLSSAE WGRLEKTRRA
351 R SDNTHLQIS NSLVFYRNAR QYWTGGLDFY RERNPADRGD NFNRYGLRFA
401 W GQEWGSGSL SSLFRLGVAK RHYEKPGFFS SPKGERRRDK ESDTSLSLWH
451 R ALHFKGITP RLTLSHRETW SNDVFNEYEK NRAFVEFNKT F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2641>:

m769.seq

```

1  T TGATAATGG TTATTTT TTTTGTGGG AAGACATTTA TGCTGCACG
51  A AACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 A AGAAACACC GCGCGAACC GATTGAGAA GCCGTCCCGA GTTCAGGCTT
151 C ATGAAGCGG AGGTCAAACC GATCGACAGG GAGAAGGTGC CGGGGCAGGT
201 G CCGGAAAAA GGAAAAGTTT TGCAGATTGA CCGCGAAACC CTGCTGAAAA
251 A TCCCGAATT GTTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 A TTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 G GATAAGATG TTGGCACTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 G TAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGCCGCCCAA
451 C CCGACGCGC CCGCCGTCCG TATGCGTTG GCGGCAGCAT TGTTGAAAA
501 C CAGGCAGAAC GAGGCGGCGG CAGACCAGTT CGACCGCTG AAGGCGGAAA
551 A CCTGCCGCC GCAGCTGATG GAGCAGGTG AGCTGTACCG CAAGGCATTG
601 C CGCAACGCG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TCACCCGCGA
651 A CACAATATC AACCAAGCCC CGAAACGGCA GCAGTACGGC AAATGGACTT
701 T CCGCAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 A AAAAATGGT CGCTGAAAA CGGCTGGTAC ACGACGGCGG GCGGCGACGT
801 G TCCTGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 G CGTTTCCCG CGGCATCGGT TTTGCCGACC GGCAGAAAGA TGCCGGGCTG
901 G CAGTGTTC ACGAACGCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 C AACGGCGCA CGCCTTTAT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 C GTTGTCTTC GCGGAGTGG GGGCGTTGA AGAATACGCG CCGGGCGCGT
1051 T CCGACAATA CCCATTGCA AATTTCGAAT TCGCTGGTGT TTTACCGGAA
1101 T GCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 C CGCGCAGCG GGGCGCAAT TTCAACCGT ACGGCCTGCG CTTTGCCTGG
1201 G GCGCAGGAAT GGGCGGCAG CGGCTGTCT TCGCTGTGCG GCCTCGGCGC

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1251

1251 GCGCAACGG CATTATGAAA AACCCGGCTT TTTCAGCGGT TTTAAAGGGG  
 1301 AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG  
 1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCCGGA  
 1401 AACCGGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG  
 1451 TCGAGTTTAA TAAACGTTT TGA

This corresponds to the amino acid sequence <SEQ ID 2642; ORF 769>:

m769.pep

1 LIMVIFYFCG KTFMPARNRW MLLPLLASA AYAETPREP DLRSRPEFRL  
 51 HEAEVKPIDR EKVPQVREK GKVLQIDGET LLKNPELLSR AMYSAVVSNN  
 101 IAGIRVILPI YLQQAQDDKM LALYAQGILA QADGRVKEAI SHYRELIAAQ  
 151 PDAPAVRMRL AALFENRQN EAAADQFDR KAENLPPQLM EQVELYRKAL  
 201 RERDAWKVNG GFSVTRHNI NQAPKQQYQ KWTFFPKQVDG TAVNYRLGAE  
 251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL  
 301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRKNTRRAR  
 351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW  
 401 GQEWGSGSL SLLRLGAAR HYKPGFFSG FKGERRRDE LNTSLSLWHR  
 451 ALHFKGITPR LTLSHRETRS NDVFNEYKN RAFVEFNKT \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 769 shows 95.1% identity over a 492 aa overlap with a predicted ORF (ORF 769) from *N. gonorrhoeae*

m769/g769 95.1% identity in 492 aa overlap

	10	20	30	40	50	59
g769.pep	LIMVIFYFCGKTFMPARNRWMLL-PLLASAAYAETPCEPDLRSRPEFRLHEAEVKPI					
m769	LIMVIFY--FCGKTFMPARNRWMLLPLLASAAYAETPREPDLRSRPEFRLHEAEVKPI					
	10	20	30	40	50	
g769.pep	60	70	80	90	100	110
	DREKVPQGVREKGVQLQVDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD					
m769	DREKVPQGVREKGVQLQIDGETLLKNPELLSRAMYSVVSNNIAGIRVILPIYLQQAQD					
	60	70	80	90	100	110
g769.pep	120	130	140	150	160	170
	KMLALYAQGILAQAEGRVKEAVSHYRELIAAQPDAPAVRMRLAALFEDRQNEAAADQFD					
m769	KMLALYAQGILAQADGRVKEAISHYRELIAAQPDAPAVRMRLAALFENRQNEAAADQFD					
	120	130	140	150	160	170
g769.pep	180	190	200	210	220	230
	RLKTEDLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIHQAPKQQYGNWTFPKQV					
m769	RLKAENLPPQLMEQVELYRKALRERDAWKVNGGFSVTRHNIHQAPKQQYGNWTFPKQV					
	180	190	200	210	220	230
g769.pep	240	250	260	270	280	290
	DGTAVNYRFGAEKKWSLKNWYTTAGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDV					
m769	DGTAVNYRLGAEEKWSLKNWYTTAGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDA					
	240	250	260	270	280	290
g769.pep	300	310	320	330	340	350
	GLAVFHERRTYGNDAYSANGARLYFNWQTPRWQTLSSAEWGRKNTRRARSNDNTHLQI					
m769	GLAVFHERRTYGNDAYSYTNGARLYFNWQTPKWQTLSSAEWGRKNTRRARSNDNTHLQI					
	300	310	320	330	340	350
g769.pep	360	370	380	390	400	410
	SNSLVFYRNARQYWTGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLRLGVA					
m769	SNSLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAWGQEWGSGSLSLRLGAA					
	360	370	380	390	400	410
g769.pep	420	430	440	450	460	470
	KRHYEKPGFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTSLSHRETSNDVFNEYE					
m769	KRHYEKPGFFSSFKGERRRDKESDTSLSLWHRALHFKGITPRLTSLSHRETSNDVFNEYE					

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m769      KRHYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTLSHRETRSNDVFNEYE
          420      430      440      450      460      470

          480      490
g769.pep   KNRAFVEFNKTFX
          |||||
m769      KNRAFVEFNKTFX
          490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2643>:

```

a769.seq
1  TTGATAATGG TTATTTTTTA TTTTGTGGG AAGACATTTA TGCCTGCACG
51  AAACAGATGG ATGCTGCTGC TGCCTTTATT GGCAAGCGCG GCATATGCCG
101 AAAGAAACACC GCGCGAACCG GATTTGAGAA GCCGTCCCGA GTTCAGGCTT
151 CATGAAGCGG AGGTCAAACC AATCGACAGG GAGAAGGTAC CGGGCAGGT
201 GCGGGAAAAA GGAAAGTTT TGCAGATTGA CGCGAAACC CTGCTGAAAA
251 ATCCCGAATT GCTGTCCCGC GCGATGTATT CCGCAGTGGT CTCAAACAAT
301 ATTGCCGGTA TCCGCGTTAT TTTGCCGATT TACCTACAAC AGGCGCAGCA
351 GGATAAGATG TTGGCACTTT ATGCACAAGG GATTTTGGCG CAGGCAGACG
401 GTAGGGTGAA GGAGGCGATT TCCCATTACC GGAATTGAT TGTCGCCCAA
451 CCGACGCGCG CCGCGTCCG TATGCGTTTG CCGCGGCGAT TGTTGAAAA
501 CAGGCAGAAC GAGGCGGCGG CAGACAGTT CGACCGCTG AAGCGGAAA
551 ACCTGCCGCC GCAGCTGATG GAGCAGGTCG AGCTGTACCG CAAGGCATTG
601 CGCGAACCGG ATGCGTGGAA GGTAAATGGC GGCTTCAGCG TTACCCGCGA
651 ACACAATATC AACCAAGCCC CGAAACGCCA GCAGTACGGC AAATGGACTT
701 TCCCGAAACA GGTGGACGGC ACGGCGGTCA ATTACCGGCT CGGCGCGGAG
751 AAAAAATGGT CGCTGAAAAA CGGCTGGTAC ACGACGCGCG GCGGCGACGT
801 GTCCGGCAGG GTTTATCCGG GGAATAAGAA ATTCAACGAT ATGACGGCAG
851 GCGTTTCCGG CGGCATCGGT TTTGCCGACC GGCACAAAGA TGCCGGGCTG
901 GCAGTGTTCC ACGAACGCCG CACCTACGGC AACGACGCTT ATTCTTACAC
951 CAACGGCGCA CGCCTTTATT TCAACCGTTG GCAAACCCCG AAATGGCAAA
1001 CGTTGTCTTC GCGGAGTGG GGGCGTTTGA AGAATACCG CCGGGCGCGT
1051 TCCGACAATA CCCATTTGCA AATTCCAAT TCGCTGGTGT TTTACCGGAA
1101 TGCGCGCCAA TATTGGATGG GCGGTTTGA TTTTACCGC GAGCGCAACC
1151 CCGCCGACCG GGGCGACAAT TTCAACGTT ACGGCCTCGC CTTTGCTTGG
1201 GGGCAGGAAT GGGGCGGCAG CGGCCTGTCT TCGCTGTTGC GCCTCGGCGC
1251 GCGGAAACGG CATTATGAAA AACC CGCTT TTTACGCGGT TTTAAAGGGG
1301 AAAGGCGCAG GGATAAAGAA TTGAACACAT CCTTGAGCCT TTGGCACCAG
1351 GCATTGCATT TCAAAGGCAT CACGCCGCGC CTGACGTTGT CGCACCAGCA
1401 AACGCGGAGT AACGATGTGT TCAACGAATA CGAGAAAAAT CGGGCGTTTG
1451 TCGAGTTTAA TAAACGTTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 2644; ORF 769.a>:

```

a769.pep
1  LIMVIFYFCG KTFMPARNRW MLLLELLASA AYAETPREP DLRSRPEFRL
51  HEAEVKPIDR EKVPQGVREK GKVLIQIDGET LLKNPELLSR AMYSAVVSNN
101 IAGIRVILPI YLQQAQQDKM LALYAQGILA QADGRVKEAI SHYRELIVAQ
151 PDAPAVRMRL AAALFENRQN EAAADQFDRL KAENLPQLM EQVELYRKAL
201 RERDAWKVNG GFSVTREHNI NQAPKRQYQ KWTFFKQVDG TAVNYRLGAE
251 KKWSLKNWY TTAGDVSGR VYPGNKKFND MTAGVSGGIG FADRRKDAGL
301 AVFHERRTYG NDAYSYTNGA RLYFNWQTP KWQTLSSAEW GRLKNTRRAR
351 SDNTHLQISN SLVFYRNARQ YWMGGLDFYR ERNPADRGDN FNRYGLRFAW
401 QQEWGGGSLG SLLRLGAARK HYEKPGFFSG FKGERRRDKE LNTSLSLWHR
451 ALHFKGITPR LTLSHRETRS NDFVNEYEKN RAFVEFNKTF *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 769 shows 99.8% identity over a 490 aa overlap with a predicted ORF (ORF 769) from *N. meningitidis*:

m769/a769 99.8% identity in 490 aa overlap

```

          10      20      30      40      50      60
a769.pep  LIMVIFYFCGKTFMPARNRWMLLLLELLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          |||||
m769      LIMVIFYFCGKTFMPARNRWMLLLLELLASAAYAETPREPDLRSRPEFRLHEAEVKPIDR
          10      20      30      40      50      60

          70      80      90      100     110     120
a769.pep  EKVPQGVREKGVLIQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM

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1253

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m769      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
           EKVPGQVREKGVQLQIDGETLLKNPELLSRAMYSAVVSNNIAGIRVILPIYLQQAQQDKM
           70      80      90      100     110     120

a769.pep   130      140      150      160      170      180
           LALYAQGILAQADGRVKEAISHYRELIVAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m769      LALYAQGILAQADGRVKEAISHYRELIVAAQPDAPAVRMRLAAALFENRQNEAAADQFDRL
           130      140      150      160      170      180

a769.pep   190      200      210      220      230      240
           KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFFPKQVDG
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m769      KAENLPPQLMQVELYRKALRERDAWKVNGGFSVTREHNINQAPKRQQYGKWTFFPKQVDG
           190      200      210      220      230      240

a769.pep   250      260      270      280      290      300
           TAVNYRLGAEEKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m769      TAVNYRLGAEEKWSLKNWYTTAGGDVSGRVYPGNKKFNDMTAGVSGGIGFADRRKDAGL
           250      260      270      280      290      300

a769.pep   310      320      330      340      350      360
           AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m769      AVFHERRTYGNDAYSYTNGARLYFNRWQTPKWQTLSSAEWGRLKNTRRARSNDNTHLQISN
           310      320      330      340      350      360

a769.pep   370      380      390      400      410      420
           SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAGWGQEWGSGLSLLRLGAAKR
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m769      SLVFYRNARQYWMGGLDFYRERNPADRGDNFNRYGLRFAGWGQEWGSGLSLLRLGAAKR
           370      380      390      400      410      420

a769.pep   430      440      450      460      470      480
           HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTSLHRETRSNDVFNEYEKN
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m769      HYEKPGFFSGFKGERRRDKELNTSLSLWHRALHFKGITPRLTSLHRETRSNDVFNEYEKN
           430      440      450      460      470      480

a769.pep   490
           RAFEVFNKTFX
           |||||||||||
m769      RAFEVFNKTFX
           490

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2645>:

```

g770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCCGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATGT
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTG CCTGTTATAT TTCGTATGCA AAAAAAGCG GCTTGAAGGA
201 AATGGTCAAT TTGGAAGAGG ACGCGTCCGA CGCATCGGT TCGTGCGTTC
251 AGACGGCATC TTCGATTCT TTTGACGAAA CCGCGGTGCG CAAACCGAAA
301 GAAGTTTTCA AGCGCGGTAC GGGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAGCCTT CGCCTATTG GTTACAGCG
401 ATAAAATCGT CCAAGGATCG CCGAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGCGACGC GCATACCGCA AACCGACGGG GTGCAAGCCG ATACTCCCG
501 CAAACTGCTT GCCGGCGCCT GCATTATTTC CAACCCGATA AAAATCCCG
551 ACAAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2646; ORF 770.ng>:

```

g770.pep
1   MNRLLLLSAA VLPTACGSGE TDKIGRASTV FNMLGKNDRI EVEGFDDPDV
51  QGVACYISYA KGGGLKEMVN LEEDASDASV SCVQTASSIS FDETAVRKPK
101 EVFKRGTFGA FKSQRIVRRY DPKRKAFAYL VYSDKIVQGS PKNSLSAVSC
151 FSGGIPQTDG VQADTSGLL AGACIIISNPI KNPDKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2647>:

```

m770.seq
1   ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCCG
51  CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC

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1254

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101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTC CAACCCGATA GAAATCTCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2648; ORF 770>:

```

m770.pep
  1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EGEFDDPDV
 51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSRIQVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC
151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENLDRK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 770 shows 93.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. gonorrhoeae*

m770/g770 93.5% identity in 186 aa overlap

	10	20	30	40	50	60
g770.pep	MNRLLLLSAAVLP TACGSGETDKIGRASTVFNILGKNDR I EGEFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDR I EGEFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
g770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKRGTFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETA VRKPKVEFKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
g770.pep	DPKRKFAYLVYSDKIVQGS PKNSLSAVSCFGSGIPQTDGVQADTSGKLLAGACIISNPI					
m770	DPKRKTFAVLVYSDKIIQGS PKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
g770.pep	KNPDKRX					
	:					
m770	ENLDRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2649>:

```

a770.seq
  1 ATGAACAGAC TGCTACTGCT GTCTGCCGCC GTCCTGCTGA CTGCCTGCGG
 51 CAGCGGCGAA ACCGATAAAA TCGGACGGGC AAGTACCGTT TTCAACATAC
101 TGGGCAAAAA CGACCGTATC GAAGTGAAG GATTGACGA TCCCGACGTT
151 CAAGGGGTTG CCTGTTATAT TTCGTATGCA AAAAAAGGCG GCTTGAAGGA
201 AATGGTCAAT TTGAAGAGG ACGCGTCCGA CGCATCGGTT TCGTGCGTTC
251 AGACGGCATC TTCGATTCTT TTTGACGAAA CCGCCGTGCG CAAACCGAAA
301 GAAGTTTTC AACAACGGTGC GAGCTTCGCG TTCAAGAGCC GGCAGATTGT
351 CCGTTATTAC GACCCCAAAC GCAAAACCTT CGCCTATTG GTGTACAGCG
401 ATAAAATCAT CCAAGGCTCG CCGAAAAATT CCTTAAGCGC GGTTCCTGT
451 TTCGGCGGCG GCATACCGCA AACCGATGGG GTGCAAGCCG ATACTCCGG
501 CAACCTGCTT GCCGGCGCCT GCATGATTC CAACCCGATA GAAATCCCG
551 ACAACGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 2650; ORF 770.a>:

```

a770.pep
  1 MNRLLLLSAA VLLTACGSGE TDKIGRASTV FNILGKNDR I EGEFDDPDV
 51 QGVACYISYA KKGGLKEMVN LEEDASDASV SCVQTASSIS FDETA VRKPK
101 EVFKHGASFA FKSRIQVRY DPKRKTFAYL VYSDKIIQGS PKNSLSAVSC

```

1255

151 FGGGIPQTDG VQADTSGNLL AGACMISNPI ENPKR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 770 shows 99.5% identity over a 186 aa overlap with a predicted ORF (ORF 770) from *N. meningitidis*:

m770/a770 99.5% identity in 186 aa overlap

	10	20	30	40	50	60
a770.pep	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDDPDVQGVACYISYA					
m770	MNRLLLLSAAVLLTACGSGETDKIGRASTVFNILGKNDRIVEGFDDPDVQGVACYISYA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a770.pep	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKFVKHGASFAFKSRQIVRY					
m770	KKGGLKEMVNLEEDASDASVSCVQTASSISFDETAVRKPKFVKHGASFAFKSRQIVRY					
	70	80	90	100	110	120
	130	140	150	160	170	180
a770.pep	DPKRRTFAYLVYSDKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
m770	DPKRRTFAYLVYSDKIIQGSFKNSLSAVSCFGGGIPQTDGVQADTSGNLLAGACMISNPI					
	130	140	150	160	170	180
a770.pep	ENPKRXX					
m770	ENLDRXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2651>:

g771.seq

```

1  ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51  GGTGCTGACG ATGCTGCTTT TGGCGGCAGT CGGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCCGAA AACATCCGCA GCGGCCTCCA ACAAGCATT
151 GCCCATACCC ACCGGAATAT CTCGTTGAT GCGGATATAC GCGCAGGCT
201 TCTGCCCGCG CCGACCGTCA TCCTGAAAAA CCGTACCATC ACCGAACCCG
251 ACGGCGGCGG GGTGCGCGTT TCCGTCAAAG AAACCAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCGGATACAG GTTGAATAAT GGGTGGTTTC
351 GGGTGC GGAT CTTGCCCTGA CGCGCGACAG AACGCGCGCT TGAACATCC
401 AAGACCTGTT CGACGCGCGG AAACACTCCG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTTC CTGCAGCAAC AGCTTATCCT
501 GAAGGAATC AGCCTCAACC TGCAATCCCC CGATTCTGCG GGGCAGCAGT
551 TTGAAAGTTC GGGCATACTG GTTTGGAGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGG TGTTCCTTTC AGACGGCATC GGCACGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGGACACGGC ATCACCATT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCGCAATC CCCGCACTGG CACTCAAAAA CAACAGCATC AAAACCGGCA
851 CGGTCAACGG CAGCTTTACC GCCGCGGCG AATATGCCCC ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCTT CAAACCAATT
1001 TCTCCCTCGG CTGCGCGTTG GTTTGGAGTC GGGACAACGG GCTGGACGCC
1051 CCGCGCCTGC ACATATCGAC CCTTCAGGAT ACCGTGACG GCCTGCCGCA
1101 ACCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCATA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACGCCCA ACCCGTTGCC
1201 GCAAAATCA AATATACGCG GGAAGCGCA CCGCACCTGG AAGCCGCCGC
1251 CGCGCTGCAA AAATTAACCC TCGCCCCCTA TCTTGACGAA TTTCGGCAAC
1301 AAAACGGCAA AATATTCCC GACATCCTCG GCAGGCTGTC CGGCAACGTC
1351 GAGGCACACC TCAAAATCGG CAGCATCCAA CTCCCCGGCT TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGACCATATC GCGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GCGCGCCATA CCGAAGCGCG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA TGCGGTATC GACCTGACCG CAAGCGGCGA AAACCGCAAA
1651 GACCTTATCC GCTCGCTGCA AGGCAGCTG TCGCTGAATA TTTCCACCGG
1701 CGCGTGGCAC GGCATCGATA TGGACAGCAT TTAAAAAAC GGCCTTCCG

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1256

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1751 GGA A A A T C T C G G G C A G C A C A C C C T T C T A C C G A T T C A C G C T C A A C A G C G A A
1801 A T T T C A G A C G C A T C A G C C G C C A C A T C G A T A C C G A A C T C T T C T C C G A C A G
1851 C C T C T A T G T T A C C A G C A A C G G C T A T A C C A A T C T G G A T A C G C A G G A A T T G T
1901 C T G A A G A T G T C C T T A T C C G C A A C G C C G T C C A T C C G A A A A A C A A C C G A T T
1951 C C C C T G A A A A T C A C C C G T A C G G T G G A C A A G C C G T C C A T T A C C G T C G A T T A
2001 C G G C A G G C T G A C C G G C G G C A T C A A T T C G C G C A A G A G A A A C A G A A A T C C
2051 T C G A A G A C A C C T G C T G G A A C A A T G G C A G T G G C T C A A A C C T A A A G A A C C G
3051 T A A

```

This corresponds to the amino acid sequence <SEQ ID 2652; ORF 771.ng>:

```

g771.pap
1 MDLLSVFHKY RLKYAVAVLT MLLLAAVGLH ASVYRTFTPE NIRSRLQOSI
51 AHTHRKISFD ADIRRRLLPR PTVILKNLTI TEPDGGRVAV SVKETKIGLS
101 WKNLWSDRIQ VEKVVVSGAD LALTRDRNGA WNIQDLFDGA KHSASVNRRI
151 VENSTVRLNF LQQQLILKEI SLNLQSPDSS GQGFESSGIL VWRKLSVPWK
201 SRGLFLSDGI GTPEISPFHF EASTSLDGHG ITISTTGSFS VRFNAGGADA
251 AGIGLRADTS FRNLHLTAQI PALALKNNNSI KTGTVNGTFT AGGEYARWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRL QTNFSLGSPL VWSRDNLDA
351 PRLHISTLQD TVDRLPQPRF ISRLDGSLSI PNLQNWNAEL NGTFDRQFVA
401 AKFKYTRREGA PHLEAAAAAQ KLNLAFLYDE FRQONGKIFP DILGRLSGNV
451 EAHLKIGISQ LPGLQLDDME TYLHADKDHI ALSRFKSGLY GGHTEGGISI
501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFSNGDAVI DLTASGENRK
551 QLIRSLQGS LSLNISNGAWH GIDMDSILKN GLSGKISGST PFYRFTLNSE
601 ISDGISRHD TELFSDSLYV TSNGYTNLDT QELSEDVLR NAVHPKNKPI
651 PLKITGTVDK PSITVDYGR L TGGINSRKEK QKILEDLLE QWQWLKPKPE
701 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2653>:

```

m771.seq
1 ATGGATTAT TATCGGTTTT CCACAAATAC CGTCTGAAAT ATGCGGTGGC
51 CGTGCTGACG ATACTGCTTT TGGCGGCAGT CCGGCTGCAC GCTTCCGTAT
101 ATCGCACCTT CACGCCTGAA AACATCCGCA GCCGCCTACA ACAAGCATT
151 GCACACACAC ACCGGA AAT CTCGTTTAT GCGGACATT AGCGCAGGCT
201 CCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCAT ACCGAACCCG
251 GCGGCGACCA GACTGCCGTT TCGTCCAAAG AAACCAA AAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTGC GGAA CTGCGCTGA CCGCGGACGG GAAAGGTGT TGGAAACATCC
401 AAGACCTGAT CGACAGCCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAAAC GCACCGTCCG CCTCAATTC CTGCAAGAAC AGCTTATCCT
501 GAAGGAAATC AACCTCAACC TGCAATCCCC CGATTTCGTC GGGCAGCCGT
551 TTGAAAGTTT GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGC TGTTCCTTTC AAACGGCATC GGGCCGCCCG AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CCGACACGGC ATTACCATTT
701 CCACACCCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCGCAACC TCCACCTGAC
801 CGCCCAAATC CCGCGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTATAC GCCGGCGGCG AATATGCCCG ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAA AACC GCCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCGGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCGTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACC TGA AATCGG AAAAGTCCAA CTTCCGGGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTCA AGGCTTTTAC GCGGCGCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGGCGGCGA AACCCGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTCCACCGG
1701 TGCATGGCAC GGTATCGACA TGGACAATAT CCTGAAAAAC GGCATTTCGG
1751 GCAAAACTGC CGACAATGCC GCACCCAGCA CACCTTCCA CCGATTACCG
1801 CTCAACAGCG AAATTTTCAA CCGCATCAGC CGCCATATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAAGCAA CGGCTATACC AATCTGGATA
1901 CCGAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGC ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCC CGCAAAGAGA
2051 AACAGAAAT CCTCGAAGAC ACCCTGCTGG AACATGGCA GTGGCTCAAA
2101 CCTAAAGAAC CGTA

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This corresponds to the amino acid sequence <SEQ ID 2654; ORF 771>:

m771.pep  
 1 MDLLSVFHKY RLKYAVAVLT ILLLAAGVLH ASVYRTFTPE NIRSRLQOSI  
 51 AHTHRRKISFD ADIQRRLPR PTVILKNLTI TEPGGDQTAV SVQETKIGLS  
 101 WKNLWSDQIQ IEKWVSSAE LALTRDGKGV WNIQDLIDSQ KRQASVNRII  
 151 VENSTVRLNF LQEQILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK  
 201 SRGLFLSNGI GPPEISPFHF EASTSLDGHG ITISTTGSPS VRFNAGGADA  
 251 AGLGRLADTS FRNLHLTAQI PALALRNNSI KIETVNGAFT AGGEYARWDG  
 301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA  
 351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQWNAEL NGTFDRQTV  
 401 AKFRYTHEDA PHLEAAVALQ KNLTPYLDD VRQONGKIFP DTLAKLSGDI  
 451 EAHKIGKVQ LPGLQLDDME TYLHADKGHI ALSRFKSGLY GGHTEGGISI  
 501 ANTRPATYRL QQNASNIQIQ PLLQLFGFH SFGNGDAVI DLTAGGETRK  
 551 ELIRSLQGS LNLISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT  
 601 LNSEISDGIS RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK  
 651 NKPIPLKITG TVDKPSITVD YGRLTGGINS RKEKQKILED TLLEQWQWLK  
 701 PKEP\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 771 shows 90.3% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. gonorrhoeae*

m771/g771 90.3% identity in 704 aa overlap

	10	20	30	40	50	60
g771.pep	MDLLSVFHKYRLKYAVAVLTMLLLAAGVLHASVYRTFTPENIRSRLQOSIAHTHRRKISFD					
m771	MDLLSVFHKYRLKYAVAVLTILLLAAGVLHASVYRTFTPENIRSRLQOSIAHTHRRKISFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g771.pep	ADIRRRLLPRPTVILKNLTITTEPDGGRVAVSVKTKIGLSWKNLWSDRIQVEKWVVSAD					
m771	ADIQRRLPRPTVILKNLTITTEPGDQTAVSVQETKIGLSWKNLWSDQIQIEKWVSSAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
g771.pep	LALTRDRNGAWNIOQLDFDGAKHSASVNRIIVENSTVRLNLFQQLILKEISLNLQSPDSS					
m771	LALTRDGKGVWNIQDLIDSQKRQASVNRIIVENSTVRLNLFQEQILKEINLNLQSPDSS					
	130	140	150	160	170	180
	190	200	210	220	230	240
g771.pep	GQPFESSGILVWRKLSVPWKSRLFLSDGIGTPEISPFHFEASTSLDGHGITISTTGSPS					
m771	GQPFESSGILVWGKLSVPWKSRLFLSNGIGPPEISPFHFEASTSLDGHGITISTTGSPS					
	190	200	210	220	230	240
	250	260	270	280	290	300
g771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALKNNSIKTGTVNGTFTAGGEYARWDG					
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG					
	250	260	270	280	290	300
	310	320	330	340	350	360
g771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRLQTNFSLGSPVWSRDNGLDAPRLHISTLQD					
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD					
	310	320	330	340	350	360
	370	380	390	400	410	420
g771.pep	TVDRLPQPRFISRLDGSLSIPNLQWNAELNGTFDRQPVAAKFYKTYREGAPHLEAAALQ					
m771	TVNRLPQPRFISRLDGSLSVNLQWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ					
	370	380	390	400	410	420
	430	440	450	460	470	480
g771.pep	KNLNLAPYLDEFROQNGKIFPDILGRLSGNVEAHLKIGSIQLPGLQLDDMETYLHADKDH					
m771	KNLNLTPYLDDVRQONGKIFPDTLAKLSGDIEAHLKIGKVQLPGLQLDDMETYLHADKGHI					

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	430	440	450	460	470	480
g771.pep	490	500	510	520	530	540
	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALSRFKSGLYGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
g771.pep	550	560	570	580	590	
	DLTASGENRKQLIRSLQGSLSLNISNGAWHGIDMSILKNGLSGKISG----STPFYRFT					
m771	DLTAGGETRKEKILIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
g771.pep	600	610	620	630	640	650
	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
g771.pep	660	670	680	690	700	
	TVDKPSITVDYGRLTGGINSRKEKQKILEDILLEQWQWLKPKPEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDILLEQWQWLKPKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2655>:

```

a771.seq
1   ATGGATTAT TATCGGTCTT CCACAAATAC CGTCTGAAAT ATGCGGTAGC
51  CGTGCTGACG ATACTGCTTT TGGCGGCAAT CGGGCTGCAC GCTTCCGTAT
101 ATCGCATCTT CACACCTGAA AACATCCGAA GCCGCCTCCA ACAAGCATT
151 GCCCATACGC ACCGGAATAT CTCGTTGAT GCGGATATAC AGCGCAGGCT
201 TCTGCCCCGG CCGACCGTCA TCCTGAAAAA CCTGACCATT ACCGAACCCG
251 GCGGCGACCG GACTGCCGTT TCCGTCCAAG AAACCAAAAT CGGATTGAGC
301 TGGAAAAACC TGTGGTCGGA TCAGATACAG ATTGAAAAAT GGGTGGTTTC
351 GAGTCCGGAA CTTGCCCTGA CGCGCGACGG GAAAGGTGTT TGGAACATCC
401 AAGACCTGAT CGACAGCAA AAACGCCAAG CCTCAGTCAA CCGCATTATC
451 GTCGAAAACA GCACCGTCCG CCTCAATTTC CTGCAGGAAC AGCTTATCCT
501 GAAAGGAATC AACCTCAACC TGCAATCCCC CGATTCTGTC GGGCAGCCGT
551 TTGAAAGTTC GGGCATACTG GTTTGGGGAA AGCTGTCCGT CCCGTGGAAA
601 AGCAGGGGGG TGTTCCCTTC AGACGGCATC GGCACGCCCA AAATCTCACC
651 GTTCCATTTT GAAGCTTCCA CTTGCTGGA CGACACGGC ATTACCATTT
701 CCACCACCGG CAGCCCTTCT GTCCGCTTCA ACGCCGGCGG AGCGGATGCC
751 GCCGGCCTCG GCCTGCGTGC AGACACTTCC TTCCGCAACC TCCACCTGAC
801 CGCCCAAATC CCTACGCTGG CACTCAGGAA CAACAGCATT AAAATTGAAA
851 CCGTCAACGG CGCATTTACC GCCGGCGGCG AATATGCCCA ATGGGACGGT
901 TCGTTCAAAC TCGACAAAGC CAACCTGCAC TCCGGCATCG CCAACATCGG
951 CAACGCCGAA ATCTCCGGCA GCTTCAAAC ACCGCGCCAC CAGACCAACT
1001 TCTCCCTCAA TTCGCCGCTC GTATGGACGG AAAACAAAGG GCTGGACGCG
1051 CCGCGCCTGT ATGTATCGAC CCTTCAGGAT ACCGTCAACC GCCTGCCGCA
1101 ACCCCGTTTC ATCAGCCGGC TCGACGGTTC GCTGTCCGTA CCGAATCTGC
1151 AAAATTGGAA TGCCGAATTA AACGGCACAT TCGACCGCCA AACCCTTGCC
1201 GCGAAATTCA GATACACACA TGAAGACGCA CCGCATCTGG AAGCCGCCGT
1251 CGCACTGCAA AAATTGAACC TGACCCCTTA TCTTGACGAC GTGCGGCAAC
1301 AAAACGGCAA AATATTTCCT GACACCCTCG CCAAGCTGTC CGGCGACATC
1351 GAGGCGCACG TGAAAATCGG AAAAGTCCAA CTTCCTCGCC TGCAACTGGA
1401 CGATATGGAA ACCTACCTCC ACGCCGACAA AGGCCATATC GCGCTCAGCC
1451 GTTTCAGTTC AGGGCTTTAC GCGCGCCATA CCGAAGGCGG CATCAGCATC
1501 GCCAACACCC GTCCCGCCAC TTACCGCCTG CAACAGAATG CAAGCAACAT
1551 CCAAATCCAA CCGCTGCTGC AAGACCTGTT CGGCTTCCAC AGCTTCAGCG
1601 GCAACGGCGA CGCGGTATC GACCTGACCG CGGGCGGCGA AACCAGAAAA
1651 GAGCTTATCC GCTCGCTTCA GGGCAGCCTG TCGCTAAATA TTTCAACGG
1701 TGCAATGGCA GGTATCGACA TGGACAATAT CCGTAAAAAC GGCATTTCCG
1751 GCAAACTGTC CGACAATGCC GCACCCAGCA CACCCTTCCA CCGATTACAG
1801 CTTCAACAGC AATATTCAGA CGGCATCAGC CGCCACATCG ATACCGAACT
1851 CTTCTCCGAC AGCCTCTATG TTACCAGCAA CGGCTATACC AATCTGGATA
1901 CGCAGGAATT GTCTGAAGAT GTCCTTATCC GCAACGCCGT CCATCCGAAA
1951 AACAAACCGA TTCCCTGAA AATCACCAGT ACGGTGGACA AACCGTCCAT
2001 TACCGTCGAT TACGGCAGGC TGACCGGCGG CATCAATTCT CGCAAGAGAA
2051 AACAGAAATC CCTCGAAGAC ACCCTGCTGG AACAATGGCA GTGGCTCAAA
2101 CCTAAGAAGC CGTAA

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This corresponds to the amino acid sequence <SEQ ID 2656; ORF 771.a>:

## a771.pep

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1 MDLLSVFHKY RLKYAVAVLT ILLLAAGLH ASVYRIFTPE NIRSRLQQSI
51 AHTHRKISFD ADIQRRLPR PTVILKNLTI TEPGGDRTAV SVQETKIGLS
101 WKNLWSDQIQ IEKVVSSAE LALTRDGKGW WNIQDLIDSQ KRQASVNRII
151 VENSTVRLNF LQEQLILKEI NLNLQSPDSS GQPFESSGIL VWGKLSVPWK
201 SRGLFLSDGI GTPKISPFHF EASTSLDGHG ITISTGSPS VRFNAGGADA
251 AGLGLRADTS FRNLHLTAQI PTLALRNNSI KIETVNGAFT AGGEYAQWDG
301 SFKLDKANLH SGIANIGNAE ISGSFKTPRH QTNFSLNSPL VWTENKGLDA
351 PRLYVSTLQD TVNRLPQPRF ISRLDGSLSV PNLQWNAEL NGTFDRQTV
401 AKFRYTHEDA PHLEAAVALQ KNLTPYLDV VRQONGKIFP DTLAKLSGDI
451 EAHLKIGKVQ LPGQLDDME TYLHADKGIH ALSRFKSGLY GGHTGGISI
501 ANTRPATYRL QONASNIQIQ PLLQDLFGFH SFSNGDAVI DLTAGGETRK
551 ELIRSLQGS LSNISNGAWH GIDMDNILKN GISGKTADNA APSTPFHRFT
601 LNSEISDGI RHIDTELFSD SLYVTSNGYT NLDTOELSED VLIRNAVHPK
651 NKPIPLKITG TVDKPSITVD YGRLTGGIN S RKEQKILED TLEQWQWLK
701 PKEP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 771 shows 98.9% identity over a 704 aa overlap with a predicted ORF (ORF 771) from *N. meningitidis*

m771/a771 98.9% identity in 704 aa overlap

a771.pep	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQQSI	10	20	30	40	50	60
m771	MDLLSVFHKYRLKYAVAVLTILLAAIGLHASVYRIFTPENIRSRLQQSI	10	20	30	40	50	60
a771.pep	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKVVSSAE	70	80	90	100	110	120
m771	ADIQRRLPRPTVILKNLTITEPGGDRTAVSVQETKIGLSWKNLWSDQIQIEKVVSSAE	70	80	90	100	110	120
a771.pep	LALTRDGKGWNIQDLIDSQKRQASVNRIIVENSTVRLNQLQEQLILKEINLNQSPDSS	130	140	150	160	170	180
m771	LALTRDGKGWNIQDLIDSQKRQASVNRIIVENSTVRLNQLQEQLILKEINLNQSPDSS	130	140	150	160	170	180
a771.pep	GQPFESSGILVWGKLSVPWKSRLGLFLSDGIGTPKISPFHFEASTSLDGHGITISTGSPS	190	200	210	220	230	240
m771	GQPFESSGILVWGKLSVPWKSRLGLFLSNGIGPPEISPFHFEASTSLDGHGITISTGSPS	190	200	210	220	230	240
a771.pep	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPTLALRNNSIKIETVNGAFTAGGEYAQWDG	250	260	270	280	290	300
m771	VRFNAGGADAAGLGLRADTSFRNLHLTAQIPALALRNNSIKIETVNGAFTAGGEYARWDG	250	260	270	280	290	300
a771.pep	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	310	320	330	340	350	360
m771	SFKLDKANLHSGIANIGNAEISGSFKTPRHQTNFSLNSPLVWTENKGLDAPRLYVSTLQD	310	320	330	340	350	360
a771.pep	TVNRLPQPRFISRLDGSLSVNLQWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ	370	380	390	400	410	420
m771	TVNRLPQPRFISRLDGSLSVNLQWNAELNGTFDRQTVAAKFRYTHEDAPHLEAAVALQ	370	380	390	400	410	420
a771.pep	KNLTPYLDVVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGIH	430	440	450	460	470	480
m771	KNLTPYLDVVRQONGKIFPDTLAKLSGDI EAHLKIGKVQLPGLQLDDMETYLHADKGIH	430	440	450	460	470	480

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	490	500	510	520	530	540
a771.pep	ALS RFK SGL YGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
m771	ALS RFK SGL YGGHTEGGISIANTRPATYRLQQNASNIQIQPLLQDLFGFHSFSGNGDAVI					
	490	500	510	520	530	540
	550	560	570	580	590	600
a771.pep	DLTAGGETRKE LIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
m771	DLTAGGETRKE LIRSLQGSLSLNISNGAWHGIDMDNILKNGISGKTADNAAPSTPFHRFT					
	550	560	570	580	590	600
	610	620	630	640	650	660
a771.pep	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
m771	LNSEISDGISRHIDTELFSDSLYVTSNGYTNLDTQELSEDVLIRNAVHPKNKPIPLKITG					
	610	620	630	640	650	660
	670	680	690	700		
a771.pep	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPEPX					
m771	TVDKPSITVDYGRLTGGINSRKEKQKILEDTLLEQWQWLKPEPX					
	670	680	690	700		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2657>:

g772.seq

1	GTGTTCCGCA	CGGTCTTGCG	GACTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGTCGGCAAG	TTCTTTCAGG	TTGTTGCGTA	TGGTTTTCGG	GCGTTGGCGG
101	AAGGCGAGTT	TCACCAAGTT	GGCGAAATGA	TGCAATTCGT	CCGCCTTGCC
151	GATACGGTGT	TTACCCGGAA	TCATGCGCAC	CACGCGGAA	TCGATTTTCG
201	GCGCGGGATC	GAACGATTCG	GGCGGCACGT	CAATCAGCAG	CTCCATATCG
251	AAAAAATATT	GCAGCATCAC	ACCCAAGCGA	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATGCGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGGCGACATC	GTCGCCACCC	TCCGCCAGTT	TGAACAAAAG	CGGCGTGGAG
401	ATGTTATACG	GCAGGTTGCC	GACGATTTTC	TTTTTGCTTG	AGATGCCGTT
451	GAAATCAAAC	TGCAACACGT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTTCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATTG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCC	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC
701	TTGCGGGGCT	TGTGTTCTTT	CATCGTGTTC	CCTCTTCGGT	TGAAACCCCG
751	CCCTTAGGGG	CGGCAGGATC	AGACTCTGTT	TGGGCGGGGC	GTAACCCCTT
801	CCAAATCAGG	ACGACACATA	GGGCGGTGCT	TTATGTGTTC	TCCTGTGTGT
851	TGGAACATAA	ATGTGTTTAC	AGTATCCGTT	TGATGTCGGC	ATTGTAA

This corresponds to the amino acid sequence <SEQ ID 2658; ORF 772.ng>:

g772.pep

1	VFGTVLRTDA	DCLQIIVVGK	FFQVVAYGFA	ALAEGEFHQF	GEMIEIVRLA
51	DTVFHRNHAH	HCGIDFRRGI	ERFGRHVNQQ	LHIEKILQHH	TQATVVVAFR
101	RGNHALDHFF	LQHKVHIGDI	VRHLRQFEQK	RRGDVIRQVA	DDFLFA*DAV
151	EIKLQHVAFV	NHQFIRKRQR	FQTAYDVAVD	FDNVQAVQLF	RQRFNGCRQT
201	RADFNHDIIR	LRAHGVNDIA	DNPRVLQKIL	PETLAGFVFF	HRVSSSVETP
251	PFRAAGSDSV	WAGRNPFQIR	TTHRAVLVVS	SCVLEHKCVY	SIRLMSAL*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2659>:

m772.seq

1	ATGTTCCGCG	CGGTCTTGCG	GATTGATGCC	GACTGCCTGC	AAATCATCGT
51	CGCCTGCAAG	CTCTTTCAGA	TTGTTGCGTA	TGGTTTTCGG	GCGTTGGTGG
101	AAGGCGAGTT	TCACCAAGTT	GGCAAAATGC	TGCAATTCGT	CCGCCTTGCC
151	GATGCGGTGT	TTACCCGGAA	TCATACGGAC	GACGCGGAA	TCCACTTTCG
201	GCGCAGGGTC	GAACGATTCG	GGCGGTACGT	CAATCAGCAT	TTCCATATCG
251	AAAAAATATT	GCAGCATCAC	GCCCAAGCGG	CCGTAGTCGT	TGCTTTTCGG
301	CGCGGCAACC	ATACGCTCGA	CCACTTCTTT	TTGCAACATA	AAGTGCATAT
351	CGACGACATC	GTCGCCACCC	TCCGCCAGCT	TGAACAAAAG	CGGTGTGGAA
401	ATGTTGTACG	GGAGGTTGCC	GACGATTTTC	TTTTTGCTTG	CGATGCCGTT
451	GAAATCAAAC	TGCAATACAT	CGCCTTCGTG	AATCACCAGT	TTATCCGCAA
501	ACGGCAGCGT	TTTCAGACGG	CATACGATGT	CGCGGTCGAT	TTTCGACAACG
551	TGCAGGCGGT	TCAGCTTTTT	CGCCAAAGGT	TCGGTAATCG	CCGCCAAACC
601	CGGGCCGATT	TCAATCACGA	CATCATCCGC	CTGCGGGCGC	ACGGCGTTGA
651	CAATATCGCT	GATAATCCGC	GTGTCCTGCA	AAAAATTCTG	CCCGAAACGC

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701 TTGCGGGCTT TGTGTTCTTT CATCGTGTTC CTTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTTT
801 CCAAATCAGG ATGGCACATA GGGCGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2660; ORF 772>:

m772.pep

```

1 MFGAVLRIDA DCLQIIVACK LFOIVAYGFA ALVEGEFHEF GKMLEIVRLA
51 DAVFHRNHTD DGGIHFRRRV ERFGRYVNOH FHIKILQHH AQAAVVVAFR
101 RGNHTLDHFF LQHKVHIDDI VRHLRQLEQK RCGNVVREVA DDFLFACDAV
151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT
201 RADEFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP
251 PFRAVESDSI WEGRNSFQIR MAHRAVLVVS SCVLKHKCVY SIRLMSAL*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 772 shows 85.2% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. gonorrhoeae*

m772/g772 85.2% identity in 298 aa overlap

	10	20	30	40	50	60
g772.pep	VFGTVLRTDADCLQIIVGKFFQVVAYGFAALAEGEFHFQ	GEMIEIVRLADTVFHRNHAH				
m772	MFGAVLRIDADCLQIIVACKLFOIVAYGFAALVEGEFHEFGKMLEIVRLADAVFHRNHTD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g772.pep	HCGIDFRRGIERFGRHVNQQLHIEKILQHHTQATVVVAFRRGNHALDHFFLQHKVHIGDI					
m772	DGGIHFRRRVVERFGRYVNOHFHIEKILQHHAQAAVVVAFRRGNHTLDHFFLQHKVHIDDI					
	70	80	90	100	110	120
	130	140	150	160	170	180
g772.pep	VRHLRQFEQKRRGDVIRQVADDFLFAFXDAVEIKLQHVAFVNHQFIRKRQRFQTAYDVAVD					
m772	VRHLRQLEQKRCGNVVREVADDFLFACDAVEIKLQYIAFVNHQFIRKRQRFQTAYDVAVD					
	130	140	150	160	170	180
	190	200	210	220	230	240
g772.pep	FDNVQAVQLFRQRFGNCRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
m772	FDNVQAVQLFRQRFGNRRQTRADFNHDIIRLRAHGVNDIADNPRVLQKILPETLAGFVFF					
	190	200	210	220	230	240
	250	260	270	280	290	299
g772.pep	HRVSSSVETPPFRAAGSDSVWAGRNPFIQIRTHRAVLVSSCVLEHKCVYSIRLMSALX					
m772	HRVSFSVETPPFRAVESDSIWEGRNSFQIRMAHRAVLVSSCVLKHKCVYSIRLMSALX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2661>:

a772.seq

```

1 ATGTTTCGGCG CGGTCTTGCG GATTGATGCC GACTGCCTGC AAATCATCGT
51 CGCCTGCAAG CTCTTTCAGA TTGTTGCGTA TGGTTTTCGG GCGTTGGTGG
101 AAGCGGAGTT TCACGAGTTT GCGGAAATGC TCGAAATCGT CCGCCTTGCC
151 GATACGGTGT TTCACCGGAA TCATGCGGAC GACGGCCGAA TCCACTTTCG
201 GCGCGGGGTC GAACGATTTC GCGGCGACGT CAATCAGCAT TTCCATATCG
251 AAGAAATATT GCAGCATCAC GCCCAAGCGG CCGTAGTCGT TGCTTTTCGG
301 CGCGGCAACC ATACGATCGA CCACTTCTTT TTGCAGCATA AAGTGCATAT
351 CGACGACATC GTCCGCCACC TCCGCCAGCT TGAACAAAG CGGCGTGGAA
401 ATGTTGTAGG GCAGGTTGCC GACGATTTC TTTTTCCTG CGATGCCGTT
451 GAAATCAAC TGCAATACAT CGCCTTCGTG AATCACCAGT TTATCCGCAA
501 ACGGCAGCGT TTCAGACGG CATACGATGT CCGGTCGAT TTCGACAACG
551 TGCAGGCGGT TCAGCTTTT CGCCAAAGT TCGTAATCG CCGCCAAACC
601 CGGACCGATT TCAATCACGA CATCATCCGC CTGCGGGCGC ACGGCGTTGA
651 CAATATCGCT GATAATCCGC GTGTCCTGCA AAAAATTCG CCCGAAACGC
701 TTGCGGGGCTT TGTGTTCTTT CATCGTGTTC CTTTTTCGGT TGAACCCCG
751 CCCTTTAGGG CGGTAGAATC AGACTCTATT TGGGAGGGGC GTAACCTCTT
801 CCAAATCAGG ACGGCACATA GGGCGGTGCT TTATGTGTGC TCCTGTGTGT
851 TGAAACATAA ATGTGTTTAC AGTATCCGTT TGATGTCGGC ATTGTAA

```

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This corresponds to the amino acid sequence <SEQ ID 2662; ORF 772.a>:

a772.pep  
 1 MFGAVLRIDA DCLOIIVACK LFOIVAYGFA ALVEGEFHEF GEMLEIVRLA  
 51 DTVFHRNHAD DGRHFRRGV ERFGRHVNH FHIEEILQHH AQAQVVAFR  
 101 RGNHTIDHFF LQHKVHIDDI VRHLRQLEQK RRGNVVGQVA DDFLFACDAV  
 151 EIKLQYIAFV NHQFIRKRQR FQTAYDVAVD FDNVQAVQLF RQRFGNRRQT  
 201 RTDFNHDIIR LRAHGVNDIA DNPRVLQKIL PETLAGFVFF HRVSFSVETP  
 251 PFRAVESDSI WEGRNSFQIR TAHRVLYVS SCVLKHKCVY SIRLMSAL\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 772 shows 95.6% identity over a 298 aa overlap with a predicted ORF (ORF 772) from *N. meningitidis*

m772/a772 95.6% identity in 298 aa overlap

	10	20	30	40	50	60
a772.pep	MFGAVLRIDADCLQIIVACKL	FQIVAYGFAALVEGEFHEF	GEMLEIVRLADTVFHRNHAD			
m772	MFGAVLRIDADCLQIIVACKL	FQIVAYGFAALVEGEFHEFG	KMLEIVRLADAVFHRNHTD			
	10	20	30	40	50	60
	70	80	90	100	110	120
a772.pep	DGRHFRRGV	ERFGRHVNH	FHIEEILQHH	AQAQVVAFR	RGNHTIDHFF	LQHKVHIDDI
m772	DGGIHFRRR	VERFGRYV	NHGFHIEK	ILQHHQAQ	VVAFRGNHT	LDHFFLQHKVHIDDI
	70	80	90	100	110	120
	130	140	150	160	170	180
a772.pep	VRHLRQLEQK	RRGNVVGQVADDF	LACDAVEIKLQYIAF	VNHQFIRKRQR	FQTAYDVAVD	
m772	VRHLRQLEQK	RCGNVVREVADDF	LACDAVEIKLQYIAF	VNHQFIRKRQR	FQTAYDVAVD	
	130	140	150	160	170	180
	190	200	210	220	230	240
a772.pep	FDNVQAVQLF	RQRFGNRRQRT	DFNHDIIRLRAHGV	NDIADNPRVLQKIL	PETLAGFVFF	
m772	FDNVQAVQLF	RQRFGNRRQRT	ADFNHDIIRLRAHGV	NDIADNPRVLQKIL	PETLAGFVFF	
	190	200	210	220	230	240
	250	260	270	280	290	299
a772.pep	HRVSFSVETP	PFRAVESDSI	WEGRNSFQIR	TAHRVLYVS	SCVLKHKCVY	SIRLMSALX
m772	HRVSFSVETP	PFRAVESDSI	WEGRNSFQIR	MAHRVLYVS	SCVLKHKCVY	SIRLMSALX
	250	260	270	280	290	

g773.seq not found yet

g773.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2663>:

m773.seq  
 1 ATGGGATTGG GTGCAACGAC TTTTGTGCGT TCGGGTGCTA TAGGCGGAGG  
 51 TCTGTGCAGT ACCGGGATTG GCTGTGCGGC CGGTGGACTT ATTGCAACGG  
 101 CAGGTATGAC CGGTGGTTAT ACACAGGCCT CAGAAGGAAG CCGGCAATTG  
 151 TTTGGCACTT ACCAGTCCGA TTTTGGTAAA AAAGTTGTCC TATCTTTGGG  
 201 TACACCAATA GAATACGAAT CGCCGTTAGT ATCTGATGCG AAAAATCTAG  
 251 CCGTATGGGG ATTGGAAACG CTGATTACGC GCAAATGGG AAACCTGGCA  
 301 ACGGGTGTGA AAACCTCCTT GACTCCGAAA ACTGCTGACG TACAGCGAAA  
 351 TATCCTGTCC CAATCCGAAG TCGGTATCAA GTGGGGCAAG GGGATTGAAG  
 401 GACAGGGAAT GCCTTGGGAG GATTATGTCG GTAAGGGCTT GTCTGCCAAT  
 451 GCAAGGTTAC CTAAAAATTT TAAAAACATT GATTATTTTG ATCGTGGTAC  
 501 AGGCACGGCA ATCAGTGCCA AAACCTCTGA TACGCAAACT ACGGCACGCC  
 551 TGTCCAAACC CGAACAGCTT TACAGTACCA TGAAAGGGTA CATCGATAAG  
 601 ACGGCAAAAT TCAAAAGTTA TGAATTATCA GAAGTACCGT TAAGGGCAGA  
 651 CATGATCAAA CAGCGCGAAA TCCATCTGGC CATACCCGCA CAAACTAATA  
 701 AGGAGCAAAG ATTGCAGTTG CAACGTGTGG TAGAGTATGG CAAAAGTCAA  
 751 AACATTACAG TCAAAATTAC GGAGATCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 2664; ORF 773>:

m773.pep  
 1 MGLGATTFVG SGAIGGGLCS TGIGCAAGGL IATAGMTGGY TOASEGSRQL  
 51 FGTYQSDFGK KVVLSLGTPI EYESPLVSDA KNLAVWGLET LITRKLGNLA  
 101 TGVKTSITPK TADVQRNLS QSEVGKWK GIEGQGPWE DYVGKGLSAN  
 151 ARLPKNFKTF DYFDRGTGTA ISAKTLDQT TARLSKPEQL YSTMKGYIDK  
 201 TANFKSYELS EVPLRADMIK QREIHLAIPA QTNKEORLQL QRVVEYGKSO  
 251 NI TVKITEIE \*

a773.seq not found yet

a773.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2665>:

g774.seq  
 1 ATGAAGACCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCTGCCTC  
 51 CTGTGCTTCC GTTTTACCCG TTCCGGAGGG CAGCCGAACC GAAATGCCGA  
 101 CACAGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC CACTCTGCAA  
 151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAT  
 201 GGAATGTGTA AACGGGAAAG TCAAAGCATT GGAGCATACG AAAATACACC  
 251 CTTCGGCAG GACATACGTC CAAAACTCG ACGACCGCAA ATTGAAAGAG  
 301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CCGTCGAAAC  
 351 CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATCAA AACGGCAGGT  
 401 TTTCTGCCCG AGCCGCCTTG TTGAAGGGGG CGGACGGCGG AGACGGCGGC  
 451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT  
 501 GGGGAACGTG GAATCTGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT  
 551 TCAAAGACAG CCCAACCGCG CCCGAAGTCA TATTCAAAT CGGCGAATGC  
 601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGCGCT  
 651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGACGCG  
 701 TACGCAAAAC ATAG

This corresponds to the amino acid sequence <SEQ ID 2666; ORF 774.ng>:

g774.pep  
 1 MKTKLPLFII WLSVSASCAS VLPVPEGSRT EMPTOENASD GIPYPVPTLQ  
 51 DRLDYLEGKI VRLSNEVEML NGKVKALEHT KIHPSGRITYV QKLDRLKLE  
 101 HYLNTGGGSA SAHTVETAQN LYNQALKHYQ NGRFSAAAAL LKGADGGDGG  
 151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEVIFKIGEC  
 201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2667>:

m774.seq  
 1 ATGAAGATCA AATTACCGCT TTTTATCATT TGGCTGTCTG TGTCCGCCTC  
 51 CTGTGCTTCC GTTTTACCCG TTCCGGCAGG CAGCCAAACC GAAATGTGCA  
 101 CACGGGAAAA TGCTTCAGAC GGCATTCCCT ATCCCGTTCC GACCTTGCAA  
 151 GACCGTTTGG ACTATCTGGA AGGCAAAATC GTCCGGCTGT CGAACGAAAT  
 201 GGAACCTTA AACGGCAAAG TCAAAGCACT GGAACACGCA AAAACACATT  
 251 CTTCGGCAG GGCATACGTC CAAAACTCG ACGACCGCAA GTTGAAAGAG  
 301 CATTACCTCA ATACCGAAGG CGGCAGCGCA TCCGCACATA CTGTCGAAAC  
 351 CGCACAAAAC CTCTACAATC AGGCACTCAA AACTATAAA AGCGGCAAGT  
 401 TTTCTGCCCG TGCTCCCTG TTGAAGGGCG CGGACGGAGG CGACGGCGGC  
 451 AGCATCGCGC AACGCAGTAT GTACCTGTTG CTGCAAAGCA GGGCGCGTAT  
 501 GGGCAACTGC GAATCCGTCA TCGAAATCGG AGGGCGTTAC GCCAACCGTT  
 551 TCAAAGACAG CCAACCGCG CCTGAAGCCA TGTTCAAAT CGGCGAATGC  
 601 CAATACAGGC TTCAGCAAAA AGACATTGCA AGGGCGACTT GGCAGCGCT  
 651 GATACAGACC TATCCCGGCA GCCCGCGGCG AAAACGCGCC GCCGACGCG  
 701 TGCGCAAAAC ATAG

This corresponds to the amino acid sequence <SEQ ID 2668; ORF 774>:

m774.pep  
 1 MKIKLPLFII WLSVSASCAS VSPVPAGSQT EMSTRENASD GIPYPVPTLQ  
 51 DRLDYLEGKI VRLSNEVETL NGKVKALEHA KTHSSGRAYV QKLDRLKLE  
 101 HYLNTGGGSA SAHTVETAQN LYNQALKHYK SGKFSAAASL LKGADGGDGG  
 151 SIAQRSMYLL LQSRARMGNC ESVIEIGGRY ANRFKDSPTA PEAMFKIGEC  
 201 QYRLQKQDIA RATWRSLIQT YPGSPAARKA AAARVRK\*

Computer analysis of this amino acid sequence gave the following results:



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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 774 shows 92.8% identity over a 237 aa overlap with a predicted ORF (ORF 774) from *N. gonorrhoeae*

m774/g774 92.8% identity in 237 aa overlap

	10	20	30	40	50	60
g774.pep	MKTKLPLFIWLSVSASCSVLPVPEGSRTQENASDGIYPVPTLQDRLDYLEGKI					
m774	MKIKLPLFIWLSVSASCSVSPVAGSQTEMSTRENASDGIYPVPTLQDRLDYLEGKI					
	10	20	30	40	50	60
	70	80	90	100	110	120
g774.pep	VRLSNEVEMLNGKVKALEHTKIHPSGRTYVQKLDLDRKLKEHYLNTGEGSASAHTVETAQN					
m774	VRLSNEVETLNGKVKALEHAKTHSSGRAYVQKLDLDRKLKEHYLNTGEGSASAHTVETAQN					
	70	80	90	100	110	120
	130	140	150	160	170	180
g774.pep	LYNQALKHYQNGRFSAAAALLKGADGGDGGGSAQRSMYLLQSRARMGNCSVIEIGGRY					
m774	LYNQALKHYKSGKFSAAASLLKGADGGDGGGSAQRSMYLLQSRARMGNCSVIEIGGRY					
	130	140	150	160	170	180
	190	200	210	220	230	
g774.pep	ANRFKDSPTAPEVIFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAAARVRKR					
m774	ANRFKDSPTAPEAMFKIGECQYRLQKDIARATWRSLIQTYPGSPAARAAAARVRKR					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2669>:

a774.seq

1	ATGAAGACCA	AATTACCGCT	TTTTATCATT	TGGCTGTCCG	TATCCGCCGC
51	CTGTTCTTCC	CCTGTTTCCC	GCAATATTCA	GGATATGCGG	CTCGAACC GC
101	AGGCAGAGGC	AGGTAGTTCG	GACGCTATTC	CCTATCCCGT	TCCCACTCTG
151	CAAGACCGTT	TGGATTATCT	GGAAGGCACA	CTCGTCCGCC	TGTCGAACGA
201	AGTGGAAACC	TTAAACGGCA	AAGTCAAAGC	ACTGGAGCAT	GCGAAAACAC
251	ACCCCTCCAG	CAGGGCATA	GTCCAAAAAC	TCGACGACCG	CAAGTTGAAA
301	GAGCATTACC	TCAATACCGA	AGGCGGCAGC	GCATCCGCAC	ATACCGTCGA
351	AACCGCACAA	AACCTCTACA	ATCAGGCACT	CAAACACTAT	AAAAGCGGCA
401	GGTTTCTGCG	CGCTGCCTCC	CTGTTGAAAG	GCGCGGACGG	AGGCGACGGC
451	GGCAGCATCG	CGCAACGCAG	TATGTACCTG	TTGCTGCAAA	GCAGGGCGCG
501	TATGGGCAAC	TGCGAATCCG	TCATCGAAAT	CGGAGGGCGT	TACGCCAACC
551	GTTTCAAAGA	CAGCCCAACC	GCGCCTGAAG	CCATGTTCAA	AATCGGCGAA
601	TGCCAATACA	GGCTTCAGCA	AAAAGACATT	GCAAGGGCGA	CTTGGCGCAG
651	CCTGATACAG	ACCTATCCCG	GCAGCCCGGC	GGCAAAACGC	GCCGCGCGAG
701	CCGTGCGCAA	ACGATAG			

This corresponds to the amino acid sequence <SEQ ID 2670; ORF 774.a>:

a774.pep

1	MKTKLPLFIIWLSVSACSS	PVSRNIQDMR	LEPQAEAGSS	DAIPYPVPTL
51	QDRLDYLEGT	LVRLSNEVET	LNGKVKALEH	AKTHPSSRAY
101	EHYLNTEGGS	ASAHTVETAQ	NLYNQALKHY	KSGRFSAAAS
151	GSIAQRSMYL	LLQSRARMGN	CESVIEIGGR	YANRFKDSPT
201	CQYRLQKDI	ARATWRS LIQ	TYPGSPAAR	AAAARVRK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 774 shows 89.5% identity over a 238 aa overlap with a predicted ORF (ORF 774) from *N. meningitidis*

m774/a774 89.5% identity in 238 aa overlap

	10	20	30	40	50	60
a774.pep	MKTKLPLFIIWLSVSACSSPVSRNIQDMRLEPQAEAGSSDAIPYPVPTLQDRLDYLEGT					
m774	MKIKLPLFIIWLSVSASCS-VSPVAGSQTEMSTRENASDGIYPVPTLQDRLDYLEGK					
	10	20	30	40	50	

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      70      80      90      100      110      120
a774.pep  LVRLSNEVETLNGKVKALEHAKTHPSSRAYVQKDDRKLKEHYLNTGGSASAHTVETAQ
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      IVRLSNEVETLNGKVKALEHAKTHSSGRAYVQKDDRKLKEHYLNTGGSASAHTVETAQ
          60      70      80      90      100      110

      130      140      150      160      170      180
a774.pep  NLYNQALKHYKSGRFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGNCESVIEIGGR
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      NLYNQALKHYKSGKFSAAASLLKGADGGDGGSIQRSMYLLQSRARMGNCESVIEIGGR
          120      130      140      150      160      170

      190      200      210      220      230      239
a774.pep  YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAKRAAAVRRRX
          :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m774      YANRFKDSPTAPEAMFKIGECQYRLQOKDIARATWRSLIQTYPGSPAAKRAAAVRRRX
          180      190      200      210      220      230

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g790.seq not found yet

g790.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2671>:

```

m790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATAGTC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ATGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTACAGC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCTTCGCA GTACACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA CTTGCTGGTG GTCGAGCCGC GTATGTGCCC
651 TGCGGACGAA GACATCGCGC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG
751 GGCAGGCCGT CTGAAGCCTT TGACCTGCCC GAAGGCAGCA CGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCGC AGGCAAGAAG
851 GCGTGTTGAT TCGGATTACC GCCCCTGATG TGTGGACGGT TGGTATGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2672; ORF 790>:

```

m790.pep
1  MARRSKTFEE AAAEVEERFG HRGIKVEFE GTAKPCVINC PKHGNQTCR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTOAYNEMT KSVAGSNSIV LNDVQGDTTI NNHHTHTNNH SDADGKALSM
151 RLTPRPLLSL RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIEKGDLLV VEPKPCPADE DIALIELSDK RLVVAHLVID IAGRMLIYQT
251 GRPSEAFDLP EGSTILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGMI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNPN NA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2673>:

```

a790.seq
1  ATGGCAAGAA GGTCAAAAAC ATTTGAAGAA GCTGCTGCTG AGGTTGAGGA
51  ACGTTTCGGT CATCGTGGCA TTAAGTTGGT CGAGTTTGAG GGTACAGCCA
101 AGCCGTGTGT AATCAACTGC CCTAAACATG GAAACCAAAC CTGTTTCGAGG
151 TACTCCAATA TGTTCATAGG AAGTAGCTGG GGTGCCCCCT CTTGTGGTAA
201 TGAGCAAGCT GCAAAAGCCG GTATAGCGAC CCTTAGGAAG AATCACATAG
251 CGTTAGAAAT GCTGAAACAG GCTGTAACAG GTATGACCAA GCAAGAGCGC
301 ATCACGACGC AAGCCTACAA TGAGATGACC AAATCCGTGG CAGGTTCAAA
351 CAGCATATC CTTAACGATG TCCAAGGCGA TACGACCATC AACAACCATC
401 ATACGCATAC GCACAACCAC AGCGATGCCG ACGGCAAAGC ACTGTCGATG
451 AGGCTCACAC CCCGTCCTTT GTTGTACAGC CGTCAGGCGG CGGCTTTCGC
501 CCGTACAGGC AAACCTACGG GCAGTTTCGA CCTGTTTGCT TCGGTGGTTCG
551 CCCCTTCACA ATATACGTTT GCCGTTGCCA TGCCCGACAC GTCCATGTCTG
601 CCGGTTATCG AAAAGGGAGA TTTGCTGGTG GTCGAGCCGC GTATGCGCCC
651 TGCGGACGAA GACATCGTAC TGATTGAACT GTCCGACAAG CGGCTGGTTCG
701 TCGCGCACCT TGTTATCGAT ATTGCGGGCA GGATGCTGAT TTATCAGACG

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751 GGCAGGCCGT CTGAAGCCCT CGACCTGCCC GAAGGCAGCG TGATTTTAGG
801 TGTGGTGCTG GAGTCAAAAA ACGGTTTATG TCCGCCGCAC AGGCAAGAAG
851 GCGTGTGTAT TCGGATTACC GCCCTGATG TGTGGACGGT TGGTACGATT
901 TCCGCTTCCA AAACGTCGTG TACGCGCCCG ACCGCAGCCC GGAAATCAGC
951 CGTATGCTTT CTTGATTTT GGCAGGCTAC GCGTGGGATA CCGAAAACCC
1001 GTTCGTGGCG AAATCCGAAC AACGCCTGT

```

This corresponds to the amino acid sequence <SEQ ID 2674; ORF 790.a>:

```

a790.pep
1  MARRSKTFEE AAEEVEERFG HRGIKLVEFE GTAKPCVINC PKHGNQTCRSR
51  YSNMFIGSSW GCPSCGNEQA AKAGIATLRK NHIALEMLKQ AVTGMTKQER
101 ITTQAYNEMT KSVAGSNSII LNDVQGDTTI NNHHTHTNH SDADGKALSM
151 RLTPRPLSD RQAAAFARTG KLTGSFDLFA SVVAPSQYTF AVAMPDTSMS
201 PVIKGDLLV VEPRMRPADE DIVLIELSDK RLVV AHLVID IAGRMLIYOT
251 GRPSEALDLP EGSVILGVVL ESKNGLCPPH RQEGVLIRIT APDVWTVGTI
301 SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 790 shows 98.2% identity over a 342 aa overlap with a predicted ORF (ORF 790) from *N. meningitidis*

```

a790/m790    98.2% identity in 342 aa overlap

          10      20      30      40      50      60
a790.pep    MARRSKTFEEAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
m790         MARRSKTFEEAAEEVEERFGHRGIKLVEFEGTAKPCVINC PKHGNQTCRSRYSNMFIGSSW
          10      20      30      40      50      60

          70      80      90     100     110     120
a790.pep    GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSII
m790         GCPSCGNEQA AKAGIATLRKNHIALEMLKQAVTGMTKQERITTQAYNEMTKSVAGSNSIV
          70      80      90     100     110     120

          130     140     150     160     170     180
a790.pep    LNDVQGDTTINNHHTHTNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
m790         LNDVQGDTTINNHHTHTNHSDADGKALSMRLTPRPLSDRQAAAFARTGKLTGSFDLFA
          130     140     150     160     170     180

          190     200     210     220     230     240
a790.pep    SVVAPSQYTF AVAMPDTSMS PVIKGDLLVVEPRMRPADE DIVLIELSDKRLVV AHLVID
m790         SVVAPSQYTF AVAMPDTSMS PVIKGDLLVVEPRMCPAEDIALIELSDKRLVV AHLVID
          190     200     210     220     230     240

          250     260     270     280     290     300
a790.pep    IAGRMLIYQTGRPSEALDLPESVILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGTI
m790         IAGRMLIYQTGRPSEAFDLPEGSTILGVVLESKNGLCPPHRQEGVLIRITAPDVWTVGMI
          250     260     270     280     290     300

          310     320     330     340
a790.pep    SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAC
m790         SASKTSCTRP TAARKSAVCF LRFWQATRGI PKTRSWRNP NAX
          310     320     330     340

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2675>:

```

g791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CTA CTGTTT
51  TGGTTTGT TTGGTTTT GTGTATTGG AGTGGGCTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAAC TGCCGT CTTTGGATTC TTG CAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGCGGATG GAGAAGTCAT
201 CCGTATGTAT GGGGAGCAGC GGCGCGAATT TACAAAATC GGCGATTTC
251 CCGAGGTGTT GCGGAATGCG GTTATTGCCG CCGAGGATAA ACGCTTTTAC
301 CCGCATTGGG GGGTGGATGT TTGGGGTGT GCCCGGCTG CCGTCGCAA
351 TGTCGTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACACAGCAGG

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401 TGGCGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTTGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCTATG
551 GTTTTGATC TGCCGCGCAA ATCTATTTCATAAAGATGT CCGAGATTG
601 ACTTTGCGG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CGGAGCGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCATTGA ATGAGGAAT GCATTATGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAATGGT GCGTCGGGAA CTGTATGAGA
851 AATATGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCACCAGATC ATCAGAAGGC GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTTCGAT CGCGGCAGCA GCTACCGCGG TGCGGAAAC TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCGCC GTTGTGTGG ATGTTACTAA
1101 AAGAAAAAT GTCTCATAC AGCTGCCCGG CGGCAGCGCG GTTGCCTTG
1151 AGAGCGCGC CTTGGGTTT GCGGCCGAG CGGTCGATAA TGAGAAATG
1201 GGGGAGGACC GTATCCGCG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGTTT AAGAGCCGTT GGTGACGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTGACCTTT AAGCCGTTT TCTATTCGGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCTGCC GGGGAAAGGG
1501 CGGAACGGT CCGTTTGAC ACCTAAAAAT TCAGACGGCA GATATTCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCGTATTTT GATGTCTATC GGTGTCGGT ACGCGCAACA GTATATCCGG
1651 CGTTTCGGCT TCAGGCGGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACGACGC CGTTGAAAGT GCGCGAGGCA TATAGTGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTCGC ACGTGATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCAGGGCA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTCGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGT ACGACCAACG ACAATAAGA
2001 TGCGTGGTTT GTCGGTTTA ACCCTGATGT GGTACTGCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG CCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAAGGG ATGAAATGC CTGAAGGTGT GGTACGACG AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAT GCTGGACAAC
2251 AGCGGTATTG CGCCGCAACC TTCCGACGG GCAAAGAAG ATGATGAAGC
2301 GGCAGTAGAA AACGAACAGC AGGGAAGGTC TGACGAAACG CGTCAGGACG
2351 TACAGGAAAC GCCGTGCTT CCGAGCAATA CGGATTCCAA ACAGCAGCAG
2401 TTGGATTCCC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2676; ORF 791.ng>:

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g791.pep
1  MVNYYSAMIK KILTTCEGLF FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWGV ARAAVGNVVS GSVQSGASTI TQOVAKNFYL SSEKTETRFK
151 NEVLAYKIE QSLSKDKILE LYFNQIYLQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR OKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRRE LYEKYGEDAY TQGFVKYTTV
301 RTDHQKAATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGGRR VALDRRALGF AARAVDNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPLQG ALVSLDAKTG AVRALVGGYD
451 FHSKTFNRAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSYIIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRPSELF ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKIY
601 DRDGLRLAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRAGYGGTI
701 AVPVWVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLMLDN
751 SGIAQPQSRK AKEDDEAAVE NEQQGRSDET RQDVQETPVL PSNTDSKQQQ
801 LDSLF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2677>:

```

m791.seq
1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTC
51  TGTTTGGTT TTTGGGTTT GTGATTATGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGCGGCT CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGAATT TACAAAAATC GCGGATTTC
251 CAGAGGTGTT GCGGAATGCG GTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGATTTGGG GGGTGGATGT TTGGGGTGT GCGGCGGCTG CCGTCGCGAA
351 TGTGCTGTCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGCGGAAAAA TTTTATTG AGCAGTGAAA AAACGTTTAC ACGCAAATTC

```

1268

```

451 AATGAGGTGT TGCTTGCCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCCGCGCAA ATCTATTTC AATAAGATGT CCGAGATTTG
601 ACTTTGGCCG AAGCCGCCAT GCTTGCGGGA CTGCCAAGG CTCCGTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCGCGAT
751 CAGGCGTTGA ATGAGGAAC TGCATTACGAG CGGTTTGTTT GGAAATCGA
801 TCAGAGTGGG TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTCGAT CGCGGCAGCA GCTACCGCGG TCGGAAAAAT TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTGCGGA
1051 CTCTATACCG TCGATAAAAT GGTTCGCCG GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTGCGGTTT GCGGCCCGCG CGGTCAATAA TGAAAAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGCGGTTGG GCGGTGTTT AAGAGCGGTT GCTGCAGGGG GCTTTGGGTT
1301 CGCTGGATGC AAAAACCGGA GCTGTGCGCG CGCTGGTCGG CGGTTATGAT
1351 TTTCACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTT TCTATTCCGC GGCATTATCT AAGGGGATGA
1451 CC GCGTCCAC AGTGGTTAAC GATGCGCCGA TTTCCCTGCC GGGGAAAGGG
1501 CC GACCGGTT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCGGTATTTT GATGTCATC GGTGTGCGTT ACGCGCAACA GTATATCCGG
1651 CGTTTTCGGT TCAGGTGCTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GGCAGGAGCA TATAGCGTAT
1751 TTGCGAACCG CGGATATAGG GTTCTTCGCG ACGTAATCGA TAAGATTTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAATG CAACCTTTGG TGGCTGGGCA
1851 AAATGCGCGC CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGGTACGG CAAGGGGGGC AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACCGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCTG GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCGCG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAATGTC CTGAAGGTGT GGTACGAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAA
2251 AGCGGTATG CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGCGACGGC AGCGCGCGGA TGACGAAGTC CGCCAAGATA
2351 TGCAAGAAAC GCCGCTGCTT CCGAGTAATA CTGTTTCCAA ACAGCAGCAG
2401 TTGGATTCTC TGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2678; ORF 791>:

```

m791.pep
1  MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG VARAAGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTRKF
151 NEVLLAYKIE QSLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LPKAPSAYNP IVNPERAKLR QKYILNNMLE EKMITVQQRD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHOKVATE ALRKALRNFD RGSSYRGAEN YIDLKSEDEV EETVSQYLSG
351 LYTVDMKMPA VVLDTKKKN VVIQLPGGRR VTLDRRALGF AARAVNNEKM
401 GEDRIRRGAV IRVKNNGGRW AVVQEPQLQG ALGSLDARTG AVRALVGGYD
451 FHSKTFNRVAV QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKRY
601 DRDGRLLRAQM QPLVAGQNAQ QAIDPRNAYI MYKIMQDVVR VGTARGAAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPDVVTA VYIGFDKPKS MGRVGYGGTI
701 AVPVVVDYMR FALKGKQKKG MKMPEGVVSS NGEYMKERM VTDPLGLTDN
751 SGIAPOPSRR AKEDDGAAE GGRQAADDEV RQDNQETPVL PSNTGSKQQQ
801 LDSLF*

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g791/m791 97.3% identity in 805 aa overlap

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          10      20      30      40      50      60
g791.pep  MVNYYSAMIKKILTTFCGLFFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          |||
m791      MVNYYSAMIKKILTTFCGLVFGFCVFGVGLVAIAILVTYPKLPSLDSLQHYQPKMPLTIY
          10      20      30      40      50      60

          70      80      90     100     110     120
g791.pep  SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
          |||
m791      SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVVDVWGVARAAVGNVVS
          70      80      90     100     110     120

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1269

	130	140	150	160	170	180
g791.pep	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ					
	130	140	150	160	170	180
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
g791.pep	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLPKAPSAYNPIVNPERAKLRQKYILNNMLE					
	190	200	210	220	230	240
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
g791.pep	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRRELYEKYGEDAYTQGFVYTTV					
	250	260	270	280	290	300
g791.pep	RTDHQKAATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
g791.pep	RTDHQKAATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDVEETVSQYLSGLYTVDKMVPA					
	310	320	330	340	350	360
g791.pep	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
g791.pep	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
m791	VVLDVTKKKNVVIQLPGGRRVALDRRALGFAARAVDNEKMGEDRIIRGAVIRVKNNGGRW					
	370	380	390	400	410	420
g791.pep	AVVQEPPLQAGLVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPPLQAGLVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
g791.pep	AVVQEPPLQAGLVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
m791	AVVQEPPLQAGLVSLDAKTGAVRALVGGYDFHSKTFNRAVQAMRQPGSTFKPFVYSAALS					
	430	440	450	460	470	480
g791.pep	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
g791.pep	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLQALTASKNMVSIRILMSI					
m791	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLQALTASKNMVSIRILMSI					
	490	500	510	520	530	540
g791.pep	GVGYAQYIRRFGRFSELPAISLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQYIRRFGRFSELPAISLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
g791.pep	GVGYAQYIRRFGRFSELPAISLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
m791	GVGYAQYIRRFGRFSELPAISLMAAGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY					
	550	560	570	580	590	600
g791.pep	DRDGRRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
g791.pep	DRDGRRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
m791	DRDGRRLAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG					
	610	620	630	640	650	660
g791.pep	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGGYGGTIAVPVWVDYMRFALKGKGK					
m791	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGGYGGTIAVPVWVDYMRFALKGKGK					
	670	680	690	700	710	720
g791.pep	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGGYGGTIAVPVWVDYMRFALKGKGK					
m791	TTNDNKDAWFVGFNPDVVTAVYIGFDKPKSMGRVGGYGGTIAVPVWVDYMRFALKGKGK					
	670	680	690	700	710	720
g791.pep	MKMPEGVVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
	730	740	750	760	770	780
g791.pep	MKMPEGVVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
m791	MKMPEGVVSSNGEYMKERMVTDPLGLMLDNSGIAPQPSRRAKEDDEAAVENEQQGRSDET					
	730	740	750	760	770	780
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDVQETPVLPSNTDSKQQQLDSLFX					
	790	800				
g791.pep	RQDVQETPVLPSNTDSKQQQLDSLFX					
m791	RQDVQETPVLPSNTDSKQQQLDSLFX					
	790	800				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2679>:

1270

a791.seq

```

1  ATGGTAAATT ATTATTCAGC TATGATTAAA AAGATTTTAA CGACTTGTTT
51  TGGTTTGGTT TTTGGGTTTT GTGTATTGGG AGTGGGTTTG GTTGCCATTG
101 CTATTTTGGT AACGTATCCG AAACGTGCCG CTTTGGATTG TTTGCAGCAT
151 TACCAGCCTA AAATGCCGTT GACTATTTAT TCGGCGGATG GGAAGTCAT
201 CGGTATGTAT GGGGAGCAGC GCGCGCAATT TACAAAAATC GGCATTTC
251 CAGAGGTGTT GCGGAATCGG GTTATCGCCG CCGAGGATAA ACGCTTTTAC
301 CGGCATTGGG GGGTGGATGT TTGGGGTGTT GCCCGCGCTG CCGTCGGCAA
351 TGTCTGTGCC GGCAGCGTGC AGTCGGGTGC GAGTACGATT ACGCAGCAGG
401 TGGCGAAAAA TTTTATTG AGCAGTAAA AAACGTTTAC ACGCAAATTC
451 AATGAGGTGT TGCTTGCCTA TAAATCGAG CAGTCTTTAA GCAAAGACAA
501 AATCCTCGAG TTGTATTCA ATCAGATTTA CCTCGGTCAG CGCGCCTATG
551 GTTTTGCATC TGCCGCGCAA ATCTATTTCA ATAAGAATGT CCGAGATTTG
601 ACTTTGGCGG AAGCCGCCAT GCTTGCGGGA CTGCCCAAGG CTCGCTCTGC
651 CTATAATCCG ATTGTTAATC CAGAACGTGC CAAGTTGCGC CAGAAGTATA
701 TTTTGAACAA TATGCTCGAG GAGAAGATGA TTACCGTGCA ACAGCCCGAT
751 CAGGCGTTGA ATGAGGAACT GCATTACGAG CGGTTTGTTT GGAATAATCGA
801 TCAGAGTGCT TTATATGTGG CGGAAATGGT GCGTCAGGAA CTGTATGAGA
851 AATACGGTGA AGATGCCTAT ACGCAGGGTT TTAAGGTTTA TACCACGGTC
901 CGCGCCGATC ATCAGAAGGT GGCAACCGAG GCATTGCGCA AGGCTCTACG
951 GAATTTGATC CGCGGCAGCA GCTACCGCGG TGCGGAAAAA TATATCGATT
1001 TGAGTAAGAG TGAAGATGTC GAGGAGACTG TCAGCCAGTA TCTGTCGGGA
1051 CTCTATACCG TCGATAAAAT GGTTCCCGCC GTTGTGTTGG ATGTGACTAA
1101 AAAGAAAAAT GTCGTCATAC AGCTGCCCGG CGGCAGGCGG GTTACGCTTG
1151 ACAGGCGCGC CTTGGGTTTT GCGGCGCGCG CGGTCAATAA TGAATAAATG
1201 GGGGAGGACC GTATCCGCAG GGGCGCGGTC ATCCGTGTCA AAAACAACGG
1251 CGGGCGTTGG GCGGTGGTTC AAGAGCCGTT GCTGCAGGGG GCTTTGGTTT
1301 CGCTGGATGC AAAAACCAGA GCTGTGCGCG CGCTGGTCCG CGGTTATGAT
1351 TTTTACAGCA AAACATTCAA TCGTGCCGTT CAGGCAATGC GGCAGCCGGG
1401 TTCGACCTTT AAGCCGTTTG TCTATTGCGC GGCATTATCT AAGGGGATGA
1451 CCGCGTCCAC AGTGGTTAAC GATGCGCCGA TTCCCTGCCC GGGGAAAGGG
1501 CGTGAACGGT CGGTTTGGAC ACCTAAAAAT TCAGACGGCA GATATTCCGG
1551 CTACATTACT TTGAGACAGG CTCTGACGGC TTCCAAGAAT ATGGTTTCCA
1601 TCCGTATTTT GATGCTATC GGTGTCGGTT ACGCGCAACA GTATATCCGG
1651 CGTTTTCGCT TCAGGTCGTC CGAGCTGCCG GCAAGCCTGT CTATGGCTTT
1701 AGGTACGGGC GAGACAACGC CGTTGAAAGT GCGGAGGCA TATAGCGTAT
1751 TTGCGAACGG CGGATATAGG GTTCTTTCGC ACGTAATCGA TAAGATTAT
1801 GACAGAGACG GCAGGTTGCG CGCCCAAATG CAACCTTTGG TGGCCGGGGA
1851 AAATGCGCCT CAGGCAATCG ATCCGCGCAA TGCCTATATT ATGTATAAGA
1901 TTATGCAGGA TGTGGTCCGT GTTGTACGG CAAGGGGGGG AGCTGCGTTG
1951 GGAAGAACGG ATATTGCCGG TAAACGGGT ACGACCAATG ACAATAAGGA
2001 TGCGTGGTTT GTCGGTTTTA ACCCTGATGT GGTACTGCCC GTATATATCG
2051 GCTTCGACAA ACCTAAGAGT ATGGGGCGTG TCGGCTACGG CGGTACGATT
2101 GCGGTGCCGG TTTGGGTGGA CTATATGCGT TTTGCGTTGA AAGGAAAGCA
2151 GGGCAAGGGG ATGAAAATGC CTGAAGGTGT GGTGAGCAGC AATGGCGAAT
2201 ACTATATGAA GGAACGTATG GTAACCGATC CGGGCTTGAC GCTGGACAAC
2251 ACGCGGTATT CGCCGCAACC TTCCCGACGG GCAAAAGAAG ATGACGGGGG
2301 CGCGGCAGAA GCGGACGCGC AGCGGCGGGA TGACGAAGTC CGCCAAGATA
2351 TGCAGGAAAC GCCGGTGCTT CCGAGTAATA CTGGTTCCAA ACAGCAGCAG
2401 TTGGAATCTC TGTTTTAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 2680; ORF 791.a&gt;:

a791.pep

```

1  MVNYYSAMIK KILTTFCGLV FGFCVFGVGL VAIAILVTYP KLPSLDSLQH
51  YQPKMPLTIY SADGEVIGMY GEQRREFTKI GDFPEVLRNA VIAAEDKRFY
101 RHWGVVDVWG ARAAVGNVVS GSVQSGASTI TQQVAKNFYL SSEKTFTTRKF
151 NEVILLAYKIE QLSKDKILE LYFNQIYLGQ RAYGFASAAQ IYFNKNVRDL
201 TLAEAAMLAG LFKAPSAYNP IVNPERAKLR OKYILNNMLE EKMITVQORD
251 QALNEELHYE RFVRKIDQSA LYVAEMVRQE LYEKYGEDAY TQGFVYTTV
301 RADHQKVATE ALRKALRNFD RGSSYRGAEN YIDLSKSEDE EETVSQYLSG
351 LYTVDKMVPA VVLDVTKKKN VVIQLPGRR VTLDRRALGF AARAVNNEKM
401 GEDRIIRGAV IRVKNNGGRW AVVQEPILQG ALVSLDARTG AVRALVGGYD
451 FHSKTFNRVA QAMRQPGSTF KPFVYSAALS KGMTASTVVN DAPISLPGKG
501 PNGSVWTPKN SDGRYSGYIT LRQALTASKN MVSIRILMSI GVGYAQQYIR
551 RFGFRSSELP ASLSMALGTG ETTPLKVAEA YSVFANGGYR VSSHVIDKLY
601 DRDGRRLRAQM QPLVAGQNAP QAIDPRNAYI MYKIMQDVVR VGTARGAAL
651 GRTDIAGKTG TTNDNKDAWF VGFNPVDTA VYIGFDKPKS MGRVGYGGTI
701 AVPVVVDYMR FALKGKQKRG MKMPEGVVS NGEYMKERM VTDPLGLTDN
751 SGIAPOPSRR AKEDDGGAAE GGRQAADDEV RQDMQETPVL PSNTGSKQQQ
801 LDSLF*

```

a791/m791 99.9% identity in 805 aa overlap

10

20

30

40

50

60

1271

a791.pep	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVITYPKLPSLDSLOHYQPKMPLTIY
m791	MVNYYSAMIKKILTTTCFGLVFGFCVFGVGLVAIAILVITYPKLPSLDSLOHYQPKMPLTIY
	10 20 30 40 50 60
a791.pep	70 80 90 100 110 120
m791	SADGEVIGMYGEQRREFTKIGDFPEVLRNAVIAAEDKRFYRHWGVDVWGVARAAVGNVVS
	70 80 90 100 110 120
a791.pep	130 140 150 160 170 180
m791	GSVQSGASTITQQVAKNFYLSSEKTFTRKFNEVLLAYKIEQSLSKDKILELYFNQIYLGQ
	130 140 150 160 170 180
a791.pep	190 200 210 220 230 240
m791	RAYGFASAAQIYFNKNVRDLTLAEAAAGLGLPKAPSAYNPVNPRAKLRQKYILNNMLE
	190 200 210 220 230 240
a791.pep	250 260 270 280 290 300
m791	EKMITVQQRDQALNEELHYERFVRKIDQSALYVAEMVRQELYEKYGEDAYTQGFVYTTV
	250 260 270 280 290 300
a791.pep	310 320 330 340 350 360
m791	RADHQKVATEALRKALRNFDGSSYRGAENYIDLSKSEDEETVSQYLSGLYTVDKMVP
	310 320 330 340 350 360
a791.pep	370 380 390 400 410 420
m791	VVLDVTKKKNVVIQLPGGRRVTLDRRALGFAARAVNNEKMGEDRIRRGAVIRVKNNGGRW
	370 380 390 400 410 420
a791.pep	430 440 450 460 470 480
m791	AVVQEPLLQALVSLDAKTGAVRALVGGYDFHSTFNRAVQAMRQPGSTFKPFVYSAALS
	430 440 450 460 470 480
a791.pep	490 500 510 520 530 540
m791	KGMTASTVVNDAPISLPKGPNGSVWTPKNSDGRYSGYITLRQALTASKNMVSIIRILMSI
	490 500 510 520 530 540
a791.pep	550 560 570 580 590 600
m791	GVGYAQYIIRRFGRSSSELPASLSMALGTGETTPLKVAEAYSVFANGGYRVSSHVIDKIY
	550 560 570 580 590 600
a791.pep	610 620 630 640 650 660
m791	DRDGRRLRAQMQLVAGQNAPOAIDPRNAYIMYKIMQDVVRVGTARGAAALGRTDIAGKTG
	610 620 630 640 650 660
a791.pep	670 680 690 700 710 720
m791	TTNDNKDAWFGFNPVVTAVYIGFDKPKSMGRVGYGGTIAVPVWVDYMRFALKGKQKG
	670 680 690 700 710 720
a791.pep	730 740 750 760 770 780
m791	MKMPEGVVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGAEGGRQAADDEV
	MKMPEGVVSSNGEYYMKERMVTDPLGLTLDNSGIAPQPSRRAKEDDGAEGGRQAADDEV



1272

730 740 750 760 770 780

790 800

a791.pep RQDMQETPVLPSNTGSKQQQLDSLFX  
|||||

m791 RQDMQETPVLPSNTGSKQQQLDSLFX  
790 800

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2681>:

g792.seq

```

1 ATGTTCCGCA TCGTCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATCACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAA
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGGTGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GTCCGTTTGT
251 CCggacacgg gggcttcGat GGGGACGGCa tTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCGAAGT GAAGGCGGGC GGATCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTCTTCC TCAACGAAAG CCGCAACTAT CTGCGCAAAG
401 GCGAAGAGGC GGCCATTACG GCAATGATGG AAGCTGTTAC CGACAAAAAC
451 AGGATTTTCG AACTGTATTT AAACCAATC GAATGGCACT ACGGCGtTTT
501 CCGCGCGGAA GCTGCGTCCC GgtatTttTA TAAAAAACCG GCcgcaGACC
551 TGACCAAAAC GCAGgcggcG aaactgacgg tactcgtccc cgccccgttt
601 taCtactctg accatccaaa aagcaaacgg ctgcgcaaca aaaccaatat
651 cgtgctcaga cgcaggggtt cggcaaatTA ccccaagcg aaacggactg
701 attgttcag atatggaaat gccgcctgaa ctgggggttcg aacggcatat
751 gttttctggg acttataa

```

This corresponds to the amino acid sequence <SEQ ID 2682; ORF 792.ng>:

g792.pep

```

1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WVPYNRISTN LKKALIASD VRFAGHGGFD GDGIQNAIRR
101 NRNSGEVKAG GSTISQQLAK NLFLNESRNY LRKGEEAAIT AMMEAVTDKN
151 RIFELYLNSI EWHYGVFGAE AASRYFYKKP AADLTQQAQ KLTVLVPAPF
201 YYSDPKSKR LRNKTNIIVL RMGSANYPKA KRTDCSRYGN AA*TGVRTAY
251 VFWDL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2683>:

m792.seq

```

1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CTTTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGATGAAGCA GTTTGAACAG
151 GAAGGTCGCG ATGTCGCACT GGATTACCGC TGGATGCCCT ACAACCGCAT
201 TTCCACCAAC CTGAAAAAAG CCCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGGCAGCG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATCAGGCGC
301 AACCGGAACA GCGGCAAAGT GAAGGCGGGC GGCTCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAAG
401 GCGAAGAGC GCGGATTACC GCGATGATGG AAGCCGTTAC CGACAAAGAC
451 AGGATTTTTG AACTGTATTT AAACCAATC GAATGGCACT ACGGCGTTTT
501 CCGCGCGGAA GCCGCGTCCC GGTATTTTAA TCAAATACCC GCCGCAAGC
551 TGACCAAAAC GCAGGCGGCA AAACGACGG CGCGCGTCCC CGCCCGCTC
601 TACTACGCCG ACCATCCGAA AAGCAAACGG CTCCGCAACA AAACCAATAT
651 CGTGCTCAAA CGCATGGGTT CGGCAGAGT GCCTGAAAGC GACACGGACT
701 GA

```

This corresponds to the amino acid sequence <SEQ ID 2684; ORF 792>:

m792.pep

```

1 MFRIVKWLIA LPVGIFIFFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKKALIASD ARFAGHGGFD WGGIQNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLNESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQQAQ KLTARVPAPL
201 YYADHPKSKR LRNKTNIIVL RMGSAELPES DTD*

```

g792 / m792 90.4% identity in 230 aa overlap

```

          10      20      30      40      50      60
g792.pep MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
          |||||
m792      MFRIVKWLIALPVGIFIFFNAYVYGNIIYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR
          10      20      30      40      50      60

          70      80      90     100     110     120
g792.pep WVPYNRISTNLKKALIASDVRFAGHGGFDGDGIQNAIRNRNSGEVKAGGSTISQQLAK

```

```
m792      WMPYKRISTNLKKALIASEDARFAGHGFDWGGIQNARRNRNSGKVKAGGSTISQQLAK  
          70           80           90           100          110          120
```

```
g792.pep   NLFLNLSRNYLRKGEEAAITAMMEAVTDKNRI FELYLNSIEWHYGVFGAEASRYFYKKP  
            |||||:|||::|||||::::|||::|::|::|::|::|::|::|::|::|::|::|:  
m792       NLFLNLSRSYIRKGEEAAITAMMEAVTDKDRI FELYLNSIEWHYGVFGAEASRYFYQIP  
          130         140        150        160        170        180
```

```
g792.pep   AADLTQQAAKLTVLPAPFFYYSDHPKSRLRNKTNI VLRMGSAANYPKAKRTDCSRYGN  
            | | :|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::||  
m792       AAKLTQQAAKLTA RVPAPLYYADHPSKSLRNKTNI VLKRMGSALPESTDIX  
          190        200        210        220        230
```

```
g792.pep   AAXTGVRTAYVFWDLX  
          250
```

```
a792.seq
1 ATGTTCCGCA TCATCAAATG GCTGATTGCC CTGCCCGTCG GCATCTTTAT
51 CT'TTTTCAAT GCCTATGTGT ACGGCAACAT CATTACCTAC CGCGCCGTCG
101 CGCCCCATCG GACTGCCTTT ATGTCGATGC GGTGAAGCA GCTTTGAACAG
151 GAAGGTGCGC ATGTGCGCAT GGATTACCGC TGATGCCCT ACAACGCAT
201 TTCACCAAC CTGAAAAAG CCTGATTGC TTCCGAAGAT GCCCGTTTCG
251 CCGGCGCAGG CGGCTTCGAT TGGGGCGGCA TTCAAAACGC CATAGGCGCG
301 AACCGGAACA CGCGCAAAAT GAAGGCGGGC GGTGCGACCA TCAGCCAGCA
351 GCTTGCCAAA AACCTGTTTT TAAACGAAAG CCGCAGCTAT ATCCGCAAGG
401 CGCAAGAAGC GGCATTATCC GCATGATGG AAGCCGTTAC CGACCAAGAC
451 AGGATTTTTG AACTGTATTT AAACCTCAAT GAATGGCACT ACGGCGTTTT
501 CGGCGCGGAA GCCGCGTCCC GGTATTTTTA TCAAAATACC CGCGCCAAAG
551 TGACCAAAACA GCAGCGCGCA AAACGACGG CGCGCGTCCC CGCCCGCGTC
601 TACTACCGCG ACCATCCGAA AAGCAAACGG CTCGCAACA AAACCAATAT
651 CTGTGCTCAGA CGCATGGGTT CGGCAGAGTT GCCTGAAAGC GACACGGACT
701 GA
```

```
a792.pap
1 MFRIIKWLIA LPVGIFIFN AYVYGNIIY RAVAPHRTAF MSMRMKQFEQ
51 EGRDVALDYR WMPYKRISTN LKALIASD ARFAGHGDF WGGIGNAIRR
101 NRNSGKVKAG GSTISQQLAK NLFLESRSY IRKGEEAAIT AMMEAVTDKD
151 RIFELYLNSI EWHYGVFGAE AASRYFYQIP AAKLTQKQAA KLTARVPAPL
201 YYADHPKSKR LRNKHNVILR RMSAELPES DTD*
```

	10	20	30	40	50	60
a792.pep	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
m792	MFRIIKWLIALPVGIFIFFNAYVYGNIIITYRAVAPHRTAFMSMRMKQFEQEGRDVALDYR					
	10	20	30	40	50	60
a792.pep	70	80	90	100	110	120
	WMPYKRISTNLKALIASEDARFAGHGGFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK					
m792	WMPYKRISTNLKALIASEDARFAGHGGFDWGGIQNAIRNRNRNSGKVKAGGSTISQQLAK					
	70	80	90	100	110	120
a792.pep	130	140	150	160	170	180
	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNLSIEWHYGVFGAEASRYFYQIP					
m792	NLFLNESRSYIRKGEEAAITAMMEAVTDKDRIFELYLNLSIEWHYGVFGAEASRYFYQIP					
	130	140	150	160	170	180
a792.pep	190	200	210	220	230	
	AAKLTKQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDIDX					
m792	AAKLTKQAAAKLTARVPAPLYYADHPKSKRLRNKTNIVLRRMGSAELPESDIDX					
	190	200	210	220	230	

q793.seq

1274

```

1  ATGTTGATTA AAAGCGAATA TAAGCCCCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATTAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC TGCTGATTG CCCGCGGGCT GTATCTGCAG
151 ACGGTAACTG ATAACCTTTT GAAAGAACAG GGCACAAACC GGATTGTGCG
201 GACTCAAGCA TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGCGCG CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GATATGAAGG AAATGCCGTC TGCCGCCCAA TTGGAACGCC TGTCCGAGCT
351 TGTTCGATGT CCGGTCGATG TTTTGAGGAA CAAACTCGAA CAGAAAGGCA
401 AGTCGTTTAT TTGGATCAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAACG
501 CCATTACCGG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGCAAG AGGTCAGGAA GGTTCGAAAC TTTCGCTTGA AGACAGCCTG
601 TAGGCGAAG ACGGCGCGGA AGTTGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCACCAGCA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCAGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGACCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAAACG ATATGATCGA ACCTGGTTCG GCAATCAAA CGTTCTGTAT
951 TCGGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCCGGA CCGTCTCCCG TGCGCGATGA TACCCATGTT
1051 TACCCCTCTT TGGATGTGCG CGGCATTATG CAGAAATCGT CCAACGTCGG
1101 CACAAGCAAA CTGCTGCGC GTTTCGGCGC CGAAGAAATG TATGACTTCT
1151 ATCATGAATT GGGCATCGGT GTGCGTATGC ACTCGGGCTT TCCGGGGGAA
1201 ACTGCAAGTT TGTGTAGAAA TTGGCGCAGG TGGCGGCCCA TCGAACAGGC
1251 GACGATGCTT TTCGTTACG GTCTGCAATT GAGCCTGCTG CAATTGGCGC
1301 GCGCCTATAC CGCACTGACG CACGACGGCG TTTGCTGCC GCTCAGCTTT
1351 GAGAAGCAGG CGGTTCGCC GCAAGGCAAA CGCATATTC AAGAATCGAC
1401 CGCGCGCGAG GTACGCAATC TGATGGTTTC CGTAACCGAG CCGGGCGGCA
1451 CCGGTACGGC GGGTGGCGTG GACGGTTTCG ATGTCGGCGC TAAACCGGCG
1501 ACGGCGCGCA AGTTCGTCAA CGGGCGTTAT GCGGACAACA AACACGTCGC
1551 TACCTTTATC GGTTTTGCCC CCGCCAAAAA CCCCCGTGTG ATTGTGGCGG
1601 TAACCATCGA CGAACCGACT GCCACGGCT ATTACGGCGG CGTAGTGGCA
1651 GGGCCGCCCT TCAAAAAAAT TATGGCGGCG AGCCTGAACA TCTTGGGCAT
1701 TTCCCGACC AAGCCACTGA CCGCCGACG CGTCAAAACA CCGTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2688; ORF 793.ng>:

```

g793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAMAVLFA CLIARGLYLO
51  TVTYNFLKEQ GDNRIVRTQA LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 DMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKQGE GLELSLEDSL
201 YGEDGAEVVL RDRQGNIVDS LDSPRNKAPQ NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPY RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDDTHV
351 YPSLDVRGIM QKSSNVGTSK LSAFGEAEM YDFYHELIGI VRMHSGFPGE
401 TAGLLRNWRR WRPIEQATMS FGYGLQLSL QLARAYALT HDGVLLPLSF
451 EKQAVAPQK RIFKESTARE VRNLMVSVTE PGGTGTAGAV DGFVDVGARTG
501 TARKFVNGRY ADNKHVATFI GFAPAKNPRV IVAVTIDEPT AHGYGGVVA
551 GPFKKIMGG SLNILGISPT KPLTAAVKT PS*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2689>:

```

m793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCCTCGG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC TGCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACTG ATAACCTTTT GAAAGAACAG GGCACAAACC GGATTGTGCG
201 GACTCAAAAC TTGCCGGCTA CACGCGGTAC GGTTCGGAC CGGAACGGTG
251 CGGTTTTGGC GTTGAGTGGC CCGACGGAGT CCCTGTTTGC CGTGCCTAAA
301 GAGATGAAGG AAATGCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTTCGATGT CCGGTTGATG TTTTGAGGAA CAAGCTCGAA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGGT TGCCGAAGAG
451 GTCAAAGCCT TGGGTTTGA AACTTTGTA TTTGAAAAAG AATTAAACG
501 CCATTACCGG ATGGGCAACC TGTTTGACA CGTCATCGGA TTTACCGATA
551 TTGACGCAAG AGGTCAGGAA GGTTCGAAAC TTTCGCTTGA AGACAGCCTG
601 TATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGGCAGACA GCGAACAGCG GCGCAACCGT
901 GCCGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAA CGTTTGTGAT
951 TCGGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA

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1001 C GCAGCCTTA TAAATCGGA CCGTCTCCCG TCGCGGATAC CCATGTTTAC
1051 C CCTCTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 A AGCAAACTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 A TGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 G CAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGGCGAC
1251 G ATGTCTTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 C CTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGGT CAGCTTTGAA
1351 A AACAGGCGG TTGCGCCGCA AGGCAAACGC ATATTCAAAG AATCGACCGC
1401 G CGCGAGGTA CGCAATCTGA TGGTTCCGT AACCGAGCCG GCGGCGACCG
1451 G TACGGCGGG TCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 G CGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAAC ACATCGCTAC
1551 C TTTATCGGT TTTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 C CATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 C CGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTC
1701 C CCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2690; ORF 793>:

```

m793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFLKEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKFSIWIK RQLDPKVAEE
151 VKALGLENFV FEKELKRHPY MGNLFAHVIG FTDIDGKGQE GLELSLEDSL
201 HGEDGAEVVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIOTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRP RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTQPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNRRW RPIEQATMSF GYGLQLSLQ LARAYTALH DGVLLPVSFE
451 KQAVAPQGRK IFKESTAREV RNLMSVTEP GGTGTAGAVD GFDVGAKTGT
501 ARKFVNGRYA DNKHIATFIG FAPAKNPRVI VAVTIDEPTA HGYGCVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAAVKTP S*

```

g793/m793 98.5% identity in 582 aa overlap

g793.pep	10	20	30	40	50	60
m793	10	20	30	40	50	60
g793.pep	70	80	90	100	110	120
m793	70	80	90	100	110	120
g793.pep	130	140	150	160	170	180
m793	130	140	150	160	170	180
g793.pep	190	200	210	220	230	240
m793	190	200	210	220	230	240
g793.pep	250	260	270	280	290	300
m793	250	260	270	280	290	300
g793.pep	310	320	330	340	350	360
m793	310	320	330	340	350	
g793.pep	370	380	390	400	410	420
m793	370	380	390	400	410	

1276

```

          430      440      450      460      470      480
g793.pep    FGYGLQLSLLQLARAYTALTHDGVLLPLSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793        FGYGLQLSLLQLARAYTALTHDGVLLPVSFEKQAVAPQGKRIFKESTAREVRNLMVSVTE
          420      430      440      450      460      470

          490      500      510      520      530      540
g793.pep    PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793        PGGTGTAGAVDGFVDGAKTGTARKFVNNGRYADNKHVATFIGFAPAKNPRVIVAVTIDEPT
          480      490      500      510      520      530

          550      560      570      580
g793.pep    AHGYYGGVVAGPPFFKKIMGGS LNILGISPTKPLTAAAVKTPSX
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m793        AHGYYGGVVAGPPFFKKIMGGS LNILGISPTKPLTAAAVKTPSX
          540      550      560      570      580

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2691>:

```

a793.seq
1  ATGTTGATTA AGAGCGAATA TAAGCTCTCG ATGCTGCCCA AAGAAGAGCA
51  GGTCAAAAAG CCGATGACCA GTAACGGACG GATCAGCTTC GTCCTGATGG
101 CAATAGCGGT CTTGTTTGCC GGTCTGATTG CTCGCGGACT GTATCTGCAG
151 ACGGTAACGT ATAACCTTTT GAAAGAACAG GCGGACAACC GGATTGTGCG
201 GACTCAAAAC TTGCCGGCTA CACGCGGTAC GGTTCGGAC CCGAACGGTG
251 CGGTTTTGCG GTTGAGTGC GCGACGGAGT CCTGTGTTGC CGTGCCTAAG
301 GAGATGAAGG AATGCCCGTC TGCCGCACAA TTGGAACGCC TGTCCGAGCT
351 TGTGATGTG CCGGTTGATG TTTGAGGAA CAAAGCTCGA CAGAAAGGCA
401 AGTCGTTTAT CTGGATTAAG CGGCAGCTCG ATCCCAAGST TGCCGAAGAG
451 GTCAAAAGCT TGGGTTTGGA AAACCTTGTA TTTGAAAAGG AATTAAACG
501 CCATTACCCG ATGGGCAACC TGTTCGACA CGTCATCGGA TTTACCGATA
551 TTGACGGCAA AGGTGAGGAA GGTTCGGAAC TTTGCTTGA AGACAGCCTG
601 CATGGCGAAG ACGGCGCGGA AGTCGTTTTC CGGGACCGGC AGGGCAATAT
651 TGTGGACAGC TTGGACTCCC CGCGCAATAA AGCCCCGAAA AACGGCAAAG
701 ACATCATCCT TTCCTCGAT CAGAGGATTC AGACCTTGGC CTATGAAGAG
751 TTGAACAAGG CGGTCGAATA CCATCAGGCA AAAGCCGGA CGGTGGTGGT
801 TTTGGATGCC CGCACGGGGG AAATCCTCGC CTTGGCCAAT ACGCCCGCCT
851 ACGATCCCAA CAGGCCCGGC CGGCGAGACA GCGAACAGCG GCGCAACCGT
901 GCGGTAACCG ATATGATCGA ACCCGGTTTC GCAATCAAAC CGTTTGTGAT
951 TGCGAAGGCA TTGGATGCGG GCAAAACCGA TTTGAACGAA CGGCTGAATA
1001 CGCAGCCTTA TAAATCGGA CCGTCTCCCG TGCGCGATAC CCATGTTTAC
1051 CCTCTTTTGG ATGTGCGCGG CATCATGCAG AAATCGTCCA ACGTCGGCAC
1101 AAGCAAACCTG TCTGCGCGTT TCGGTGCCGA AGAAATGTAT GACTTCTATC
1151 ATGAGTTGGG CATCGGTGTG CGTATGCACT CGGGCTTTCC GGGCGAAACT
1201 GCAGGTTTGT TGAGAAATTG GCGCAGGTGG CGGCCTATCG AACAGCGGAC
1251 GATGTCCTTC GGTACGGCC TGCAATTGAG CCTGCTGCAA TTGGCGCGCG
1301 CCTATACCGC ACTGACGCAC GACGGCGTTT TACTGCCGCT GAGCTTTGAA
1351 AAACAGGCGG TTGCGCCGCA AGGCAACGCG ATATCAAAAG AATCGACCGC
1401 GCGCGAGGTA CGCAATCTGA TGGTTTCCGT AACCGAGCCG GCGGCGACCG
1451 GTACGGCGGG TGCGGTGGAC GGTTCGATG TCGGCGCGAA AACCGGCACG
1501 GCGCGCAAGT TCGTCAACGG GCGTTATGCC GACAACAAC ACATCGCTAC
1551 CTTTATCGGT TTGCCCCCG CCAAAAATCC CCGTGTGATT GTGGCGGTAA
1601 CCATTGACGA ACCGACTGCC CACGGTTATT ACGGCGCGCT AGTGGCAGGG
1651 CCGCCCTTCA AAAAAATTAT GGGCGGCAGC CTGAACATCT TGGGCATTTT
1701 CCCGACCAAG CCACTGACCG CCGCAGCCGT CAAAACACCG TCTTAA

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This corresponds to the amino acid sequence <SEQ ID 2692; ORF 793.a>:

```

a793.pep
1  MLIKSEYKPR MLPKEEQVK PMTSNGRISF VLMAIAVLFA GLIARGLYLQ
51  TVTYNFKLEQ GDNRIVRTQT LPATRGTVSD RNGAVLALSA PTESLFAVPK
101 EMKEMPSAAQ LERLSELVDV PVDVLRNKLE QKGKSFIIWK RQLDPKVAEE
151 VKALGLENFV FEKELKRHYD MGNLFAHVIG FTDIDKGQGE GLELSLEDLS
201 HGEDGAEEVL RDRQGNIVDS LDSPRNKAPK NGKDIILSLD QRIQTLAYEE
251 LNKAVEYHQA KAGTVVVLDA RTGEILALAN TPAYDPNRPQ RADSEQRNR
301 AVTDMIEPGS AIKPFVIAKA LDAGKTDLNE RLNTOPYKIG PSPVRDTHVY
351 PSLDVRGIMQ KSSNVGTSKL SARFGAEMY DFYHELIGIV RMHSGFPGET
401 AGLLRNWRWW RPIEQATMSF GYGLQLSLLQ LARAYTALH DGVLLPVSFE
451 KQAVAPQGR IFEKSTAREV RNLMSVTEP GGTGTAGAVD GFDVGARTGT
501 ARKFVNNGRY DNKHVATFIG FAPAKNPRVI VAVTIDEPTA HGYGGVVAG
551 PPFKKIMGGS LNILGISPTK PLTAAVKTP S*

```

a793/m793 100.0% identity in 581 aa overlap

1277

a793.pep	10	20	30	40	50	60
	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
m793	MLIKSEYKPRMLPKKEQVKKPMTSNGRISFVLMAIAVLFAGLIARGLYLQTVTYNFLKEQ					
	10	20	30	40	50	60
a793.pep	70	80	90	100	110	120
	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
m793	GDNRIVRTQTLPATRGTVSDRNGAVLALSAPTESLFAVPKEMKEMPSAAQLERLSELVDV					
	70	80	90	100	110	120
a793.pep	130	140	150	160	170	180
	PVDVLRNKLKQKGSFIWIKRQDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
m793	PVDVLRNKLKQKGSFIWIKRQDPKVAEEVKALGLENFVFEKELKRHYPMGNLFAHVG					
	130	140	150	160	170	180
a793.pep	190	200	210	220	230	240
	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
m793	FTDIDGKGQEGLELSLEDSLHGEGDAEVVLRDRQGNIVDSLSPRNKAPKNGKDIILSLD					
	190	200	210	220	230	240
a793.pep	250	260	270	280	290	300
	QRIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
m793	QRIQTLAYEELNKAVEYHQAKAGTVVVLARTGEILALANTPAYDPNRPGRADSEQRNR					
	250	260	270	280	290	300
a793.pep	310	320	330	340	350	360
	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
m793	AVTDMIEPGSAIKPFVIAKALDAGKTDLNERLNTQPYKIGSPVRDTHVYPSLDVRGIMQ					
	310	320	330	340	350	360
a793.pep	370	380	390	400	410	420
	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
m793	KSSNVGTSKLSARFGAEEMYDFYHELIGIVRMHSGFPGETAGLLRNWRRWRPIEQATMSF					
	370	380	390	400	410	420
a793.pep	430	440	450	460	470	480
	GYGLQLSLQLARAYTALHDGVLLPVSEKQAVAPQKRIKKESTAREVRNLMVSVTEP					
m793	GYGLQLSLQLARAYTALHDGVLLPVSEKQAVAPQKRIKKESTAREVRNLMVSVTEP					
	430	440	450	460	470	480
a793.pep	490	500	510	520	530	540
	GGGTAGAVDGFVDGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
m793	GGGTAGAVDGFVDGAKTGTARKFVNGRYADNKHIATFIGFAPAKNPRVIVAVTIDEPTA					
	490	500	510	520	530	540
a793.pep	550	560	570	580		
	HGYGGVVAGPPFKKINGGSLNILGISPTKPLTAAAVKTPSX					
m793	HGYGGVVAGPPFKKINGGSLNILGISPTKPLTAAAVKTPSX					
	550	560	570	580		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2693>:

g794.seq

```

1  gtgcgtttca ATCATTTCAT AATGGTAACG ATTATTATAT ATGTGATTTC
51  CCCTGCAAAAC AAGCCGGTCC GCCGCCCGCG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTCACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAACGA AATCGCTGTA TATGTCCAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGTGCCGG CATACCCGTC
301 AATCCCGCGT CCACGATGAA GCTCGTTACC GCGTTTGCCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTCA ATCAGGAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 CAAAGGCATC CGCAATATCA CGGGCGCCT GATGCTCGAC CACAGCTGT

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1278

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551 GGGGCGAAGT CGGCAGTCCC GACCATTTTG AAGCCGACAG CGGTTCCGCG
601 TTTATGACGC CCCCAATCC GACTATGCTG TCTGCCGGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CT'TTGCCGCA TATTTTGGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTCCGTCAA AAACTGATG CGCGCATCTT TTTCGGGCAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA AAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGCCA AAGTTTACC
901 AACCGCTGGC TGCTCGCGG CGGACGGATT TCAGACGGCA TCGGCATAGC
951 CGACACACCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCCAAACCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTGATTGCG
1051 CGT'TCCGTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGAGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACCGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT GCCCATCGCG GGCACAGACG
1301 GGACTTTACG CAACCGCTTC AAACAAGCG CGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCCGA CTTGGACAAC TTCGTTGCCA AAAACATCAT CTCCGGCGGC
1501 GACGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2694; ORF 794.ng>:

```

g794.pep
1  VRFNHFMIVT IIIYVISPAN KPVRRPGVPT YPALPYNCFF YVTDSPMNF
51  KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRAGIPV
101 NPA STMKLVT AFAAFKTFGS NYRWATEFKS NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLRDKGI RNITGRMLLD HSLWGEVGSF DHEADSGSP
201 FMT'PPNPTML SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSVKKLM RASFSGNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NRWLLGGGRI SDGIGIADTP EGAQTLAVAH SKPMKEILD MNKRSNLLIA
351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE
401 RVT'ARMMAQM LETAYFSPFA QDFIDTLPIA GTDGTLRNRF KQSGGLRLRK
451 TGT'LNNVRAL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVAKNIISGG
501 DGWLDALMC KERRA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2695>:

```

m794.seq
1  GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTC
51  CCTTGCAAAC AAGCCGGCCC GCCGCCACAG CGTCCCACT TATCCGGCTT
101 TGCCTTATAA TTGCTTTTTT TATGTAACAG ATTACCTAT GAATTTCCCC
151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC
201 GCTCGATACC GGCCGCATTC CGCAAAACGA AATCGCCGTA TATGTCGAAG
251 AGCTTGACAG CGGAAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGTTC
301 AACCCCGCCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAC
351 CTTCCGCAGC AATTACCGCT GGGCGACCGA GTTAAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTAT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CTGCTTGAT GCTCAAAAAC AGTTGCGCGA
501 ACAAGGCATA CTCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGGCGAAGT CGGCAGCCCC GACGATTTCC AAGCCGACAG CGGTTCCGCC
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCCGAA CGCAATGCCG CCGGCAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCCGA TATTTTCGCC CAAAACAAC TGAATAATAC CGCCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTCGGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCCGG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGTA TCGGCATAGC
951 CGACACGCGG GAAGGCGCGC AGACATTGC CGTTGCACAC GCCAAACCGA
1001 TGAAGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGT'TCCGTCT TCCTCAAAC CCGCGGCGAC GGCAAACTGC CCGCCGTTTC
1101 CGAACAGGCG GCGTCTGCCG TCCGGCGCGA ACTTGCCGTA TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTGG GAAAACGGTT CGGGCCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GCGCAAAATG TTGGAACCGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGACACGCT ACCCATCGCC GGCACAGACG
1301 GAACTTTACG CAACCGCTTC AAACAAGCG CGGGCTGTT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTATT GGCTGGGCGA
1401 CAAACCGATG GCGGTGGTCG TCATCATCAA CAGCGGCCGC GCCGTTTCCC
1451 TGCTGCCAGA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGGCGGC
1501 GATGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2696; ORF 794>:

```

m794.pep
1  VRLNHFMIA IIIYVISPAN KPARRHSVPT YPALPYNCFF YVTDLPMNFP
51  KTAASLLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSVPV

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1279

101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD  
 151 PVFNQENLLD AQKOLREQGI LNTGHLMLD HSLWGEVGSF DDFEADSGSP  
 201 FMTTPNPMTL SAGMVMVRAE RNAAGSTDIL TDPPLPHIFA QNNLKITASQ  
 251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT  
 301 NHWLLGGGRI SDGIGIADTP EGAQTLAVAH AKPMKEILTD MNKRSNLI  
 351 RSVFLKLGGD GKLPVSEQA ASAVRRELAV SGIDVADLVL ENGSGLSRKE  
 401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLLRLK  
 451 TGTNNVRAL AGYWLGDKPM AVVVIINSR AVSLPDLN FVANNIISGG  
 501 DGWLDKLMC KERRA\*

g794/m794 95.5% identity in 515 aa overlap

	10	20	30	40	50	60
g794.pep	VRFNHFIMVTIIIVISPAKPVRRPGVPTYPALPYNCFYVTDSPMNFPKTAASLLLL					
m794	VRLNHFIMIAIIIVISPAKPARRHVSPTYPALPYNCFYVTDLPNMFPKTAASLLLL					
	10	20	30	40	50	60
g794.pep	ASLAHAHALDTGRIPONEIAVYVQELDSGKVIIDHRAGIPVNPASTMKLVTAFKTFGS					
m794	ASLAHAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS					
	70	80	90	100	110	120
g794.pep	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRLDKGIRNITGRMLD					
m794	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKOLREQIILNITGHLMLD					
	130	140	150	160	170	180
g794.pep	HSLWGEVGSFDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
m794	HSLWGEVGSFDDFEADSGSPFMTPPNPMTLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
g794.pep	QNNLKITASQAACPSVKKLMRASFSNGTLKLRGNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
g794.pep	NRWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSNLIARSVFLKLGGD					
m794	NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTMNKRSNLIARSVFLKLGGD					
	310	320	330	340	350	360
g794.pep	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA					
m794	GKLPVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERVARTARMAQMLETAYFSPFA					
	370	380	390	400	410	420
g794.pep	QDFIDTLPIAGTDLNRNRFKQSGGLLRLKTGTNNVRALAGYWLGDKPMVAVVVIINSR					
m794	QDFIDTLPIAGTDLNRNRFKQSGGLLRLKTGTNNVRALAGYWLGDKPMVAVVVIINSR					
	430	440	450	460	470	480
g794.pep	AVSLPDLNDFVAKNIISGGDGWLDKLMCKERRAX					
m794	AVSLPDLNDFVANNIISGGDGWLDKLMCKERRAX					
	490	500	510			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2697>:

a794.seq

1 GTGCGTCTCA ATCATTTCAT AATGATAGCG ATTATTATAT ATGTGATTTT  
 51 CCCTGCAAAC AAGCCGGCCC GCCGCCACAG CGTTCCCACT TATCCGGCTT  
 101 TGCCATTATA TTGCTTTTTT TATGTAACAG ATTTACCTAT GAATTTCCCC  
 151 AAAACAGCGG CCTCCCTGCT GCTGCTTCTC GCCTCCCTCG CCGCACACGC  
 201 GCTCGATACA GGTCCGATTC CGCAAACGA AATCGCCGTA TATGTCCAAG  
 251 AGCTTGACAG CGGAAAGTC ATCATTGACC ACCGCTCGGA TGTCCCGGTC



1280

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301 AACCCGCGCT CCACAATGAA ACTCGTTACC GCGTTTGCCG CCTTCAAAAC
351 CTT CGGCAGC AATTACCGCT GGGCGACCGA GTTTAAAGC AACGGTACGG
401 TAAACGACGG CACGCTTGAC GGAAACCTGT ATTGGGCGGG CAGCGGCGAC
451 CCCGTTTTCA ATCAGGAAAA CCTGCTTGCC GTCCAACGCC AGTTGCGCGA
501 ACAAGGCATA CGCAATATCA CGGGACACCT GATGCTCGAC CACAGCCTGT
551 GGGCGGAAGT CGGCAGCCCC GACGATTCG AAGCCGACAG CGGTTCGCGG
601 TTTATGACGC CCCCCAATCC AACTATGCTG TCTGCCGTA TGGTTATGGT
651 GCGCGCGGAA CGCAATGCCG CCGACAGTAC CGACATCCTC ACCGATCCGC
701 CTTTGCCGCA TATTTTCGCC CAAAACAAC TGAATAATAC CGCTCCCAA
751 GCTGCCTGCC CTTGATCAA AAACTGATG CGTGCATCTT TTTCCGACAA
801 TACGCTGAAA TTGCGCGGCA ATATTCCCGA GAGCTGTTG GGCAAGCCTG
851 TCGGTGTCCG GATGTTCGCG CTTGACGAAC TGATCCGGCA AAGTTTACC
901 AACCACTGGC TGCTCGGCGG CGGACGGATT TCAGACGGCA TCGGCATATC
951 CGACACGCCG GAAGGCGCGC AGACGCTTGC CGTTGCACAC TCAAGCCGA
1001 TGAAGGAAAT TTTGACGGAC ATGAACAAGC GTTCGGACAA TCTAATTGCG
1051 CGTTCCTGCT TCCTCAAACT CGGCGGCGAC GGCAAACTGC CCGCGGTTTC
1101 CGAACAGGCA GCGTCTGCCG TCCGGCGTGA ACTTGCCGTG TCGGGCATCG
1151 ATGTTGCGGA TTTGGTTTTG GAAAACGGTT CAGGTCTGTC CAGAAAAGAA
1201 AGGGTAACGG CGAGAATGAT GGCACAAATG TTGGAAACGG CTTATTTCAG
1251 CCCGTTTGCA CAAGATTTC TCGATACGCT GCCCATCGCC GGCACAGACG
1301 GGCATTTACG CAACCGCTTC AAACAAGCG CCGGCGCTGT GCGCTTAAAA
1351 ACCGGCACGC TCAACAATGT CCGCGCCCTT GCAGGTTATT GGCTGGGCGA
1401 CAAACCGGAT GCGGTGGTCG TCATCATCAA CAGCGGCGCG GCCGTTTCCC
1451 TGTGCCCGCA CTTGGACAAC TTCGTTGCCA ACAACATCAT CTCCGCGCGC
1501 GATGGCTGGC TGGATGCGAA ACTGATGTGC AAAGAACGCC GAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2698; ORF 794.a>:

```

a794.pep
1  VRLNHFIMIA IIIYVISPAN KPARRHSVPT YPALPYNCF YVTDLPMNFP
51  KTAASLLLL ASLAHALDT GRIPONEIAV YVQELDSGKV IIDHRSDVPV
101 NPASTMKLVT AFAAFKTFGS NYRWATEFES NGTVNDGTLD GNLYWAGSGD
151 PVFNQENLLA VQRQLREQGI RNITGHLMLD HSLWGEVSGP DDFEADSGSP
201 FMTPPNPTML SAGMVMVRAE RNAADSTDIL TDPPLPHIFA QNNLKITASQ
251 AACPSIKKLM RASFSDNTLK LRGNIPESCL GKPVGVRMFA LDELIRQSFT
301 NHWLLGGGRI SDGIGISDTP EGAQTLAVAH SKPMKEILD MNKRSNLI
351 RSVFLKLGSD GLPAVSEQA ASAVRELA VSGIDVADLV ENGSGLSRKE
401 RVTARMAQM LETAYFSPFA QDFIDTLPIA GTDGLRNRF KQSGGLRLK
451 TGTLLNNVRL AGYWLGDKPM AVVVIINSGR AVSLLPDLN FVANNIISGG
501 DGWLDKILMC KERRA*

```

a794/m794 98.6% identity in 515 aa overlap

	10	20	30	40	50	60
a794.pep	VRLNHFIMIAIIIYVISPAN KPARRHSVPTYPALPYNCFYVTDLPMNFPKTAASLLLL					
m794	VRLNHFIMIAIIIYVISPAN KPARRHSVPTYPALPYNCFYVTDLPMNFPKTAASLLLL					
	10	20	30	40	50	60
a794.pep	ASLAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS					
m794	ASLAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS					
	70	80	90	100	110	120
a794.pep	ASLAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS					
m794	ASLAHALDTGRIPONEIAVYVQELDSGKVIIDHRSDVPVNPASTMKLVTAFKTFGS					
	70	80	90	100	110	120
a794.pep	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLAVQRQLREQGIRNITGHLMLD					
m794	NYRWATEFESNGTVNDGTLDGNLYWAGSGDPVFNQENLLDAQKQLREQGILNITGHLMLD					
	130	140	150	160	170	180
a794.pep	HSLWGEVSGPDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAADSTDILTDPPLPHIFA					
m794	HSLWGEVSGPDDFEADSGSPFMTPPNPTMLSAGMVMVRAERNAAGSTDILTDPPLPHIFA					
	190	200	210	220	230	240
a794.pep	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	250	260	270	280	290	300
a794.pep	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
m794	QNNLKITASQAACPSIKKLMRASFSNTLKLGRNIPESCLGKPVGVRMFALDELIRQSFT					
	310	320	330	340	350	360
a794.pep	NHWLLGGGRISDGIGISDTPGAQTLAVAHSKPMKEILDMNKRSNLIARSVFLKLGSD					

1281

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|||||
m794      NHWLLGGGRISDGIGIADTPEGAQTLAVAHAKPMKEILTDMNKRSDNLIARSVFLKLGGD.
          310      320      330      340      350      360

          370      380      390      400      410      420
a794.pep  GKLPVAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          |||||||
m794      GKLPVAVSEQAASAVRRELAVSGIDVADLVLENGSGLSRKERV TARMMAQMLETAYFSPFA
          370      380      390      400      410      420

          430      440      450      460      470      480
a794.pep  QDFIDTLPIAGTDGTLNRNFKQSGGLRLKTGT LNNVRALAGYWLGD KPMVAVVVIINSGR
          |||||||
m794      QDFIDTLPIAGTDGTLNRNFKQSGGLRLKTGT LNNVRALAGYWLGD KPMVAVVVIINSGR
          430      440      450      460      470      480

          490      500      510
a794.pep  AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
          |||||||
m794      AVSLLPDLDNFVANNIISGGDGWLD AKLMCKERRAX
          490      500      510

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2699>:

g900.seq

```

1   ATGccgTCTG AAATGCCGTC TGAAACGTGG CAGGCGGAGG TTCGGACGGC
51  ATTGGGTTTA TTTCAACGGG CGGATGCCGA CCGCATCGCG TACTTTATCC
101 AACAAATCGC GCGCTTCTTT GCGCGCTTTT TCGCGCctg cctGCAAAAT
151 CTCTTCGATT TGCGAAGGAT TAGAGGTCAA TCGGTTGTAG CGTTCGCGCA
201 GTTCTGCCAA TTCGGCGTTG ATTTTCGCCG CCGAAAGTTT TTTCCGCTCG
251 CCCCAAGCCA AGCCGTCGGC AAGCATTGTC GTAAATTCCG CCGTTTCAGA
301 CGGCGTGGAG AAGGCTTTAT AGATTTCAAA CAAAGGGCTT TCGTCGGGCT
351 GTTTCGGCTC GCCCGGCTCT TTCATGTTGG TAATGATTTT GTTGACCGAT
401 TTTTGGGTTT TTTTGTCTGT TTCCCAAAGC GGAATGGTAT TGCCGTAGGA
451 TTTGGACATT TTGCGTCCGT CCAAACCGAC CAAGAGTTCG ACGTTTTCGT
501 CGATTTTCAC TTCGGGCagg GTGaagagtt cTTGGAaacc gtgggtgaag
551 cggccggcAa tgtcgcgcg cATTTCgacg tgttgGATTT GGTGCGGCCC
601 GACGGGGACT TCGTTGGCGT TGAACATCAA AATGTCGCA GTCATCAGAA
651 TCGGATAACT GAACAAACCC ATTTCCACAC CGAAATCGGG GTCTTCCTGC
701 CCGTTTTCCG CATTGGCTTG AACGGCGGCT TTGTAGGCGT GGGCGCGGTT
751 CATCAAACCC TTGGCGGTGA TGCAGGTCAG AATCCAGTTC AACTCCATCA
801 CTTCGGGAAT GTCGCTTTGG CGGTAGAAGG TGGTGCCTC GGGGTGAGT
851 CCGCAGGCAA GCCAAGTGGC GGCAACGGCt tgGGTGGATT GGTGAATCAT
901 CTCCTGCTCG TGGCATTGTA TGATGCCGTG GTAATCGCG AGGAAGAGGA
951 AGGATTCGGT ATCGGGGTTT TCGCGCGCGC GGACGGCGGG CGCGATGGCG
1001 CCGACGTAGT TGCCAGATG CGGGGTGCCG GTGGTGGTTA CGCCGGTCAG
1051 AACTCGTTTT TTGCTCATAA AAATGTCCTT ACGGCAGCAA TGCCGTCTGA
1101 AAGGGAAAa. gatgCGCGA TTATACCGA TTTGCCACAT ACATCCAGCC
1151 GacaACagac TTTTCATAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2700; ORF 900.ng:

g900.pep

```

1   MPSEMPSETW QAEVRTALGL FORADADRIA YFIQQFARFF ARFLRACLON
51  LFDLRRIRGQ CVVAFQFCQ FGVDfRRRKf FRLAPSQAVG KHLRKfRRfR
101 RRGEgFIDFK QRAfVGLfRL ARLfHVGNDF VDRfLGfFFV FPKRNGIavg
151 FGHFASVQTD QEFdVfVDFH FGQGEfFLET VGEAAGNVAR HFDVLDLVAP
201 DGDFVGVehQ NVGSHQNRIT EQTHfHTEIG VFLPVfRIGL NGGFVGVgAV
251 HQTLGGDAGQ NPVQLHHfGN VALAVEGGAL GVESAGKPSG GNGLGGLVNH
301 LLLVAFDDAV VIGEEEGFG IGVLRRADGG ADGADVVAQM RGAGGGYAGQ
351 NSFFAHKNVL TAAMPSEREK DAPIIPDLPH TSSRQQTfPY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2701>:

m900.seq

```

1   ATGCCGTCG AAACGCGGCA GCGGAGGTT CCGACGGCAT CGGGTTCATT
51  TCAACGGGCG GATGcCGACC GCATCg.TA CTTTGTCCAA TAATTCGCGT
101 GCTTCTTTAC GCGCTTTCGC CCGCCTGCC TGCAAAATCT CTTGATTG

```

1282

```

1 51 CGAAGGGTCG GCGGTCAGCT CGTTGTAGCG TTCGCGCGGT TCGGCGAGTT
2 01 CGGCGTTGAT TTTCGCGGCC AAAAGTTTTT TGGCTTCACC CCACGCCAAG
2 51 CCGTCGGCAA GCATTTTCGT AAATTCACC GTTTCAGACG GCGTGGAGAA
3 01 GGCTTTGTAG ATTTCAAACA ATGGGCTTTC GTCGGGCTGT TCGGCTCGC
3 51 CCGGCTCTTT CATATTGGTG ATGATTTTGT TGACCGATT TTGGGTTTTT
4 01 tTGTCGTTTT CCCAAAGCGG AATGGTGTG CCGTAGGATT TGGACATTTT
4 51 GCGTCCGTCC AAACCGACCA AGAGTTCGAC GTTTTCATCG ATTTTCACTT
5 01 CGGGCAGGGT GAAGAGTTCC CGGAAGCGGT GGTGAAGCG GCCGCGATG
5 51 TCGCGCGCCA TTTCGACGTG TTGGATTGG TCGCGCCCGA CgGGCaCTTC
6 01 GTTGGCGTTG AACATCAGAA TATCGGCAGT CATCAGAATC GGATAACTGA
6 51 ACAAACCCAT TTCCACACCG AAATCAGGGT CTTCCTGCCC GTTTTCTGCA
7 01 TTTGCCTGCA CGGCGGCTTT GTAGGCATGG GCGCGGTTCA TCAAACCTT
7 51 GGCAGTGATG CAGGTCAGAA TCCAGTTCAA TTCCATCACT TCgGAGTGT
8 01 GCGTTTGCGG GTAGAAGGTG GTGCGCTCGG GGTTCGAGTCC GCAGGCAAGC
8 51 CAAGTGGCGG CAACGGCTTG GGTGGATTGG TGAATCATCT CCGGCTCGTG
9 01 GCATTTGATG ATACCGTGGT AATCGGCGAG GAAGAGGAAG GATTCGGTAT
9 51 CGAGGTTTTG CGCCGCGCGG ACGGCGGGC GGATGGCGCC GACGTAGTTG
10 01 CCCAGATGCG GGATGCCGGT GGTGGTTACG CCGGTCAGAA CTCGTTTTTT
10 51 GTCATAAAA ATGTCCTTGC GGCATCAATG CCGTCTGAAA GGGAAAAAGA
11 01 TGTGCCGATT ATACCGGATT TGCCACCTAC ATCCAGCCGA CAACAGACTT
11 51 TTCCATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2702; ORF 900>:

m900.pep

```

1 MPSETRQAEV RTASGSFQRA DADRIXYPVQ *FACFFTRFR RACLQNLFDL
51 RRVGGQLVVA FARFGEFGVD FRRQKFFGFT PRQAVGKHFR KFHRFRRRGE
101 GFVDFKQWAF VGLFRLARLF HIGDDFVDRF LGFFVVPKR NGVAVGFGHF
151 ASVQTDQEFV VFIDFHFGQG EEFPEAVVEA AGDVARHFDV LDLVAPDGHF
201 VGVHQNIGS HQNRITEQTH FHTAIRVFLP VFCICLHGGF VGMGAVHQT
251 GSDAGQNFVQ FHHFGSVALA VEGGALGVES AGKPSGGNGL GGLVNHLRLV
301 AFDDTVVIGE EEEFGFIEVL RRADGGADGA DVVAQMRDAG GGYAQNSFF
351 AHKNVLAASM PSEREKDVPI IPDLPTSSR QQTFFPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 900 shows 87.0% identity over a 386 aa overlap with a predicted ORF (ORF 900.ng) from *N. gonorrhoeae*:

m900/g900

	10	20	30	40	50
m900.pep	MPSETRQAEVRTASGSFQRADADRIXYPVQX*FACFFTRFRACLQNLFDLRRVGGQ				
g900	MPSEMPSETWQAEVRTALGLFQRADADRIAYFIQQFARFFARFLRACLQNLFDLRRIRGQ				
	10	20	30	40	50
	60	70	80	90	100
m900.pep	LVVAFARFGEFGVD FRRQKFFGFT PRQAVGKHFRKFHRFRRRGE GFVDFKQWAFVGLFRL				
g900	CVVAFQAQFCQFGVD FRRRKFFRLAPSQAVGKHLRKFRFRRRRGE GFIDFKQRAFVGLFRL				
	70	80	90	100	110
	120	130	140	150	160
m900.pep	ARLFHIGDDFVDRFLGFFVVPKRNGVAVGFGHFASVQTDQEFVDFIDFHFGQGEFPEA				
g900	ARLFHVGNDFVDRFLGFFVVPKRNGIAVGFGHFASVQTDQEFVDFVDFHFGQGEFLET				
	130	140	150	160	170
	180	190	200	210	220
m900.pep	VVEAAGDVARHFDVLDLVAPDGHFVGVHQNIGSHQNRITEQTHFHTAIRVFLPVFCICL				
g900	VGEAAGNVARHFDVLDLVAPDGHFVGVHQNIGSHQNRITEQTHFHTAIGVFLPVFRIGL				
	190	200	210	220	230
	240				

```

      240      250      260      270      280      290
m900.pep  HGGFVGMGAVHQTLGSDAGQNPVQFHHFGSVALAVEGGALGVESAGKPSGGNGLGGLVNH
          :|||:|||||:|||||:|||:|||||
g900      NGGFVGVGAVHQTLGGDAGQNPVQLHHFGNVALAVEGGALGVESAGKPSGGNGLGGLVNH
          250      260      270      280      290      300

      300      310      320      330      340      350
m900.pep  LRLVAFDDTVVIGEEEEFGFIEVLRRADGGADGADVVAQMRDAGGGYAGQNSFFAHKNVL
          | |||:|||||
g900      LLLVAFDDAVVIGEEEEFGFIVLRRADGGADGADVVAQMRGAGGGYAGQNSFFAHKNVL
          310      320      330      340      350      360

      360      370      380
m900.pep  AASMPSEREKDVPIIPDLPTSSRQQTFFPYX
          :|||:|||||
g900      TAAMPSEKDAPIIPDLPHPTSSRQQTFFPYX
          370      380      390

```

a900.seq	(partial)					
1	GAGGTCGGA	CGGCATTGGG	TTTATTTCAA	CGGGCGGATA	CCGACCGCAT	
51	CACGTACTTT	GCCCAATAAT	TCGCGTGCCT	CTTTACGCGC	TTTTTTCGCG	
101	CTGCCTGCA	AAATCTCTTC	GATTTCGCAA	GGGTCGGCGG	TCCGCTCGTT	
151	GTAGCGTTCG	CGCGGTTTCG	CGAGTTCGCG	GTTGATTTTC	GCGGCCAAAA	
201	GTTTTTTTGC	CTCGCCCCAA	GCCAAGCCGT	CGGCAAGCAT	TTTCGTAAT	
251	TCTGCCGTTT	CAGACGGCGT	GGAGAAAGCT	TTGTAGATTT	CAAACAGAGG	
301	GCTTTCGTCG	GGCTTCTTCG	GCTCGCCCCG	CTCTTTCATA	TTGGTGATGA	
351	TTTTTGTGAC	CGATTTTTCG	GTTTTTTTGT	CGTTTTCCCA	AAGCGGAATG	
401	GTGTTGCCGT	AGGATTTCGA	CATTTTTCGT	CCGTGCCAAG	CACCAAGAGT	
451	TTCGACGTTT	TCGTGATTTT	TCACTTCGGG	CAGTGTGAAG	AGTTCCCGGA	
501	AGCGGTGGTT	GAAGCGGCGG	GCAATATCGC	GTGCCATTTC	AACGTGTTGG	
551	ATTTGGTCGC	GACCGACTGG	AACCTCATGG	GCATTGAACA	TGAGAATGTC	
601	GGCAGTCATG	AGGATAGGTT	AGCTGTACAA	ACCCATTTC	ACGCCGAAAT	
651	CGGGGTCTTC	CTGCCCCGTT	TCCGCATTTC	CCTGCACGGC	GGCTTTGTAG	
701	GCGTGGGCGC	GGTTCATCAA	ACCCTTGCGC	GTGATGCAGG	TCAGAATCCA	
751	GTTCAATTCC	ATCACTTCGG	GAATGTCGCT	TTGACGGTAG	AAGGTGGTGC	
801	GCTCGGGGTG	GAGTCCGACG	GCAAGCCAAG	TGGCGGCAC	GGCTTTGGGTG	
851	GATTGGTGAA	TCATCTCCGG	CTCGTGGCAT	TGTGATGATC	CGTGTTAATC	
901	GGCGAGGAAG	AGGAAGGATT	CGGTATCAGG	GTTTTGCGCC	GCGCGGACGG	
951	CGGGGCGGAT	AGCACCAGAC	TAGTTGCCCA	GATGCGGGAT	GCCGGTGGTG	
1001	GTTACGCCGG	TCGAACCTCG	TTTTTTGCTC	ATAAAAAATG	CCTTGGCGCA	
1051	TCATGCCCGT	CTGAAGGGA	AAAAGATGCG	CCGATTATAC	CCGATTTCGC	
1101	ACCTACATCC	AGCCGACAAC	AGACTTTTCC	ATATTAA		

a900.pap	(partial)				
1	EVRTALGLFQ	RADTDRTITYF	AQ*FACFFTR	FLRACLQNLF	DLRRVGGQLV
51	VAFARFGFGE	VDFFRRQKDFD	LAPSQAVGKH	FRKFCRFRRR	GESFVDFKQR
101	AFVGLLRRLR	LFHIGDDFVD	RELGFVVFP	KRNGVAVGFG	HFASVQTNQE
151	FDVFVDHFHG	QCEEFPEAVV	EAGNIACHF	NLDVLVATDV	NFMGIEHNEV
201	GSHEDRVAVQ	THFHA <u>IGVF</u>	<u>LVVFRICLHG</u>	GFVGVGAVHQ	TLGGDAQGNP
251	VQFHHFGNVA	LTVEGAGLV	ESAGKPSGGN	GLGLVNHLR	LVAFDTVVI
301	GEEEGFGFIR	VLRRDGGAD	STDVVAQMRD	AGGGYAGQNS	FFAHKNVLAA
351	SMPSEREKDA	PIIPDLPTS	SRQOTFPY*		

```

      10      20      30      40      50      60
m900.ppep  MPSETRQAEVRTASGSFORADADRIXFYVQXFACFFTRFRRAQLQLNLFDLRRVGGQLVVA
           |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a900       EVRTALGLFQRADTDRIYFAQXFACFFTRFLRAQLQLNLFDLRRVGGQLVVA
           10      20      30      40      50
           70      80      90      100     110     120

```

m900. pep	FARFGEFGVD	FRRQKFFG	GFTPRQ	AVGKHF	KFRK	FHRFR	RRRGEG	FVDFKQ	WAFVGL	FRLARLF
a900	FARFGEFGVD	FRRQKFFC	LAPSQAV	GKHF	KFCR	FRRRGES	FVDFKQ	RAFVGL	LLRLARLF	
	60	70	80	90	100	110				
m900. pep	130	140	150	160	170	180				
a900	HIGDDFVD	RFLGFFV	VPKRN	GVAVG	FGHFAS	VQTDQ	EFDV	FIDF	HFGQ	EEFPEAV
	120	130	140	150	160	170				
m900. pep	190	200	210	220	230	240				
a900	AGDVARH	FVDL	VAPD	GHFV	GVGHQ	NI	GSQNR	ITEQ	TFHTE	IRVFL
	180	190	200	210	220	230				
m900. pep	250	260	270	280	290	300				
a900	VGMGAV	HQTL	GS	DAGQ	NPVQ	FHHF	GS	VALA	VEGG	ALGV
	240	250	260	270	280	290				
m900. pep	310	320	330	340	350	360				
a900	AFDDTV	VIGEE	EEG	FGI	EV	LRRAD	GGAD	GV	VVAQ	MRDAG
	300	310	320	330	340	350				
m900. pep	370	380								
a900	PSEREK	DVPI	IPDL	PPTSS	RQQT	FPYX				
	360	370								

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2705>:

```
m901.seq
  1  ATGCCCGATT  TTTCGATGTC  CAATTTGGCC  GTTGCCCTTTT  CCATCACATT
51  GGCTGCCGGT  TTGTTTACCG  TATTakGyAG  TGGCTTGGTG  ATGTTTTCCA
101 AAACGCCATA  TCCGCGTGTG  TTGTCGTTTG  GTTGGCGCTT  TGCCGCGGGT
151 GCGATGGCTA  ATGTTTCCCT  GACGGAGATT  TTTCAgTAAGT  CCAGCGAGGC
201 GTTCGCTGAA  ATTTATGATA  AAGACCACGC  GTTTGCGGCG  GCGACCATGG
251 CATTTTTTGGC  CGGGATGGGC  GGCATTGCGC  TGATTGACCG  TCTGGTGCCG
301 AACCCGCATG  AAACTTTAGA  CGCGCAAGAC  CCGTCGTTTC  AAGAAAGCAA
351 ACGCCGCCAT  ATCGCGCGAG  TCGGCATGAT  GGC CGCGTTT  GCGATTACTG
401 CGCACAATT  CCCGGAAGGC  TTGGCGACGT  TTTTGTGCCAC  ATTGGA AAAAT
451 CCAGCAGTCG  GCGATGCTTT  GGCCTTGGCG  ATTGCCATCC  ATAATATTCC
501 GGAGGGCATT  TCCATCGCCG  CGCCGGTTTA  TTTTGCCACC  CCGACCGGTA
551 AGAAAACGGT  GTGGGCGTGT  CTGCTATCCG  GCTTGGCCGA  GCCGTTGGGG
601 GCGGCTTTGG  GCTATTGGT  TTTGCAGCCG  TTTTGTGTCG  CTGCCGTGTT
651 TGGTTCGGTA  TTCGCGGTGA  TAGCCGGTGT  GATGGTGT TTGGCGTTGG
701 ACGAGCTGnt  GCCGGCTGCC  AAACGCTATT  CAGACGGCCA  TGAAACCGTT
751 TACGGCCTGA  CAACGGGTAT  GCGGTGATT  GCCGTCAGCC  TGGTATTGTT
801 CCATTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 2706; ORF 901>:

```
m901.pep
  1  MPDFSMSNLA VAFSITLAAG LFTVLXSLGV MFSKTPNPRV LSFGLAFAGG
 51  AMVVYSLTEI FSKSSEAFAE IYDKDHAFAA ATMAFLAGMG GIALIDRIVP
```

1285

101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN  
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG  
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV  
 251 YGLTGMMAVI AVSLVLFHF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2707>:

a901.seq  
 1 ATGCCCGATT TTTCGATGTC CAATTTGGCC GTTGCCTTTT CCATTACGTT  
 51 GGCTGCCGGT TTGTTTACCG TATTAGGCAG CGGCTTGGTG ATGTTTCCCA  
 101 AAACGCCCAA TCCGCGCGTG TTGTCGTTTG GTTTGGCATT TGCCGCGCGT  
 151 GCGATGGTGT ATGTTTCCCT GACGGAGATT TTCAGTAAGT CCAGCGAGGC  
 201 GTTCGCTGAA ATTTATGATA AAGACCACGC GTTTCGCGCG GCGACCATGG  
 251 CATTTTGGC AGGGATGGGC GGCATTGCGC TGATTGACCG TCTGGTGCCG  
 301 AACCCGCATG AAACCTTAGA CGCGCAAGAC CCGTCGTTTC AAGAAAGCAA  
 351 ACGCCGCCAT ATCGCGCGAG TCGGCATGAT GCGCGCGTTT GCGATTACTG  
 401 CGCACAATTT CCCCAGAGGC TTGGCGACGT TTTTGGCCAC ATTGGAAAT  
 451 CCAGCAGTCG GGATGCCCTT GGCTTGGCG ATTGCCATCC ATAATATTCC  
 501 GGAGGGCATT TCCATCGCG CGCCGGTTTA TTTTGGCCAC CGCAGCCGTA  
 551 AGAAAACGGT GTGGGCGTGT CTGCTATCCG GCTTGGCCGA GCCGTTGGGG  
 601 GCGGCTTTGG GCTATTGGT TTGCGAGCG TTTTGTGCG CTGCCGTGTT  
 651 TGGTTCGGTA TTCGGCGTGA TAGCCGGTGT GATGGTGT TGGCGTTGG  
 701 ACGAGCTGCT GCCGCTGCC AAACGCTATT CAGACGGCCA TGAAACCGTT  
 751 TACGGCCTGA CAATGGGCAT GCGGTGATT GCCGTCAGCC TGGTATTGTT  
 801 CCATTTTAA

This corresponds to the amino acid sequence <SEQ ID 2708; ORF 901.a>:

a901.pep  
 1 MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG  
 51 AMVYVSLTEI FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP  
 101 NPHETLDAQD PSFQESKRRH IARVGMMAAF AITAHNFPEG LATFFATLEN  
 151 PAVGMPLALA IAIHNIPEGI SIAAPVYFAT RSRKKTWAC LLSGLAEPLG  
 201 AALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA KRYSDGHETV  
 251 YGLTGMMAVI AVSLVLFHF\*

m901/a901 98.9% identity in 269 aa overlap

m901.pep	10	20	30	40	50	60
	MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
a901	10	20	30	40	50	60
	MPDFSMSNLA VAFSITLAAG LFTVLGSGLV MFSKTPNPRV LSFGLAFAGG AMVYVSLTEI					
m901.pep	70	80	90	100	110	120
	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHETLDAQD PSFQESKRRH					
a901	70	80	90	100	110	120
	FSKSSEAF AE IYDKDHAF AA ATMAFLAGMG GIALIDRLVP NPHETLDAQD PSFQESKRRH					
m901.pep	130	140	150	160	170	180
	IARVGMMAA FAITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
a901	130	140	150	160	170	180
	IARVGMMAA FAITAHNFPEGLATFFATLEN PAVGMPLALA IAIHNIPEGISIAAPVYFAT					
m901.pep	190	200	210	220	230	240
	RSRKKTWAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
a901	190	200	210	220	230	240
	RSRKKTWAC LLSGLAEPLGAALGYLVLPQ FLSPAVFGSV FGVIAGVMVF LALDELLPAA					
m901.pep	250	260	270			
	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					
a901	250	260	270			
	KRYSDGHETV YGLTGMMAVI AVSLVLFHF					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2709>:

```

g902.seq
1  ATGCCGTC CG AACCCGAACG GCGGCATGGC AATACTGCCC TACCCTTCCC
51  GATAGCCGCA CGCCCAACGG TCGGTTTTTC CGGCAAGCCT TTCAAGATAA
101 CCGGCAAGTG TGTCTATTG CGCCGCCGCA TTGTCCAAGC GGTGATTTC
151 ACGCCGCGCC TGTTCGCCGT CGGCATTTC GCCGATGTAC CAGCCTATGT
201 GTTTGCGTGC GATGCGCACA CCGACGGTCT CACCATAAAA CGCGTGCATG
251 GCGCGGATGT GGTTCAAAAT GCGGCTCTG CATTCTGCCA AACTCAAGGC
301 AGGCGGTAA ACGCCGTGTT CGGCATAATG CTTCAAATCG CGGAAAAACC
351 ACGGCCTGCC TTGCGCGCCG CGCCCTATCA TGATGCCGTC GCGGCGGTT
401 TGTTCGAGGA cggCGGCGGC TTTTgcggc GAagtGATGT CGCGGTTGac
451 cCaggCCGGG ATGTTcAGAc ggCTTTTGGT CTCGGcgatg agttCGTAAC
501 gcGCCTCGCC TTGTACATT TCGGTGcgcg CGcgcccggtg aacggcaaGg
551 gcggcaatgc cgcaatcttc ggcgattttg gcgacggcgG gcaggttttg
601 atcgtcgtcg tgccaacca AacggGTTTT GaggGTAACG GGTAcgcCCG
651 CCGCCTTgac caccgcctcc aAAatggcGg caaccagcgg CTGTCCTGC
701 ATCagcGCGC TACCGGCTTG GACGTGCAC ACTTTcTtgg cgggGCAGCC
751 CATAttgATG TCGATGACCT GCGCCCCGAG TCCGACGTg taacgcgcg
801 ca tCCGCCAT CtgttcggGg TCGTCGCCG CAATCTGCAC GGCAACGATG
851 CCGcctcat cggcaAAAtc actgcggtgc aGGGTTTTTC CGGTATTcCT
901 GAGCGTCGGA TCGCTGGCCA GCATTTCGCA CACCGCCCAA CCTGCGCCAA
951 ACGCCCGACA GAGCGGCGG AAGGGTTTGT CGGCAATGCC CGCCATCGC
1001 GCAAGTGC GA TGGGTTGTC GATAAAATAA CCGCGATGT GCATAATGGG
1051 CCGCGTTTC AAAAAAGTGC GCCATTGTAC ATTTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2710; ORF 902.ng>:

```

g902.pep
1  MPSEPERRHG NTALPFPIAA RPTVGFSKPK FKITGKCVVL RRRIVQAVDF
51  TPRLFAVGHF ADVPAYVFAC DAHTDGLTIK RVHGADVQVN GGSAPCQTQG
101 RR *NAVFGIM LQIAEKPRPA LRAAPYHDAV GGGLFEDGGG FLRRSDVAVD
151 PGRDVQTAFG LGDEFVTRLA FVHLRARAPV NGKGGNAAlF GDFGDGGQVL
201 IVVVPTQTGF EGNgyARRLD HRLQNGGNQR LVLHORATGL DVAHFLGGAA
251 Hl DVDDLrPE SDVVTRRlRH LFGVAAGNLH GNDAAFIGKI TAVQGFSGIP
301 ERRIAGQHFA HRPTCAKRPT EAAEGFVGNA RHRRKCDGVV DKlTADVHNG
351 PAFQKSAPLY IF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2711>:

```

m902.seq
1  TTGCACTTTC AAAGGATAAT CAAGTGTTCa GAAGGCATTt GGGCGGTAGG
51  CGCACGCCCA ACTGTcGGTT TTTTCGGCAa GTCTTTCAAG ATAACCTGCA
101 AGCATGTCTG ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCAGCAGC
151 TgTCTgTTCG CCGTcGGGCA TTTCGTcGAT GTACCAGCCT ATGTGTTTGC
201 GTGCGATGCG CACACCGCGG GTGTcGCGGT AAAACGCGTG TATGCGCGCG
251 ATGTGgTTCA AAATAGCGGC GCGcATTCT GCCAAACTCA AGGCAGGCGG
301 CAAAACACCG TGTTcGGCAT AATGTTTCAa ATCGCGGAAG AACCACGGCC
351 TGCCTTcGCG GCCGCGCCCT ATCATAATGC CGTcGGCGGC GgTTTgTTTG
401 AGGACGGCTT GGGCTTTTtG CGGCGAAGTA ATGTcGCGT TGACCCAGAC
451 CGGGATgTTC AGACGGCATT TGGTTTcGGC GATGAGTTCG TAACCGCTT
501 CGCCTTTGTA CATTTGCGTA CGCGTcGCTC CGTGGACGGC AAGGGCGCGG
551 ATGCCGCAAT CTTCGCGCAT TTTGGCGATG ACggGcAGGT TTTGATGGTC
601 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCTGCCGCAC
651 GGACGACGGC TTCCAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
701 GCGCTACCGG CTTGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
751 GATGTCGATA AGCTGCGCCC CAAGGCTGAC GTTGTAAcGC GCGGCATCCG
801 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
851 TCATCGGCAa AATCGCTGCG GTGCAAGGT TTTCTAGTAT TTCTGAGCGT
901 CGGGTCGCTG GTCAGCATTt CGCACACCGC CCAACCTGCG CCAAAATCTC
951 GGCAAAAGTC GCGGAACGGT TTGTcGGTAA TGCCCGCCAT CGGcGCAAGT
1001 GCGATGGGGT TGTCGATAAA ATAGCCCGCG ATGTGCATAA TGGATCCCGG
1051 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2712; ORF 902>:

m902.pep  
 1 LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT  
 51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQQTQGR  
 101 QNTVFGIMFQ IAEPRPALR AAPYHNAVGG GLFEDGLGFL RRSNVAVDPD  
 151 RDVQTAFGFG DEFVTRFAFV HLRTRASVDG KGGDAIFGD FGDDGQVLMV  
 201 VVPQTGTFEG NGYACRTDDG FONGGNQRLV LHQRATGLDI ADFFSGTAHV  
 251 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER  
 301 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDCGVVDK IAADVHNGSA  
 351 FQKSTPLYIF \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 902 shows 80.9% identity over a 345 aa overlap with a predicted ORF (ORF 902.ng) from *N. gonorrhoeae*:

m902/g902

	10	20	30	40	50
m902.pep	LHFQRIIKCS EGIWAVGARP TVGFFGKSFK ITCKHVVLRR RTVQAVDFTT CLFAVGHF				
	::				
g902	MPSEPERRHGN TALPFP IAA RPTVGFSGKPFKITGKC VVLR RRIVQAVDFTT PRLFAVGHF				
	10	20	30	40	50
	60	70	80	90	100
m902.pep	VDVPAYVFACDA HTGGVAVKRV YGADVQNSG GAFQQTQGR RQNTVFGIMFQ IAEPRPA				
	:				
g902	ADVVPAYVFACDA HTDGLTI KRVHGADV VQNGGSAFCQTQGR RXNAVFGIMLQIAEKPRPA				
	70	80	90	100	110
	120	130	140	150	160
m902.pep	LRAAPYHNAVGG GLFEDGLGFL RRSNVAVD PDRDVQTAFGFGDEFVTRFAFVHLRTRASV				
	:				
g902	LRAAPYHDAVGG GLFEDGGGFL RRSNVAVD PGRDVQTAFGLGDEFVTRLAFVHLRARAPV				
	130	140	150	160	170
	180	190	200	210	220
m902.pep	DGKGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFONGGNQRLVLHQRATGL				
	:				
g902	NGKGGNAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRLDHRLQNGGNQRLVLHQRATGL				
	190	200	210	220	230
	240	250	260	270	280
m902.pep	DIADFFSGTAHV DDKLRPKADV VTRGIRHLLRIASGNLHGNNAAFIGKIAAVQGFSSIS				
	:          :				
g902	DVAHFLGGAHIDVDDL RPESDVVTRIRHLFGVAAGNLHGNDAAFIGKITAVQGFSGIP				
	250	260	270	280	290
	300	310	320	330	340
m902.pep	ERRVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLY				
	:				
g902	ERRIAGQHFAHRPTCAKRPTAAEGFVGNARHRRKCDGVVDKITADVHNGPAFQKSAPLY				
	310	320	330	340	350
	360				
m902.pep	IFX				
g902	IFX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2713>:

a902.seq

1 TTGCACTTC AAAGGATAAT CAAGTGTTC GAAGGCATT GGGCGGTAGG  
 51 CGCAGCCCA ACTGTCGGT TTTTCGGCA GTCTTCAAG ATAACCTGCA



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```

1 01 AACATGTCGT ATTGCGCCGC CGCACTGTCC AAGCGGTTGA TTTCACGACG
1 51 TGTCTGTTTCG CCGTCGGGCA TTTCGTGAT GTACCAGCCT ATGTGTTTGC
2 01 GTGCGATGCG CACACCGGCG GTGTCGCGT AAAACGCGTG CATGGCTCGG
2 51 ATGTGGTTCA AAATAGTGGC GGTACATTCT GCCAAACTCA AGGCAGGCGG
3 01 TAAACACCG TGTTGCGCGT AATGTTTCAA ATCGCGGAAG AACCACGGTC
3 51 TGCTTGCGC GCCGCGCCCT ATCATAATGC CGTCTGCGGC GGTTGTTTTC
4 01 AGGACGGCTT GGGCTTTTTC CGGCGAGGTA ATGTCGCGCT TGACCCAGAC
4 51 CCGGATGTTT AGACGGCATT TGGTTTCGGC AATCAGGTCG TAAGCCGCTT
5 01 CGCCTTTGTA CATTGCGTG CGCGTGCCTC CGTGGACGGC AAGGCGGGCA
5 51 ATGCCGCAAT CTTCGGCGAT TTTGGCGATG ACGGGCAGGT TTTGATGGTC
6 01 GTCGTGCCAA CCCAAACGGG TTTTGAGGGT AACGGGTACG CCCGCCGCTT
6 51 TGACCACCGC CTCCAAATG GCGGCAACCA GCGGCTCGTT CTGCATCAGC
7 01 GCGGTACCGG CTTGGACATT GCAGACTTTT TTAGCGGGAC AGCCCATGTT
7 51 GATGTCGATA AGCTCGCGCC CAAGGCTGAC GTTGTAAACG CCGGCATCCG
8 01 CCATCTGCTG CGGATCGCTT CCGGCAATCT GCACGGCAAC AATGCCGCCT
8 51 TCATCGGCAA AATCGCTGCG GTGCAAGGTT TTTCTAGTAT TTCTGAGCGT
9 01 CGGGTCGCTG GTCAGCATTT CGCACACCGC CCAACCTGCG CCAAATCTC
9 51 GGCAAAGTCG GCGGAACGGT TTGTCGGTAA TGCCCGCCAT CGGCGCAAGT
10 01 GCGATGGGGT TGTCGATAAA ATAGCCGCGC ATGTGCATAA TGGATCCGCG
10 51 TTTCAAAAAA GTACGCCATT GTACATTTT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2714; ORF 902.a>:

## a902.pep

```

1 LHFQRIIKCS EGIWAVGARPTVGFPGKSEF ITCKHVLLRR RTVQAVDFTT
51 CLFAVGHFVD VPAYVFACDA HTGGVAVKRV HGSDVVQNSG GTFCQTQGRR
1 01 *NTVFGVMFQ IAEPRALS AAPYHNAVCG GLFEDGLGFL RRGNAVDPD
1 51 RDVQTAFGFG NQVVSRAFAV HLRARASVDG KGNAAIFGD FGDDGQVLMV
2 01 VVPTQTGFEG NGYARRFDHR LQNGGNQRLV LHQRATGLDI ADFFSGTAHV
2 51 DVDKLRPKAD VVTRGIRHLL RIASGNLHGN NAAFIGKIAA VQGFSSISER
3 01 RVAGQHFAHR PTCAKISAKS AERFVGNARH RRCDDGVVDK IAADVHNGSA
3 51 FQKSTPLYIF *

```

m902/a902 94.7% identity in 360 aa overlap

	10	20	30	40	50	60
m902.pep	LHFQRIIKCSEGIWAVGARPTVGFPGKSEF ITCKHVLLRRRTVQAVDFTTCLFAVGHFVD					
a902	LHFQRIIKCSEGIWAVGARPTVGFPGKSEF ITCKHVLLRRRTVQAVDFTTCLFAVGHFVD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m902.pep	VPAYVFACDAHTGGVAVKRVHGSDVVQNSG GAFQQTQGRRQNTVFGIMFQIAEPRPALR					
a902	VPAYVFACDAHTGGVAVKRVHGSDVVQNSG GTFQQTQGRRXNTVFGVMFQIAEPRSALR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m902.pep	AAPYHNAVGGGLFEDGLGFLRRSNVAVDPDRDVQTAFGFGDEFVTRFAFVHLRTRASVDG					
a902	AAPYHNAVCGGLFEDGLGFLRRGNVAVDPDRDVQTAFGFGNQVVSRAFAVHLRARASVDG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m902.pep	KGGDAIFGDFGDDGQVLMVVVPTQTGFEGNGYACRTDDGFQNGGNQRLVLHQRATGLDI					
a902	KGGNAAIFGDFGDDGQVLMVVVPTQTGFEGNGYARRFDHRLQNGGNQRLVLHQRATGLDI					
	190	200	210	220	230	240
	250	260	270	280	290	300
m902.pep	ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSISER					
a902	ADFFSGTAHVVDVKLRPKADVTRGIRHLLRIASGNLHGNNAFIGKIAAVQGFSSISER					
	250	260	270	280	290	300
	310	320	330	340	350	360
m902.pep	RVAGQHFAHRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF					

```

a902      |||||
          RVAGQHFHFRPTCAKISAKSAERFVGNARHRRKCDGVVDKIAADVHNGSAFQKSTPLYIF
          310      320      330      340      350      360

m902.pep    X
             |
a902        X

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2715>:

```

g903.seq
1  ATGGCAACAC AGGTAGGCGG TGCAAattcg gatgaggCAA GCCCCTGCTT
51 TCCTATTCTT GAGGTGGAA TGGTGGGTGA aGaaacggct aaATTCCGgt
101 tTGCCTCaa ccaTGCCTTG tgccAAACAC ATTTTGtttc cGcaagtgt
151 CTGcATGcgg gcgacatTAA TCAAatcaTG TCCTTAGCAC AAAATGCTTT
201 GATCGGCAGG GGATATACCA CGACCGGTAT CTTGGCTGCG CCACAGGATT
251 TGAATAGTGG caaGCTTCAA TTAaccctga tgccggGCTA TctgcgctcC
301 ATAcgaATCG atcgggtccaa cgatgatcaa ACCCATgcAG GACGTATTGC
351 AGCATTCCAA AACAAATTTC CCACCCGCTC GAACGATCTG TTGAATCTGC
401 GTGATTGGA ACAAGGACTG GAAAATCTCA AATGTCTCCC GACTGCGGAA
451 GCCGATCTCC AAATCgttcc cgtagAGAGA GAACcAAACC AAAGTGATGT
501 CGTGGTGCAA TGGCGGTAAC GTCTGCTGCC CTACTGTGTG AGTGTGGGGA
551 TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG AAATATCACT
601 TTCTCTGCCG ACAATCCTTT TggactgAGT GATATGTTCT ATGTAAATTA
651 TGGACGTTCA ATTGGCGGTA CGcccgATGA GGAAATTTT GACGGCCATC
701 GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC AGCCCCTTTC
751 GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT ACCATCAGGC
801 GGTTCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA AGTTACAACA
851 CTGATTTCCG CTTCAACCGC CTGTTGTATC GTGATGCCAA ACGCAAAACC
901 TATCTCAGTG TAAACTGTG GACGAGGGAA ACAAAAAGTT ACATTGATGA
951 TGCCGAAGT ACTGTACAAC GGCGTAAAC CACAGGTTGG TTGGCAGAAC
1001 TTTCCACAA AGGATATATC GGTCGCAGTA CGGCAGATT TAAGTTGAAA
1051 TATAAACACG GCACCGCAT GAAAGATGCT CTGCGCGCGC CTGAAGAAGC
1101 CTTTGGCGAA GGCACGTCAC GTATGAAAT TTGGACGGCA TCGGCTGATG
1151 TAAATACTCC TTTTCAAATC GGTAAACAGC TATTTGCCTA TGACACATCC
1201 GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG ACAAACTGGC
1251 TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA ATGAGTTTGC
1301 CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG GCAATTTAAA
1351 CAGGCCATC AGCTTATCT TGGGGCTGAT GTAGGACATG TTTCAGGACA
1401 ATCCGCCAAA TGGTTATCGG GCCAAACTCT AGCCGGCACA GCAATTGGGA
1451 TACGCGGCA GATAAGCTT GCGCGCAACC TGCATTACGA TATATTACC
1501 GGCCGTGCAT TGAAAAGCC cgaatatTTT CAGACGAAGA Aatgggtaac
1551 ggggtTTCAG gtgggttatt cgTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2716; ORF 903.ng>:

```

g903.pep
1  MATQVGGANS DEASPCFPIS EVELVGEETA KFRFALNHAL CQTHFVSGKC
51 LHAGDINQIM SLAQNALIGR GYTTTRILAA PQDLNSGKLQ LTLMPGYLRS
101 IRIDRSNDDQ THAGRIAAFO NKFPTRSNDL LNLRLDLEQGL ENLKCLPTAE
151 ADLQIVPVER EPNQSDVVVQ WRXRLLPYCV SVGMDNSGSE ATGKYQGNIT
201 FSADNPFGLS DMFYVNYGRS IGGTPDEENF DGHKKEGGSN NYAVHYSAPP
251 GKWTWAFNHN GYRYHQAVSG LSEVYDYNKG SYNDFGFNR LLYRDAKRKT
301 YLSVKLWTRE TKSYYDDAEL TVQRRKTTGW LAELSHKGYI GRSTADFKLK
351 YKHGTGMKDA LRAPEEAFGE GTSRMKIWTA SADVNTPFQI GKQLFAYDTS
401 VHAQWNKTPL TSQDKLAIGG HHTVRGFDGE MSLPAERGKY WRNDLSWQFK
451 PGHQLYLGLAD VGHVSGQSAK WLSGQTLAGT AIGIRGQIKL GGNLHYDIFT
501 GRALKKPEYF QTKKWVTGFO VGYSF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2717>:

```

m903.seq
1  ATGCAGCGTC AGCAGCACAT AGATGCTGAA TTGTTAACTG ATGCAAATGT
51 CCGTTTCGAG CAACCATTTG AGAAGAACAA TTATGTCCTG AGTGAAGATG
101 AAACACCGTG TACTCGGGTA AATTACATTA GTTTAGATGA TAAGACGGTG

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1 51 CGCAAATTTT CTTTCTTCC TTCTGTGCTC ATGAAAGAAA CAGCTTTTAA
2 01 AACTGGGATG TGTTTAGGTT CCAATAATTT GAGCAGGCTA CAAAAAGCCG
2 51 CGCAACAGAT ACTGATCGTG CGTGGCTACC TCACTTCCCA AGCTATTATC
3 01 CAaCCACAGA ATATGGATTC GGAATTCTG AAATTACGGG TATCAGCAGG
3 51 CGAAATAGGG GATATCCGCT ATGAAGAAAA ACGGGATGGG AAGTCTGCCG
4 01 AGGGCAGTAT TAGTGCATTC AATAACAAAT TTCCCTTATA TAGGAACAAA
4 51 ATTCTCAATC TTCGCGATGT AGAGCAGGGC TTGGAAGAAC TCGCTCGTTT
5 01 GCCGAGTGTT AAAACAGATA TTCAGATTAT ACCGTCCGAA GAAGAAGGCA
5 51 AAAGCGATTT ACAGATCAAA TGGCAGCAGA ATAAACCCAT ACGGTTTCAGT
6 01 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
6 51 TGCCTCTTGA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTtTATG
7 01 TTTCATATGG ACGCGGTTTG GCGCACAAAA CCGACTTGAC TGATGCCACC
7 51 GGTACGGAAA CTGAAAGCGG ATCCAGAAAGT TACAGCGTGC ATTATTCGGT
8 01 GCCCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
8 51 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAAACAA
9 01 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGACTTCA
9 51 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
10 01 TCGACGATGC CGAAATCGAA GTACAACGCC GCCGCTCTGC AGGCTGGGAA
10 51 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
11 01 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCTGCACCGG
11 51 AAGAAAACGG CGGCGATATT CTTCCAGGTA CATCTCGTAT GAAAATCATT
12 01 ACTGCCAGTT TGGACGCAGC CGCCCCATTT AytTTAGGCA AACAGCAGTT
12 51 TTTCTACGCA ACCGCCATTC AAGCTCAATG GAACAAAACG CCGTTGGTTG
13 01 CCCAAGATAA ATTGTCAATC GGCAGCGGCT ACACCGTTCG CGGATTTCAT
13 51 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
14 01 AACTTGGTAT TTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
14 51 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
15 01 GGTGCAGTGG TCGCTTCAG AGGAGGGCAT AAAGTAGGCG GTATGTTTGC
15 51 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
16 01 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2718; ORF 903>:

m903.pep

```

1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV
51  RKFSFLPSVL MKETAFKTM CLGSNNLSRL QKAAQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEKRDG KSAEGSISAF NNKFLYRNK
151 IILNRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFYVSYGRGL AHKTDLTDAT
251 GTETESGSRs YSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSSLAAERM LWRNRLHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAIYL RWQLDGKLSY KRGTMGRQSM PAPEENGDDI LPGTSRMKII
401 TASLDAAAPF XLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVRGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTINTVYG FNLNYSF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 903 shows 48.9% identity over a 519 aa overlap with a predicted ORF (ORF 903.ng) from *N. gonorrhoeae*:

m903/g903

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          |:::| |:::| |:::| |:::| |:::| |:::|
g903      MATQVGANSDEASPCFP ISEVELVGEETAKFRFALNHA
          10      20      30

          70      80      90     100     110     120
m903.pep  MKETAFKTMCLGSNNLSRL QKAAQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
          :| | | | |:::| |:::| |:::| |:::| |:::| |:::|
g903      LCQTHFVSGKCLHAGDINQIMSLAQNALIGRGYTTTRILAAPQDLNSGKQLTLMPGYLR
          40      50      60      70      80      90

```

[illegible]

a903.seq

1	ATGCAGCGTC	AGCAGCACAT	AGATGCTGAA	TTGTTAACTG	ATGCAAATGT
51	CCGTTTCGAG	CAACCATTGG	AGAAGAACAA	TTATGTCCTG	AGTGAAGATG
101	AAACACCGTG	TACTCGGGTA	AATTACATTA	GTTTAGATGA	TAAGACGGCG
151	CGCAAAATTT	CTTTTCTTCC	TTCTGTGCTC	ATGAAAGAAA	CAGCTTTTAA
201	ACCTGGGATG	TGTTTAGGTT	CCAATAATT	GAGCAGGCTA	CAAAAAGCCG
251	CGCAACAGAT	ACTGATTGTG	CGTGCGTACC	TCACTTCCCA	AGCTATTATC
301	CAACCACAGA	ATATGGATTG	GGGAATTCTG	AAATTACGGG	TATCAGCAGG
351	CGAAATAGGG	GATATCCGCT	ATGAAGAAAA	ACGGGATGGG	AAGTCTGCCG
401	AGGCGAGTAT	TAGTGCGATT	AATAACAAAT	TTCCCTTTAT	TAGGAACAAA
451	ATTCTCAATC	TTCCGCGATG	AGAGCAGGGC	TTGGAAAACC	TGCGTCGTTT
501	GCCGAGTGTT	AAAACAGATA	TTCAGATTAT	ACCGTCCGAA	GAGAAGGCA
551	AAAGCGATTT	ACAGATCAAA	TGGCAGCAGA	ATAAACCCAT	ACGGTTTCAGT

1292

```

601 ATCGGTATAG ATGATGCGGG CGGCAAAACG ACCGGCAAAT ATCAAGGAAA
651 TGTCGCTTTA TCGTTCGATA ACCCTTTGGG CTTAAGCGAT TTGTTTTATG
701 TTTTCATATGG ACGCGGTTTG GTGCACAAAA CGGACTTGAC TGATGCCACC
751 GGTAACGAAA CTGAAAGCGG ATCCAGAAGT TACAGCGTGC ATTATTCGGT
801 GCGCGTAAAA AAATGGCTGT TTTCTTTTAA TCACAATGGA CATCGTTACC
851 ACGAAGCAAC CGAAGGCTAT TCCGTCAATT ACGATTACAA CGGCAAACAA
901 TATCAGAGCA GCCTGGCCGC CGAGCGCATG CTTTGGCGTA ACAGGTTTCA
951 TAAAACTTCA GTCGGAATGA AATTATGGAC ACGCCAAACC TATAAATACA
1001 TCGACGATGC CGAAATCGAA GTGCAACGCC GCCGCTCTGC AGGCTGGGAA
1051 GCCGAATTGC GCCACCGTGC TTACCTCAAC CGTTGGCAGC TTGACGGCAA
1101 GTTGTCTTAC AAACGCGGGA CCGGCATGCG CCAAAGTATG CCCGCACCTG
1151 AAGAAAACGG CGGCGGTACT ATTCCAGGCA CATCCCGTAT GAAAATCATA
1201 ACCGCCGATG TGGATGCAGC GGCCCGGTTT ATGTTGGGCA AACAGCAGTT
1251 TTTCTACGCA ACCGCCATTG AAGCTCAATG GAACAAAACG CCTTTGGTTG
1301 CCCAAGACAA GTTGTCTATC GGCAGCGCGT ACACCGTNG CGGATTTGAT
1351 GGGGAGCAGA GTCTTTTCGG AGAGCGAGGT TTCTACTGGC AGAATACTTT
1401 AACTTGGTAT TTTTCATCCGA ACCATCAGTT CTATCTCGGT GCGGACTATG
1451 GCCGCGTATC TGGCGAAAGT GCACAATATG TATCGGGCAA GCAGCTGATG
1501 GGTGCACTGG TCGGNTTCAG AGGAGGNCAT AAAGTAGGCG GTATGTTTGC
1551 TTATGATCTG TTTGCCGGCA AGCCGCTTCA TAAACCCAAA GGCTTTCAGA
1601 CGACCAACAC CGTTTACGGC TTCAACTTGA ATTACAGTTT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 2720; ORF 903.a>:

```

a903.pep
1  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTA
51  RKFSFLPSVL MKETAFTKGM CLGSNNLSRL OKAAQQILIV RGYLTSQAI
101 QPQNMDSGIL KLRVSAGEIG DIRYEEKRDG KSAEGSISAF NNFPLYRNK
151 ILNLRDVEQG LENLRLPSV KTDIQIIPSE EEGKSDLQIK WQONKPIRFS
201 IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFVVSYGRGL VHKTDLTDAT
251 GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
301 YQSSLAERML LWRNRFHKTS VGMKLWTRQT YKYIDDAEIE VQRRRSAGWE
351 AELRHRAYLN RWQLDGKLSY KRGTMGRQSM PAPEENGGGT IPGTSRMKII
401 TAGLDAAAPF MLGKQOFFYA TAIQAQWNKT PLVAQDKLSI GSRYTVXGFD
451 GEQSLFGERG FYWQNTLTWY FHPNHQFYLG ADYGRVSGES AQYVSGKQLM
501 GAVVGFRGGH KVGGMFAYDL FAGKPLHKPK GFQTTNTVYG FNLNYSF*

```

m903/a903 98.4% identity in 547 aa overlap

```

          10      20      30      40      50      60
m903.pep  MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKTV RKFSFLPSVL
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a903       MQRQQHIDAE LLTDANVRFE QPLEKNNYVL SEDETPCTRV NYISLDDKT ARKFSFLPSVL
          10      20      30      40      50      60

          70      80      90     100     110     120
m903.pep  MKETAFTKGM CLGSNNLSRL OKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a903       MKETAFTKGM CLGSNNLSRL OKAAQQILIV RGYLTSQAI IQPQNMDSGIL KLRVSAGEIG
          70      80      90     100     110     120

          130     140     150     160     170     180
m903.pep  DIRYEEKRDG KSAEGSISAF NNFPLYRNK ILNLRDVEQG LENLRLPSV KTDIQIIPSE
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a903       DIRYEEKRDG KSAEGSISAF NNFPLYRNK ILNLRDVEQG LENLRLPSV KTDIQIIPSE
          130     140     150     160     170     180

          190     200     210     220     230     240
m903.pep  EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFVVSYGRGL
          | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a903       EEGKSDLQIK WQONKPIRFS IGIDDAGGKT TGKYQGNVAL SFDNPLGLSD LFVVSYGRGL
          190     200     210     220     230     240

          250     260     270     280     290     300
m903.pep  AHKTDLTDAT GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ
          : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a903       VHKTDLTDAT GTETESGSR SSVHYSVPVK KWLFSFNHNG HRYHEATEGY SVNYDYNKGQ

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1293

	250	260	270	280	290	300
	310	320	330	340	350	360
m903.pep	YQSSLAERMLWRNRLHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRLAYLN					
a903	YQSSLAERMLWRNRFHKT SVGMKLWTRQTYKYIDDAEIEVQRRRSAGWEAELRHRLAYLN					
	370	380	390	400	410	420
m903.pep	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
a903	RWQLDGKLSYKRGTMQRQSMPEENGDDILPGTSRMKIITASLDAAAPFXLGKQQFFYA					
	430	440	450	460	470	480
m903.pep	TAIQAQWNKTPLVAQDKLSIGSRYTVRGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
a903	TAIQAQWNKTPLVAQDKLSIGSRYTVXGFDGEQSLFGERGFYWQNTLTWYFHPNHQFYLG					
	490	500	510	520	530	540
m903.pep	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
a903	ADYGRVSGESAQYVSGKQLMGAVVGFRRGGHKVGGMFAYDLFAGKPLHKPKGFQTTNTVYG					
	490	500	510	520	530	540
m903.pep	FNLNYSFX					
a903	FNLNYSFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2721>:

g904.seq

```

1  ATGATGCAGC ACAATCGTTT CTTGCGGTC GGGGCCGGTg gaGACGATGG
51  CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGCA ATGCGTCGTA GCTTTTCACG CCGACAGTCG ATTCGCGCCA
151 GCCGGGCATG GTTTCGTAAA TCGGTTTGCA GGTTCACACC GCATCCGAAC
201 CGCAAGGCAG GATGTCGGTT TTGCCGCCG CTGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATGCA
301 CATAACGGAA ATGCCGTTGA TTTGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACAGGCC GCAGCGGCGC GCGCGGCCG TTACCGAACC GAATTCGTGT
401 CCGCGCTCCG CCAAACCTGC GCCTACTTCG TCGAACCAAT CCGTCGGGAA
451 CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCAAAACAT
501 AATCCAGCAT TTGAGGACCT ACGCCGCGC CTGCCGAAGC CGCGCGGGCG
551 AGACAGTTGG ACGAGGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TCGCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTGTTTCAA CACGCgggaC acgtcgGCAA TCATCGGCGC AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCACGTCT TCCGCTTTAA CCGGTCCGGC
751 GTTATGCAGG TATTGGAGTT GGACGTTGTA ATAGGCAAGG ACGGCATCCA
801 GTTTTTACAG CAGTTTTTCA GGATGCAGCA AATCGCGGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CTTTTCGCGC GCGATGCTTC GCGGGCTTGG TCGAGCGCGA
951 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
1001 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
1051 GGCTTCGGGg gaaacgAcaa cGCCCCAACC gatGAAGCAA TCCAATCCTT
1101 CGTGCAGGAT ACCGCTCGGA ATCAGGCGCA AAATGTTTTT TTTGCCGCGG
1151 ACGACCAAGG TATGGCCCGC ATTGTGGCCG CCTTGAAGC GCACgacGct
1201 gCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
1251 CCACTGTgc gccGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
1301 ATCGatatTA A

```

This corresponds to the amino acid sequence <SEQ ID 2722; ORF 904.ng>:

g904.pep

```

1  MMQHNRFFAV GAGGDDGDRR AADFFNPFQI CFGIGRQCVV AFHADS RFAP

```

```

51 AGHGFVNRFA GFHRIRARQ DVGFAAAWQF VADADIDGFN AVHYIEFGNA
1 01 HTGNAVDLDG AFQGGGKPA AAARAAGYRT EFVSALRQTC AYFVEQFGRE
1 51 RARTDARGIG FDDAQNI IQH LRTYARACRS RAGETVGRGN EGVSAVVDVQ
2 01 QRTLRAFQKQ FFAVFVFFVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRSR
2 51 VMQVLELDV IGKDG IQFFT QFFRMQQIGG ANGAACHFVF VGRADAAAGR
3 01 ADFAFARCF AGLVERDVVR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
3 51 GFGGNDNART DEAIQSFVQD TARNQAQNGF FAADDQGMAR IVAALEAHDA
4 01 AGFFRQPVND FTFTLVAPLC ADYINIFSHS HITRY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2723>:

```

m904.seq
1 ATGATGCAGC ACAATCGTTT CTTCTCGGTC GGGGCCGgTG GAGACGATGG
51 CGACCGGCGC GCCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCG
1 01 TTTTCGGGCA ATGCGCCGTA GTCCTTCACG CCGAAAGTGG ATTTCGCGCA
1 51 GCCGGGCATG GTTTCGTAAA TCGGCTTGCA GGTTCACACC GCATCGGAAC
2 01 CGCAAGGCAG GATGTCGGTT TTGCCCGCGT CGGGCAATTC ATAGCCGACG
2 51 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TAGTAATACA
3 01 CATACCGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
3 51 CAAACCGACC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
4 01 CCGCGTTCTG CCAAACCTAC GCCTACTTCG TCGAACAAAT CGGTCCGGAA
4 51 CCGGCCCGAA CCGACGCGCG TGGTATAGGC TTTGACGATG CCCAAAACAT
5 01 AATCCAGCAT TTGAGGACCT ACGCCGCGC CTGCCGAAGC TGCGCCCGCC
5 51 AGACAGTTGG ACGAGGTAAC GAAGGGATAA GTGCCGTAGT CGATGTCCAA
6 01 CAACGCACCT TCGCGCCTT CAAACAGCAG TTTTTCGCCG TTTTGTGTTT
6 51 TCTCGTTCAA CACGCGGGAC ACGTCGGTAA TCATCGGCGC AATGCGCGGC
7 01 GCGACTTTT CGATAACCGC CATCACGTCT TCCGCTTAA CCGGCTCGGC
7 51 ATTGTGCAGA TGTTCAGTT GGACATTGTA ATAGGCAAGG ACGGCATCCA
8 01 GTTTTTCACG CAGTTTtTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
8 51 CGGCGTGCCA CTTTGTCTTC GTAGGAGGG CCGATGCCGC GGCCGGTCGT
9 01 GCCGATTTTG CTTTTCGCCG GCG.ATcTTC GCGGGCTTGG TCAGCGCGCA
9 51 TGTGGTAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
10 01 TCACGTTT TCACGCTGC CCGGTTCAAC TCGTCGATT CGCCCAACAG
10 51 GGCTTCGGGG GAGACGACAA CGCCGAACC GATGAAGCAG TCCAAACTTT
11 01 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTTGCCGCCG
11 51 ACAACCAAGG TATGGCCCGC ATTGTGGCCG CTTGGAAGC GCACCaCGCC
12 01 GCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
12 51 CCCACTGTGC GCCGATTAsT ACAACATTT TAGCCATAGC CATATAACCT
13 01 ATCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2724; ORF 904>:

```

m904.pep
1 MMQHNRFSSV GAGGDDGDRR AADFFNPFQI CFGVFGQCAV VLHAESGFAP
51 AGHGFVNRFA GFHRIGTARQ DVGFAAVGQF IADADIDGFN AVHYIEFSNT
101 HTGNAVDLDG AFQGGGKPA AAACASGYRT EFVSALRQTC AYFVEQFGRE
151 RARTDARGIG FDDAQNI IQH LRTYARACRS CARQTVGRGN EGISAVVDVQ
201 QRTLRAFQKQ FFAVFVFLVQ HAGHVGNHRR NARRDFFDNR HHVFRFNRLG
251 IVQMLQLDIV IGKDG IQFFT QFXRMQQIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAXIF AGLVERDVVR QDQAGRRDF QTAFDVFHAC RVQLVDFAQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMAR IVAALEAHHA
401 AGFFRQPVND FTFTLVAPLC ADXYNIFSHS HITRY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 904 shows 90.4% identity over a 436 aa overlap with a predicted ORF (ORF 904.ng) from *N. gonorrhoeae*:

m904/g904

```

          10      20      30      40      50      60
m904.pep MMQHNRFSSVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRFA
          |||||:|||||:|||||:|||||: ||:|:|:|:| |||||:|
g904      MMQHNRFFAVGAGGDDGDRRAADFFNPFQICFGIGRQCVVAFHADS RFAPAGHGFVNRFA
          10      20      30      40      50      60
          70      80      90     100     110     120

```

1295

m904 . pep	GFHRIGTARQDVGFAAVQGFIADADIDGFNAVHYIEFSNHTGNAVDLDGAFQGGGIKPA
g904	GFHRIRTARQDVGFAAAWQFVADADIDGFNAVHYIEFGNAHTGNAVDLDGAFQGGGIKPA
	70 80 90 100 110 120
m904 . pep	AAACASGYRTEFVS AFCQTYAYFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
g904	AAARAAGYRTEFVSALRQTCA YFVEQFGRERARTDARGIGFDDAQNI IQHLRTYARACRS
	130 140 150 160 170 180
m904 . pep	CARQTVGRGNEGISAVVDVQORTLRAF KQOFFAVFVFLVQHAGHVGNHRRNARRDFFDNR
g904	RAGETVGRGNEGVSAVVDVQORTLRAF KQOFFAVFVFFVQHAGHVGNHRRNARRDFFDNR
	190 200 210 220 230 240
m904 . pep	HHVFRFNRLGIVQMLQLDIVIGKDG IQFFTOFXRMQQIGGANGAACHFVFVGRADAAAGR
g904	HHVFRFNRSQVLELDVVGKDG IQFFTOFFRMQQIGGANGAACHFVFVGRADAAAGR
	250 260 270 280 290 300
m904 . pep	ADFAFAARIFAGLVERDVVRQDQ RAGRRDFQTA FDFVHACRVQLVDF AQQGFGGDDNART
g904	ADFAFAARCFAGLVERDVVRQDQ RAGRRDFQTA FDFVHACRVQLVDF AQQGFGGNDNART
	310 320 330 340 350 360
m904 . pep	DEAVQTFMQDAARNQAQNGFFAADNQGMARIVAAL EAHHAAGFFRQPVNDFTTFLVAPLC
g904	DEAIQSFVQDTARNQAQNGFFAADNQGMARIVAAL EAHDAAGFFRQPVNDFTTFLVAPLC
	370 380 390 400 410 420
m904 . pep	ADXYNIFSHSHITYRYX
g904	ADYYNIFSHSHITYRYX
	430

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2725>:

a904 . seq

```

1  ATGATGCAGC ACAATCGTTT CTTCGCGGTC GGGGCCGGTG GAGACGATGG
51  CGACCGGCGC ACCGCAGACT TCTTCAATCC GTTTCAAATA TGCTTTGGCA
101 TTGGCAGGTA ATGCGTCGTA GCTTTTCACG CCGAAAGTGG ATTCGCTCCA
151 ACCGGGCATG GTTTCGTAAA TCGGCTTGCA GGCTTCTACC GCATCAGAGC
201 CGCAAGGCAG GATGTCGGTT TTGCGCCGCT CGGGCAATTC GTAGCCGACG
251 CAGATATTGA TGGTTTCAAC GCCGTCCATT ACATCGAGTT TGGTAATACA
301 CATAACGGAA ATGCCGTTGA TTTGGATGGA GCGTTTCAGG GCGGCGGCAT
351 CAAACCAAGC GCAGCGGCGT GCGCGTCCGG TTACCGAACC GAATTCGTGT
401 CCGCGTTCTG CCAAACCTGC TCCGACTTCG TCGAACAATT CCGTCGGGAA
451 CGGGCCCCGAA CCGACGCGCG TGGTATAGGC TTGACGATG CCCAAACAT
501 AATCCAGCAT TTGAGGCGCT ACGCCCGCGC CTGCCGAAGC CGCGCCGGCG
551 AGGCAGTTGG ACGAAGTAAC GAAGGGGTAA GTGCCGTAGT CGATGTCCAA
601 CAACGCACCT TGC GCGCCTT CAAACAGCAG TTTTTCGCGG TTTTGTGTTT
651 TTTTCGTTCA CACGCGGGAC ACGTCGGTAA TCATCGGCGT AATGCGCGGC
701 GCGACTTTTT CGATAACCGC CATCAGTCT TCCGCTTTCA CCGACTCGGC
751 ATTGTGCAGA TGTGTCAGT GGACGTTGTA ATAAGCAAAG ACGGCATCCA
801 GTTTTTTACG CAGTTTTTCA GGATGCAGCA AATCGGCGGC GCGAATGGCG
851 CGGCGTGCCA CTTTGTCTTC GTAGGCAGGG CCGATGCCGC GGCCGGTCGT
901 GCCGATTTTG CCTTGCCGCG GCGATGCTTC TCGGCTTGG TCGAGCGCGA

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1296

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9 51 TGTGATAAGG CAGGATCAGC GGGCAGGTCG GCGCGATTTT CAGACGGCCT
10 01 TCGACGTTTT TCACGCCTGC CGCGTTCAAC TCGTCGATTT CGCCCAACAG
10 51 GGCTTCGGGG GAGACGACAA CGCCCGAACC GATGAAGCAG TCCAGACTTT
11 01 CATGCAGGAT GCCGCTCGGA ATCAGGCGCA AAATGGTTTT TTGCGCGCCG
11 51 ACAACCAAGG TATGACCCGC ATTGTGGCCG CCTTGGGAAG GCACCACGCC
12 01 TCCGGCTTCT TCCGCCAGCC AGTCAACGAT TTTACCTTTA CCCTCGTCGC
12 51 CCCACTGTGC GCCGATTACT ACAACATTTT TAGCCATAGC CATATAACCT
13 01 .TCGATATTA A

```

This corresponds to the amino acid sequence <SEQ ID 2726; ORF 904.a>:

## a904.pep

```

1 MMQHNRF FAV GAGGDDGDRR TADFFNPFQI CFGIGR*CVV AFHAESGFAP
51 TGHGFVNRLA GFYRIRARQ DVGFAAVGQF VADADIDGFN AVHYIEFGNT
101 HTGNAVLDG AFQGGGKPA AAACASGYRT EFVS AFCQTC SDFVEQFGRE
151 RARTDARGIG FDDAQNIQH LRAYARACRS RAGEAVGRSN EGVSAVVDVQ
201 QRTLRAF KQ FFAVFVFFVQ HAGHVG NHRR NARRDFFDNR HHVFRF HRLG
251 IVQMLQLDVV ISKDG IQFFT QFFRMQ QIGG ANGAACHFVF VGRADAAAGR
301 ADFAFAARCF SGLVERDVIR QDQ RAGRRDF QTA FDVFHAC RVQLVDF AQQ
351 GFGGDDNART DEAVQTFMQD AARNQAQNGF FAADNQGMTR IVAALEAHHA
401 SGFFRQPVND FTTLVAPLC ADYYNIFSHS HITXRY*

```

m904/a904 91.3% identity in 436 aa overlap

	10	20	30	40	50	60
m904.pep	MMQHNRF	SVGAGGDDGDRRAADFFNPFQICFGVFGQCAVVLHAESGFAPAGHGFVNRLA				
a904	MMQHNRF	FAVGAGGDDGDRRTADFFNPFQICFGIGRXC VVAFHAESGFAPTGHGFVNRLA				
	10	20	30	40	50	60
	70	80	90	100	110	120
m904.pep	GFHRIGTARQDVGF	AAVVGQFIADADIDGFNAVHYIEFSNTH	TGN	AVDLDGAFQGGGKPA		
a904	GFYRIRARQDVGF	AAVVGQFVADADIDGFNAVHYIEFGNTH	TGN	AVDLDGAFQGGGKPA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m904.pep	AAACASGYRTEFV	S AFCQTYAYFEVQFGRERARTDARGIGFDDAQNIQH	LR	TYARACRS		
a904	AAACASGYRTEFV	S AFCQTCSD FVEQFGRERARTDARGIGFDDAQNIQH	LR	AYARACRS		
	130	140	150	160	170	180
	190	200	210	220	230	240
m904.pep	CARQTVGRGNEG	ISAVVDVQRTLRAF KQFFAVFVFLVQHAGHVG NHRRNARRDFFDNR				
a904	RAGEAVGRSNEG	VS AVVDVQRTLRAF KQFFAVFVFLVQHAGHVG NHRRNARRDFFDNR				
	190	200	210	220	230	240
	250	260	270	280	290	300
m904.pep	HHVFRFNRLGIV	QMLQLDIVIGKDG IQFFTQFXRMQ QIGGANGAACHFVFVGRADAAAGR				
a904	HHVFRFHRLGIV	QMLQLDVVISKDG IQFFTQFFRMQ QIGGANGAACHFVFVGRADAAAGR				
	250	260	270	280	290	300
	310	320	330	340	350	360
m904.pep	ADFAFAAXIFAG	LVERDVVRQDQ RAGRRDFQTA FDVFHACRVQLVDF AQQFGGDDNART				
a904	ADFAFAARCF	SGLVERDVIRQDQ RAGRRDFQTA FDVFHACRVQLVDF AQQFGGDDNART				
	310	320	330	340	350	360
	370	380	390	400	410	420
m904.pep	DEAVQTFMQDA	AARNQAQNGFFAADNQGMARIVAAL	EAHHAAGFFRQPVNDFTTLVAPLC			
a904	DEAVQTFMQDA	AARNQAQNGFFAADNQGMTRIVAAL	EAHHAAGFFRQPVNDFTTLVAPLC			
	370	380	390	400	410	420

1297

m904.pép ADXYNIFSHSHITYRYX  
 || ||||| ||||  
 a904 ADYYNIFSHSHITXRYX  
 430

g906.seq not found yet  
 g906.pép not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2727>:

m906.seq  
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC  
 51 GTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGGTCA TTTGGGAAT  
 101 T'GAAAAATTA CGCCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC  
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG  
 201 CCGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA  
 251 GGA AAAAGG CTGGTGTCTG AAGGGTTTCG ACCCTTATCC CGAAAACAAA  
 301 AAATACGAAT GGCCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2728; ORF 906>:

m906.pép  
 1 MKYIVSISLA MGLAACSFEGG FKPNPWAAS FWELKNYANP YPGSASAALD  
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPENK  
 101 KYEWPREEGK TK\*

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2729>:

g907.seq (partial)  
 1 ATGAAAAAAC CGACCGATAC CCTACCCGTC AATCTgcaAC GCCGCCGCCT  
 51 GCTGTGTGCC GCCGGCGCGC TGTGTATCAG CCCGCTGGCG CACGCCGGCG  
 101 CGCAACGTGA AGAAACGctt gCCGACGATG TGGCTTCCGT GATGAGGAGT  
 151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTGACA ATCCGAAAGA  
 201 GGGCGAACGT TGGTTGTCCG CGATGTCGGC ACGTTTGCA AGATTCTGTC  
 251 CCGACGAGGG GGAGCGGCGC AGGCTGCTGG TCAATATCCA ATACGAAAGC  
 301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGa ttgaagtgga  
 351 aagcgggtac cgagctcgaa tcatatca..

This corresponds to the amino acid sequence <SEQ ID 2730; ORF 907.ng>:

g907.pép (partial)  
 1 MKKPTDTLPV NLQRRRLCA AGALLISPLA HAGAOREETL ADDVASVMRS  
 51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPDEGERR RLLVNIQYES  
 101 SRAGLDTQIV LGLIEVESGY RARIIS...

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2731>:

m907.seq  
 1 ATGAGAAAAC CGACCGATAC CCTACCCGTT AATCTGCAAC GCCGCCGCCT  
 51 GTTGTGTGCC GCCGGTGGCT TGTGCTCAG TCCTCTGGCG CACGCCGGCG  
 101 CGCAACGTGA GGAACGCTT GCCGACGATG TGGCTTCCGT GATGAGGAGT  
 151 TCTGTGCGCA GCGTCAATCC GCCGAGGCTG GTGTTTGACA ATCCGAAAGA  
 201 GGGCGAGCGT TGGTTGTCTG CCATGTCGGC ACGTTTGCA AGGTTCGTCC  
 251 CCGAGGAGGA GGAGCGGCGC AGGCTGCTGG TCAATATCCA GTACGAAAGC  
 301 AGCCGGGCGG GTTTGGATAC GCAGATTGTG TTGGGGCTGA TTGAGGTGGA  
 351 AAGCGCGTTC CGCCAGTATG CAATCAGCGG TGTCGGCGCG CGCGGCCTGA  
 401 TGCAGGTTAT GCCGTTkTGG AAAAActACA TCGCAAAACC GGCGCACAAAC  
 451 CTGTTGACA TCCGCACCAA CCTGCGTTAC GGCTGTACCA TCCTGCGCCA  
 501 TTACCGGAAT CTTGAAAAAG GCAACATCGT CCGCGCGCTT GCCCGCTTTA  
 551 ACGGCAGCTT GGGCAGCAAT AAATATCCGA ACGCCGTTTT GGgCGCGTGG  
 601 CGCAACCGCT GGCAGTGGCG TTGA

This corresponds to the amino acid sequence <SEQ ID 2732; ORF 907>:

m907.pép  
 1 MRKPTDTLPV NLQRRRLCA AGALLSPLA HAGAOREETL ADDVASVMRS  
 51 SVGSVNPRL VFDNPKEGER WLSAMSARLA RFVPEEEERR RLLVNIQYES  
 101 SRAGLDTQIV LGLIEVESAF RQYAISGVGA RGLMQVMPXW KNYIGKPAHN

1298

151 LFDIRTNLRY GCTILRHYRN LEKGNIVRAL ARFNGSLGSN KYPNAVLGAW  
201 RNRWQWR\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 907 shows 92.9% identity over a 126 aa overlap with a predicted ORF (ORF 907.ng) from *N. gonorrhoeae*:

g907/m907

	10	20	30	40	50	60
g907.pep	MKKPTDTLPVNLQRRRLCAAGALLISPLAHAGAOREETLADDVASVMRSSVGSVNPRL					
	:                   :					
m907	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAOREETLADDVASVMRSSVGSVNPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
g907.pep	VFDNPKEGERWLSAMSARLARFVPDEGERRLLVNIQYESSRAGLDTQIVLGLIEVESGY					
	:					
m907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	70	80	90	100	110	120
g907.pep	RARIIS					
m907	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2733>:

a907.seq

1	ATGAAAAAAC	CGACCGATAC	CCTACCCGTC	AATCTGCAAC	GCCGCCGCCT
51	ATTGTGTGCT	GCCGGCGCGC	TGTTGCTCAG	CCCGCTGGCA	CAAGCCGCGC
101	CGCAACGTGA	AGAAACGCTT	GCCGACGATG	TGGCTTCCGT	GATGAGGAGC
151	TCTGTCCGCA	GCATAAATCC	GCCGAGGCTG	GTGTTGACGA	ATCCGAAAGA
201	GGCGGAGCGT	TGGCTGTCCG	CGATGTCTGC	TGGTTGGCA	AGGTTCGTCC
251	CCGATGAGGA	GGAGCGGCGC	AGGCTGCTGG	TCAATATCCA	GTACGAAAGC
301	AGCCGGGCGC	GTTTGGATAC	GCAGATTGTG	TTGGGGCTGA	TTGAGGTGGA
351	AAGCGCGTTC	CGCCAGTATG	CAATCAGCGG	TGTCGGCGCG	CGCGGCCTGA
401	TGCAGGTTAT	GCCGTTTGG	AAAACTACA	TCGGCAAACC	GGCGCACAAAC
451	CTGTTGACGA	TCCGCACCAA	CCTGCGTTAC	GGCTGTACCA	TCCTGCGCCA
501	TTACCGGAAT	CTTGAAAAAG	GCAACATCGT	CCGCGCACTC	GCCCGTTTGA
551	ACGGTAGCCT	CGGCAGCAAT	AAATATCCGA	ACGCCGTTTT	GGGCGCGTGG
601	CGCAACCGCT	GGCAGTGGCG	TTGA		

This corresponds to the amino acid sequence <SEQ ID 2734; ORF 907.a>:

a907.pep

1	MKKPTDTLPV	NLQRRRLCA	AGALLSPLA	QAGAOREETL	ADDVASVMRS
51	SVGSINPPRL	VFDNPKEGER	WLSAMSARLA	RFVPDEEERR	RLLVNIQYES
101	SRAGLDTQIV	LGLIEVESAF	RQYAISGVGA	RGLMQVMPFW	KNYIGKPAHN
151	LFDIRTNLRY	GCTILRHYRN	LEKGNIVRAL	ARFNGSLGSN	KYPNAVLGAW
201	RNRWQWR*				

m907/a907 97.6% identity in 207 aa overlap

	10	20	30	40	50	60
m907.pep	MRKPTDTLPVNLQRRRLCAAGALLSPLAHAGAOREETLADDVASVMRSSVGSVNPRL					
	:                   :					
a907	MKKPTDTLPVNLQRRRLCAAGALLSPLAQAGAOREETLADDVASVMRSSVGSINPPRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m907.pep	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					
	:					
a907	VFDNPKEGERWLSAMSARLARFVPEEEERRLLVNIQYESSRAGLDTQIVLGLIEVESAF					

1299

	70	80	90	100	110	120
m907. pep	130	140	150	160	170	180
	RQYAISGVGARGLMQVMPXWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
a907	RQYAISGVGARGLMQVMPFWKNYIGKPAHNLFDIRTNLRYGCTILRHYRNLEKGNIVRAL					
	130	140	150	160	170	180
m907. pep	190	200				
	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
a907	ARFNGSLGSNKYPNAVLGAWRNRWQWRX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2735>:

g908. seq

```

1   ATGAG.AAAA GCCGTCTAAG CCGGTATAAA CAAAATAAAC TCATTGGGCT
51  ATTTGTCGCA GGTGTAAC TG CAAGAACAGC GGCAGAGTTG GTAGGCATTA
101 ATAAAAATAC CGCAGCCTAT GATTTTCATC GTTTACGATG ACTGATTTAT
151 CAAAACGCTC CGCATTGAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 acaagtgaac cctgacagta ttggtttatac ggattgttat CgTAGCTATG
401 ATGTATTAGA Tgtgagcgaa tttagccatt Ttagcttcgc tgaacttcg
451 ttttcgtaTC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA.
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2736; ORF 908.ng>:

g908. pep

```

1   MKKSRLSRYK QNKLIGLFVA GVTARTAAEL VGINKNTAAY DFHRLR*LIY
51  QNGPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPVNTQTAT LFPPIREQVK PDSIVYTDY RSYDVLVDSE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2737>:

m908. seq

```

1   ATGAGAAAAA GTCGTCTAAG CCAGTATAAA CAAAmTAAAC TCATTGAACT
51  GTTTGTCACA GGTGTAAC TG CAAGAACGGC AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATAC CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC CGCATTGAGA AATGTTTGAT GGCGAAGTAG AAGCAGATGA
201 AAGTTATTTT GGCGGACAAC GCAAAGGCAA ACGCGGTCGC GGTGCTGCCG
251 GTAAAGTCGC CGTATTCGGT CTTTGAAGC GAAATGGTAA GGTTTATACG
301 GTTACAGTAC CGAATACTCA AACCCTACT TTATTTCTTA TTATCCGTGA
351 ACAAGTGAAA CCTGACAGCA TTTTATATAC GGATTGTAT CGTAGCTATG
401 ATGTATTAGA TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A

```

This corresponds to the amino acid sequence <SEQ ID 2738; ORF 908>:

m908. pep

```

1   MRKSRLSOYK QXKLIELFVT GVTARTAAEL VGVNKNTAAY YFHRLRLLIY
51  QNSPHLEMF D GEVEADESYF GGQRKGKRGR GAAGKVAVFG LLKRNGKVYT
101 VTPVNTQTAT LFPPIREQVK PDSIFYTDY RSYDVLVDRE FSHFSFAETS
151 FSYQSQHTFC RTTKPY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 908 shows 93.4% identity over a 166 aa overlap with a predicted ORF (ORF 908.ng) from *N. gonorrhoeae*:

g908/m908

	10	20	30	40	50	60
g908. pep	MXKSRLSRYKQNKLIGLFVAGVTARTAAELVGINKNTAAYDFHRLRLXLIYQNGPHLEMF					

	:           :           :           :           :
m908	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNNTAAYYFHRLRLLIYQNSPHLEMF
	10 20 30 40 50 60
	70 80 90 100 110 120
g908.pep	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNKGVYTVTVPNTQTATLFPPIIREQVK
m908	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNKGVYTVTVPNTQTATLFPPIIREQVK
	70 80 90 100 110 120
	130 140 150 160
g908.pep	PDSIVYTD CYRSYDVLDVSEFSHF SFAETSFSYQSQHTFCR TTKPYX
m908	PDSIFYTD CYRSYDVLDVREFSHF SFAETSFSYQSQHTFCR TTKPYX
	130 140 150 160

```
a908.seq
1  ATGAGAAAAA  GTCGTCTAAG  CCAGTATAAA  CAAAATAAAC  TCATTGAGCT
51  ATTTGTGCGCA GGTGTAAC TG  CAAGAACGCG AGCAGAGTTA GTAGGCGTTA
101 ATAAAAATACT CGCAGCCTAT TATTTTCATC GTTTACGATT ACTTATTTAT
151 CAAAACAGTC  CGCATTTGGA AATGTTTGAT GCGCAAGTAG AAGCAGATGA
201 AAGTTATTTT  GCGCGACAAC GCAAAGGCAA ACGCGGTGCG GGTGCTGCCG
251 GTAAAGTCGC  CGTATTCGGT CTTTGAAGC  GAAATGGTAA GGTTTATACG
301 GTTACAGTAC  CGAATACTCA AACCGCTACT TTATTTCCCTA TTATCCGTGA
351 ACAAGTGAAA  CCTGACAGCA TTGTTTATAC GGATTGTTAT CGTAGCTATG
401 ATGTATTAGA  TGTGCGCGAA TTTAGCCATT TTAGCTTCGC TGAAACTTCG
451 TTTTCGTATC  AATCACAGCA CACATTTTGC CGAACGACAA AACCATATTA
501 A
```

**a908.pep**

1	MRKSRLSQYK	QNKLIELFVA	GVTARTAAEL	GVGNKNTAAY	YFHLRLLLIY
51	QNSPHLEMF	GEVEADESYF	GGQRKGKRGR	GAGKVAVFG	LLKRNGKVYT
101	VTQNTQTAT	LFPIIREQVK	PDSIVYDCY	RSYDVLVDRE	FSHFSFAETS
151	FSYQSTQTE	RTTKPY*			

	10	20	30	40	50	60
m908.pep	MRKSRLSQYKQXKLIELFVTGVTARTAAELVGVNKNTAAYYFHRLRLLIFYQNSPHLEMFD					
a908	MRKSRLSQYKQNKLIELFVAGVTARTAAELVGVNKNTAAYYFHRLRLLIFYQNSPHLEMFD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m908.pep	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTVPTQTATLFPPIIREQVK					
a908	GEVEADESYFGGQRKGKRGRGAAGKVAVFGLLKRNGKVYTVTVPTQTATLFPPIIREQVK					
	70	80	90	100	110	120
	130	140	150	160		
m908.pep	PDSIFYTDCYRSYDVLVDVREFSHFSFAETSFYSQSQHTFCRRTTKPYX					
a908	PDSIVYTDYRSYDVLVDVREFSHFSFAETSFYSQSQHTFCRRTTKPYX					
	130	140	150	160		

The following partial sequence was obtained from genomic DNA  
g909.seq (partial)

```
1  atgcgtaaaa ccgtacttat cCTgaccatc tccgcgcgcc ttttgtcggg
51  ctgcacatgG gaaacttatc aagacggcag cggcaaaacc gccgtccgtg
101 caaaatgttc caccggcacg ccgctgtgtt ggcaagacgg gcgcgcgtcc
```

1301

151 aaaaaggtgg actgcgacga gtacggtggc gaacgccggg ccgtgttgcg  
 201 caaccaaag cgggggaagc ccgcgacgag gagagccgca acgctgggga  
 251 aaccgagttt ccgggcgagg gacggggggg ggcgggtgaa cagggcagaa  
 301 acgggggagg ggaagcgatc ggcgagg..

This corresponds to the amino acid sequence <SEQ ID 2742; ORF 909.ng>:

g909.pep (partial)

1 MRKTVLILTI SAALLSGCTW ETYQDGSgKT AVRACSTGT PLCWQDGRGS  
 51 KKVDCDEYGG ERRAVLNRNQK RGKPTRRAA TLGKPSFRAR DGGGRVNRAE  
 101 TGEGKRSAR..

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2743>:

m909.seq

1 ATGCGTAAAA CCTTCCTCTT CCTGACCGCT GCCGCCGCC TTTGTGCGG  
 51 CTGCGCGTGG GAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC  
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG  
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC  
 201 CAATCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA  
 251 AACCAAAGTT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2744; ORF 909>:

m909.pep

1 MRKTFLFLTA AAALLSGCAW ETYQDNGKT AVRQKYPAGT PVEYQDGSYS  
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQPKFQNR \*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 909 shows 53.3% identity over a 90 aa overlap with a predicted ORF (ORF 909.ng) from *N. gonorrhoeae*:

m909/g909

	10	20	30	40	50	60
m909.pep	MRKTFLFLTAALLSGCAWETYQDNGKTAVRQKYPAGTPVEYQDGSYSKNMNYNQYRP					
		:	:	:	:	:
g909	MRKTVLILTISAALLSGCTWETYQDGSgKTAVRAKSTGTPLCWQDGRGSKKVDCEYGG					
	10	20	30	40	50	60
	70	80	90			
m909.pep	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX					
	:		::	::	: :	
g909	ERRAVLNRNQKRGKPTRRAATLGKPSFRARDGGGRVNRAETGEGKRSAR					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2745>:

a909.seq

1 ATGCGTAAAA CCTTCCTTAT CCTGATGACT GCCGCCGCC TTTGTGCGG  
 51 CTGCGCGTGG GAACTTATC AAGACGGCAA CGGCAAGACC GCCGTCCGTC  
 101 AAAAATATCC CGCCGGCAGC CCCGTTTATT ACCAAGACGG CAGCTACTCG  
 151 AAAAATATGA ACTACAACCA ATACCGTCCC GAACGCCATG CCGTGTTACC  
 201 CAACCAAACC GGCAACAACG CCGACGAAGA GCATCGCCAA CACTGGCAAA  
 251 AGCCCAAATT TCAAAACCGA TAA

This corresponds to the amino acid sequence <SEQ ID 2746; ORF 909.a>:

a909.pep

1 MRKTFLILMT AAALLSGCAW ETYQDNGKT AVRQKYPAGT PVEYQDGSYS  
 51 KNMNYNQYRP ERHAVLPNQT GNNADEEHRQ HWQPKFQNR \*

m909/a909 96.7% identity in 90 aa overlap

	10	20	30	40	50	60
m909.pep	MRKTFLFLTAALLSGCAWETYQDNGKTAVRQKYPAGTPVEYQDGSYSKNMNYNQYRP					
		:	:	:	:	:
a909	MRKTFLILMTAAALLSGCAWETYQDNGKTAVRQKYPAGTPVEYQDGSYSKNMNYNQYRP					
	10	20	30	40	50	60

1302

	70	80	90
m909.p	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
a909	ERHAVLPNQTGNNADEEHRQHWQPKFQNRX		
	70	80	90

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2747>:

```

g910.seq
1  ATGAAAAAAC TGTTATTGGC CGCCGTTGTT TCCCTAAATG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACTACTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2748; ORF 910.ng>:

```

g910.p
1  MKKLLLAADV SLNAATAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDYW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2749>:

```

m910.seq
1  ATGAAAAAAC TGTTATTGGC TGCCGTTGTT TCTCTGAGTG CCGCTGCCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCCATTTTG
101 AACAAAACCG CACAAAAGCT GTGAAAATGT TGGAGCAGCG CGGTTATCAG
151 GTTTACGATG TCGATGCCGA CGACCATTGG GGTAAGCCTG TGCTGGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATCGTGTG TCTTACCCCG
251 ACCTGAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2750; ORF 910>:

```

m910.p
1  MKKLLLAADV SLSAAAFAG DSAERQIYGD PHFEQNRTKA VKMLEQRGYQ
51  VYDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 910 shows 96.8% identity over a 94 aa overlap with a predicted ORF (ORF 910.ng) from *N. gonorrhoeae*:

g910/m910

	10	20	30	40	50	60
g910.p	MKKLLLAADVSLNAATAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDYW					
m910	MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDVDADDDHW					
	10	20	30	40	50	60

	70	80	90
g910.p	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX		
m910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX		
	70	80	90

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2751>:

```

a910.seq
1  ATGAAAAAAC TGTTATTGGT CGCCGTTGTT TCCTTGAGTG CCGCAACCGC
51  ATTTGCCGGC GACTCTGCCG AGCGTCAGAT TTACGGCGAT CCCTATTTTG
101 AACAAAACCG CACAAAAGCC GTGAAAATGT TGGAACAGCG CGGTTATCAG
151 GTTCACGATG TCGATGCCGA CGACCATTGG GGCAAACCTG TTTTGAAGT
201 GGAAGCCTAT AAAGACGGCC GCGAATACGA CATTGTGTG TCTTACCCCG
251 ACCTGAAAT CATCAAAGAG CAGCTCGATC GCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2752; ORF 910.a>:

a910.p

1303

1 MKKLLLVAVV SLAATAFAG DSAERQIYGD PYFEQNRTKA VKMLEQRGYQ  
51 VHDVDADDDHW GKPVLEVEAY KDGREYDIVL SYPDLKIIKE QLDR\*

m910/a910 95.7% identity in 94 aa overlap

	10	20	30	40	50	60
m910.pep	MKKLLLAADVSLSAAAFAGDSAERQIYGDPHFEQNRTKAVKMLEQRGYQVYDADDDHW					
a910	MKKLLLVAVVSLAATAFAGDSAERQIYGDYPFEQNRTKAVKMLEQRGYQVHDVDADDDHW					
	10	20	30	40	50	60
	70	80	90			
m910.pep	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
a910	GKPVLEVEAYKDGREYDIVLSYPDLKIIKEQLDRX					
	70	80	90			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2753>:

g911.seq

1	ATGAAAAGA	ACATATTGGA	ATTTTGGGTC	GGACTGTTTC	TCTTGATCGG
51	CGCGGCGGCG	GTTGCCTTTC	TCGCTTTCCG	CGTGGCGGGC	GGCGCGGCGT
101	TCGGCGGTTT	GGACAAACT	TACGCCGTTT	ATGCCGATT	CGGCGACATC
151	GGCGGTTTGA	AGGTCAATGC	CCCCGTCAA	TCCGCAGGCG	TATTGGTCCG
201	GCGCGTCGGC	GCTATCGGGC	TTGACCCGAA	ATCCTATCAG	GCGAGGGTGC
251	GCCTTGATT	GGACGGCAAG	TATCAGTTCA	GCAGTGACGT	TTCCGCGCAA
301	ATCCTGACTT	CGGGACTTTT	GGGCGAACAG	TACATCGGGC	TGCAGCAGGG
351	CGGCGATACG	GAAAACCTTG	CTGCCGGCGA	CACCATCTCC	GTAACCAAGT
401	CTGCAATGGT	TCTGGAAAAC	CTGATCGGTA	AATTCATGAC	CAGCTTCGCC
451	GAGAAAAACG	CTGAGGGCGG	CAATGCGGAA	AAAGCCGcag	aAtaa

This corresponds to the amino acid sequence <SEQ ID 2754; ORF 911.ng>:

g911.pep

1	MKKNILEFWV	GLFVLIGAAA	VAFLAFRVAG	GAAFGGSDKT	YAVYADFGDI
51	GGLKVNAPVK	SAGVLVGRVG	AIGLDPKSYQ	ARVRLDLGK	YQFSSDVSAQ
101	ILTSGLLGEQ	YIGLQQGGDT	ENLAAGDTIS	VTSSAMVLEN	LIGKFMTSFA
151	EKNAEAGNAE	KAAE*			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2755>:

m911.seq

1	ATGAAGAAGA	ACATATTGGA	ATTTTGGGTC	GGACTGTTTC	TCCTGATTGG
51	CGCGGCGGCG	GTTGCCTTTC	TCGCTTTCCG	CGTGGCGGGC	GGTGCAGGCGT
101	TCGGCGGTTT	GGACAAACT	TACGCCGTTT	ATGCCGATT	CGGCGACATC
151	GGCGGTTTGA	AGGTCAATGC	CCCCGTCAA	TCCGCAGGCG	TATTGGTCCG
201	GCGCGTCGGC	GCTATCGGAC	TTGACCCGAA	ATCCTATCAG	GCGAGGGTGC
251	GCCTTGATT	GGACGGCAAG	TATCAGTTCA	GCAGCGACGT	TTCCGCGCAA
301	ATCCTGACTT	CGGGACTTTT	GGGCGAGCAG	TACATCGGGC	TGCAGCAGGG
351	CGGCGACACG	GAAAACCTTG	CTGCCGGCGA	CACCATCTCC	GTAACCAAGT
401	CTGCAATGGT	TCTGGAAAAC	CTTATCGGCA	AATTCATGAC	GAGTTTGGCC
451	GAGAAAAATG	CCGACGGCGG	CAATGCGGAA	AAAGCCGCCG	AATAA

This corresponds to the amino acid sequence <SEQ ID 2756; ORF 911>:

m911.pep

1	MKKNILEFWV	GLFVLIGAAA	VAFLAFRVAG	GAAFGGSDKT	YAVYADFGDI
51	GGLKVNAPVK	SAGVLVGRVG	AIGLDPKSYQ	ARVRLDLGK	YQFSSDVSAQ
101	ILTSGLLGEQ	YIGLQQGGDT	ENLAAGDTIS	VTSSAMVLEN	LIGKFMTSFA
151	EKNADGGNAE	KAAE*			

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 911 shows 99.4% identity over a 164 aa overlap with a predicted ORF (ORF 911.ng) from *N. gonorrhoeae*:

g911/m911

10	20	30	40	50	60
----	----	----	----	----	----



1304

```

g911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
g911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQGGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
m911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQGGGDT
          70      80      90      100     110     120

          130     140     150     160
g911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNAEGGNAEKAAEX
          |||||||||||||||||||||||||||||||||||||||:|||||||
m911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2757>:

```

a911.seq
1   ATGAAAAAGA ACATATTGGA ATTTTGGGTC GGACTGTTCG TCCTGATTGG
51  CGCGCGGCGG GTTGCCTTTC TCGCTTTCCG CGTGGCCGGC GGTGCGGCGT
101 TCGGCGGTTC GGACAAAAC TACGCCGTTT ATGCCGATT TCCTGACATC
151 GCGCGTTTGA AGGTCAATGC CCCCCTCAAA TCCGCAGGCG TATTGGTCGG
201 GCGCGTCGGC GCTATCGGAC TTGACCCGAA ATCCTATCAG GCGAGGGTGC
251 GCCTCGATT GGACGGCAAG TATCAGTTCA GCAGCGACGT TTCCGCGCAA
301 ATCTGACTT CGGGACTTTT GGGCGAGCAG TACATCGGGC TGCAGCAGGG
351 CGGCGACACG GAAAACCTTG CTGCCGCGCA CACCATCTCC GTAACCAATT
401 CTGCAATGGT TCTGGAAAC CTTATCGGCA AATTCATGAC GAGTTTTCGC
451 GAGAAAAATG CCGACGGCGG CAATGCGGAA AAAGCCGCCG AATAA

```

This corresponds to the amino acid sequence <SEQ ID 2758; ORF 911.a>:

```

a911.pep
1   MKKNILEFWV GLFVLIGAAA VAFLAFRVAG GAFFGGSDKT YAVYADFGDI
51  GGLKVNAPVK SAGVLVGRVG AIGLDPKSYQ ARVRDLDLGK YQFSSDVSAQ
101 ILTSGLLGEQ YIGLQGGGDT ENLAAGDTIS VTSSAMVLEN LIGKFMTSFA
151 EKNADGGNAE KAAE*

```

m911/a911 100.0% identity in 164 aa overlap

```

          10      20      30      40      50      60
m911.pep  MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      MKKNILEFWVGLFVLIGAAVAFLAFRVAGGAFFGGSDKTYAVYADFGDIGGLKVNAPVK
          10      20      30      40      50      60

          70      80      90      100     110     120
m911.pep  SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQGGGDT
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a911      SAGVLVGRVGAIGLDPKSYQARVRDLDLGKYQFSSDVSAQILTSGLLGEQYIGLQGGGDT
          70      80      90      100     110     120

          130     140     150     160
m911.pep  ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
          |||||||||||||||||||||||||||||||||||||||
a911      ENLAAGDTISVTSSAMVLENLIGKFMTSFAEKNADGGNAEKAAEX
          130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2759>:

```

g912.seq
1   gtgAAAAaat cctcctTcat cagcGCATTG GGCATCGgtA TTTTGAGCAT
51  CGGCATGGCA TTGCCTCCC CGGCCGACGC AGTGGGACAA ATCCGCCAAA
101 ACGCCACACA GGTTTTGACC ATCCTCAAAA GCGGCGACGC GGCTTCTGCA

```

q912. pep

1	VKKSSFISAL	GIGILSIGMA	FASPADAVGO	IRONATQVLT	ILKSGDAASA
51	RPKAEAYAVP	YFDFQRM TAL	AVGNPWR TAS	DAQQALAKE	FQTL LIR TYS
1 01	GTMLKFKNAT	VNVKDNPIVN	KGGKEIVVRA	EVGIPGQKPV	NMDFTTYQSG
1 51	GKYRTYNVAI	EGTSLVTVYR	NQFGEIIKAK	GIDGLIAELK	AKNGGK*

m912. Seq

1	ATGAAAAAAT	CCTCCCTCAT	CAGCGCATTG	GGCATCGGTA	TTTTGAGCAT
51	CGGCATGGCA	TTTGCCGCCC	CTGCCGACGC	GGTAAGCCAA	ATCCGTCAAA
1 01	ACGCCACTCA	AGTATTGAGC	ATCTTAAAAA	ACGGCGATGC	CAACACCGCT
1 51	CGCCAAAAAG	CCGAAGCCTA	TGCGATTCCC	TATTTTCGATT	TCCAACGTAT
2 01	GACCGCATTG	CGGTCGGCA	ACCCTTGGCG	CACCGCGTCC	GACGCGCAAA
2 51	AACAAGCGTT	GGCCAAAGAA	TTTCAAACCC	TCTGTATCCG	CACCTATTCC
3 01	GGCACGATGC	TGAAATTAAA	AAACGCCAAC	GTCAACGCTA	AAGACAAATCC
3 51	CATCGTCAAT	AAAGCGGCA	AAGAAATCAT	CGTCCGCGCC	GAAGTCGGCG
4 01	TACCCGGGCA	AAACCCCGTC	AACATGGACT	TCACCACCTA	CCAAAGCGGC
4 51	GGTAAATACC	GTACCTACAA	CGTCGCCATC	GAAGGCGGAA	GCCTGGTTAC
5 01	CGTGTACCGC	AACCAATTCT	GCGAAATTAT	CAAAAGCGAA	GGCGTGGACG
5 51	GACTGATTGC	CGAGTTGAAA	GCCAAAAACG	GCGGCAATAA	A

m912.per

1	MKKSSLSIAL	GIGILSIGMA	FAAPADAVSQ	IRQNATQVLS	ILKNGDANTA
51	RQKAEAYAIP	YFDFQRM TAL	AVGNPWRTAS	DAQQALAKE	FQTILLIRTYS
1 01	GTMLKLKNAN	VNVKDNPIVN	KGGKEIIVRA	EVGVPGQKPV	NMDFTTYQSG
1 51	GKYRTYNVAI	EGASLVTVYR	NQFG EIIKAK	GVDGLIAELK	AKNGGK*

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 912 shows 91.8% identity over a 196 aa overlap with a predicted ORF (ORF 912.ng) from *N. gonorrhoeae*:

q912/m912

[illegible]

1306

m912

```

|:|||||
GVDGLIAELKAKNGGKX
190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2763>:

a912.seq

```

1 ATGAAAAAAT CCTCCTTCAT CAGCGCATTG GGCATCGGTA TTTGAGCAT
51 CGGCATGGCA TTTGCCGCCC CTGCCGACGC GGTAACCAA ATCCGTCAA
101 ACGCCACTCA AGTATTGAGC ATCTTAAAAA GCGGTGATGC CAACACCGCC
151 CGCCAAAAAG CCGAAGCCTA TGCGATTCCC TATTTTCGATT TCCAACGTAT
201 GACCGCATTG GCGGTCGGCA ACCCTTGGCG CACCGCGTCC GACGCGCAA
251 AACAAGCGTT GGCCAAAGAA TTTCAAACCC TGCTGATCCG CACCTATTCC
301 GGCACGATGC TGAAATTAAT AAACGCCAAC GTCAACGTCA AAGACAATCC
351 CATCGTCAAT AAAGCGCGCA AAGAAATCAT CGTCCGCGCC GAAGTCGGCG
401 TACCCGGGCA AAAACCCGTC AACATGGACT TCACCACCTA CCAAAGCGGC
451 GGTAAATACC GTACCTACAA CGTCGCCATC GAAGGCGCGA GCCTGGTTAC
501 CGTGTACCGC AACCAATTCG GCGAAATTAT CAAAGCGAAA GCGGTGGACG
551 GACTGATTGC CGAGTTGAAG GCTAAAAACG GCAGCAAGTA A

```

This corresponds to the amino acid sequence <SEQ ID 2764; ORF 912.a>:

a912.pep

```

1 MKKSSFISAL GIGILSIGMA FAAPADAVNQ IRQNTQVLS ILKSGDANTA
51 RQKAEAYAIP YFDFQRM TAL AVGNPWRTAS DAQKQALAKE FQTLIRITYS
101 GTMLKLKNAN VNVKDNPIVN KGGKEIIVRA EVGVPGQKPV NMDFTTYQSG
151 GKYRTYNVAI EGASLVTYR NQFGEI IKAK GVDGLIAELK AKNGSK*

```

m912/a912 98.0% identity in 196 aa overlap

m912.pep	10	20	30	40	50	60
	MKKSSLISALGIGILSIGMAFAAPADAVSQIRQNTQVLSILKNGDANTARQKAEAYAIP					
a912	MKKSSFISALGIGILSIGMAFAAPADAVNQIRQNTQVLSILKSGDANTARQKAEAYAIP					
	10	20	30	40	50	60
m912.pep	70	80	90	100	110	120
	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN					
a912	YFDFQRM TALAVGNPWRTASDAQKQALAKEFQTLIRITYSGTMLKLKNANVNVKDNPIVN					
	70	80	90	100	110	120
m912.pep	130	140	150	160	170	180
	KGGKEIIVRAEVLGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK					
a912	KGGKEIIVRAEVLGVPGQKPVNMDFTTYQSGGKYRTYNVAIEGASLVTYRNQFGEI IKAK					
	130	140	150	160	170	180
m912.pep	190					
	GVDGLIAELKAKNGGKX					
a912	GVDGLIAELKAKNGSKX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2765>:

g913.seq

```

1 atGAAAAAAA CCGCCTACGC CATCCTCCTG CTGATCGGGT TCGCTTCCGC
51 CCTGCAATT GCAGAAACCC GCCCGCCGA CCCTTATGAA GGCTACAACC
101 GCGCCGTTTC CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCCCT
151 GCGCGCGCG GCTACGCAA AGTTACGCCG AAACCCGTCC GCGCGGCGT
201 GTCCAATTTT TTTAACAACC TGCGCGACGT GGTCAATTTC GGCAGCAATA
251 TCTTGCGTTT GGAcATCAAA cgcgcAAGcg aAGACctcgT CCGcgtcggc
301 atCAATACCA CCTTCGGTTT GGgcgGGCTC ATTGATATTG CCGGcgcGGg
351 cggcgttccc gacaataaaa AcacTttgGg cgacacgttt gcctcgtGGG
401 GctgGAAAAa cagcaATTAT TTCGTgttgc CCGtcttagg cccgtccacc

```

g913.p ep

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2767>:

m913.seq

This corresponds to the amino acid sequence <SEQ ID 2768; ORF 913>:

m913.pgp

Computer analysis of this amino acid sequence gave the following results:

### Homology with a predicted ORF from *N. gonorrhoeae*

ORF 913 shows 94.9% identity over a 277 aa overlap with a predicted ORF (ORF 913.ng) from *N. gonorrhoeae*:

q913/m913

[illegible]

1308

	130	140	150	160	170	180
g913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYPPKNIVFHTFAGRWGTT					
m913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTFPVGRWGTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g913.pep	AAAAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDIDIDEL					
m913	AVSAVSTREGLLDLTDSLDEAAIDKYSYTRDLYMKVRARQTGATPAEGTEDNIDI--DEL					
	190	200	210	220	230	
	250	260	270			
g913.pep	VESAETGAAEPAVHEDSVSETQAEAAAGEAETQPGTQPX					
m913	VESAETGAAETAVQEDSVSETQAEAAAGEAETQPGTQPX					
	240	250	260	270		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2769>:

```

a913.seq
1   ATGAAAAAA CCGCCTATGC CTTCCTCCTG CTGATCGGGT TCGCTTCCGC
51  CCCTGCATTT GCCGAAACCC GCCCGGCCGA CCCTATGAA GGCTACAACC
101 GCGCCGTTTT CAAATTCAAC GACCAAGCCG ACCGCTACAT TTTCGCCCTT
151 GCCGCGCGCG GCTACCGCAA AGTTGCGCCG AAACCCGTCC GCGCCGGCGT
201 GTCCAATTTT TTTAACAACC TGTGCGACGT GGTCACTTC GGCAGCAATA
251 TCTTGCGCTT AGACATCAA CGCGCAAGCG AAGACCTGT CCGCGTCGGT
301 ATCAACACCA CTTTCGGTTT GGGCGGGCTT ATCGACATCG CCGGCGCGGG
351 CGGCATTCCC GACAATAAAA ACACCTTGGG CGACACGTTT GCTTCGTGGG
401 GATGGAAAAA CAGCAATTAT TTCGTGTTGC CCGTCTTAGG GCCGTCCACC
451 GTCCGCGACG CGCTCGGCAC GGGTATTACC TCCGTTTATT CGCCCAAGAA
501 TATCGTCTTC CGCACCCCTG TCGGACGCTG GGGCACGACT GCCGTATCCG
551 CCGTCAGTAC GCGCGAAGGC CTGCTCGATT TGACCGACAG TCTGGACGAA
601 GCCGCATCGC ACAAATACAG CTACACGCGC GACCTCTATA TGAAAGTCCG
651 TGCGCGGCAG ACCGGTGCAA CACCTGCCGA AGGTACGGAA GATAACATCG
701 ACATCGACGA ATTGGTCGAA AGTGCCGAAA CCGGCGCGGC GGAAACTGCC
751 GTTCAAGAAG ATTCCGTATC CGAAACACAG GCAGAAGCAG CAGGGGAAGC
801 CGAAACGCAA CCTGGAACAC AACCTGGAAC ACAACCTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 2770; ORF 913.a>:

```

a913.pep
1   MKKTAYAFLL LIGFASAPAF AETRPADPYE GYNRAVFKFN DQADRYIFAP
51  AARGYRKVAP KPVVAGVSNF FNNLCDVVSF GSNILRLDIK RASEDLVRVG
101 INTTFGLGGL IDIAGAGGIP DNKNTLGDTF ASWGWKNSNY FVLPVLPST
151 VRDALGTGIT SVYSPKNIVF RTPVGRWGTT AVSAVSTREG LLDLTDSLDE
201 AADKYSYTR DLYMKVRARQ TGATPAEGTE DNIDIDELVE SAETGAAETA
251 VQEDSVSETQ AEAAGEAETQ PGTQPGTQP*
  
```

m913/a913 100.0% identity in 275 aa overlap

	10	20	30	40	50	60
m913.pep	MKKTAYAFLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
a913	MKKTAYAFLLLIGFASAPAF AETRPADPYEGYNRAVFKFNDQADRYIFAPAARGYRKVAP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m913.pep	KPVVAGVSNEFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
a913	KPVVAGVSNEFNNLCDVVSFGSNILRLDIK RASEDLVRVGINTTFGLGGLIDIAGAGGIP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m913.pep	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTFPVGRWGTT					
a913	DNKNTLGDTFASWGWKNSNYFVLPVLPSTVRDALGTGITSVYSPKNIVFRTFPVGRWGTT					

1309

	130	140	150	160	170	180
	190	200	210	220	230	240
m913.pép	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
a913	AVSAVSTREGLDLTDSLDEAAIDKYSYTRDLYMKVRRARQTGATPAEGTEDNIDIDELVE					
	190	200	210	220	230	240
	250	260	270			
m913.pép	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPX					
a913	SAETGAAETAVQEDSVSETQAEAAEAEETQPGTQPGTQPX					
	250	260	270	280		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2771>:

g914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCAGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GacgtttGag gCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGG AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACCGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTCTCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAGTGTC AGTCGTGTTT TGCCGATTCT
451 taggctTCGA CGATTTTTTG CACCAGAGGA TGCCGGACAA CGTCTTCGCC
501 GTGAAGGTA TGGAATACA GTCCTGCCAC GCCGTGCAGT TTCTCACGTG
551 CGTCTTTCAA TCCCATTG ATGTTTTTGG GCAGGTcgaT TTGGCTGGTG
601 TCGCGGTAA TGACGGCTTT CGCgcccgaag ccGATGCGGG TCAGGAACAT
651 TTTCAATTTGT TCGGGCGTGg tgTtttGgcC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAg cgTCTGCCG CGCATATAG

```

This corresponds to the amino acid sequence <SEQ ID 2772; ORF 914.ng>:

g914.pep

```

1  MKKCILGILT ACAAMPAFAD RISDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFD*CI GWTDKETDTE LGFRLCFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTRG CRTTSPVKV WKYSPATPCS FSRASFNPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2773>:

m914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTGCG CGTATTGGAA AGCGGCGGCA ATACCGTCAA AATCGACCTT
151 TTCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACCGG ATAAAGAAAC
351 GGATACGGAT ACGGAGCTTG GCTTCCGTAT CTGTTTTTCT CTGCCTGATT
401 TTCCATGCAT CCGGTTTCAG ACGGCATTGG AATGTCAGTC GTGTTCTGCC
451 GATTCGTAGG CTTGACGAT TTTTTCACCA AAAGGATGCC GGACAACGTC
501 TTCGCCGGA AAGGTGTGGA AATACAGCCC TTCCACGTTG TGCAGTTTCT
551 CACGCGCATC TTTTAATCCC GATTTGATGT TTTGGGCAG GTCGATTGG
601 CTGGTGTGCG CGGTAATGAC GGCTTTCGCG CCGAAGCCGA TCGGGTCAG
651 GAACATTTTC ATTTGTTCCG GCGTGGTGTT TTGCGCTTCG TCGAGGATGA
701 TGTATGCGCC GTTGAAGCTC CTGCCGCGCA TATAG

```

This corresponds to the amino acid sequence <SEQ ID 2774; ORF 914>:

m914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGGNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCDEA
101 IRCRKFDXCI GWTDKETDTE TELGFRICFS LPDFPCIGFQ TALECQSCSA

```

1310

151 DSXASTIFCT KGCRTTSSPV KWKYSPSTL CSFSRASFP DLMFLGRSIW  
 201 LVSPVMTAFA PKPMVRNIF ICSGVVFCAS SRMMYAPLSV LPRI\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 914 shows 96.7% identity over a 244 aa overlap with a predicted ORF (ORF 914.ng) from *N. gonorrhoeae*:

g914/m914

	10	20	30	40	50	60
g914.pep	MKKCILGILTACAAMPAFADRISDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
m914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLESGGNTVKIDLFGSNSTMYVC					
	10	20	30	40	50	60
	70	80	90	100	110	119
g914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCGDEAIRCRKFDXCIGWTDKETDT-					
m914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCDEDAIRCRKFDXCIGWTDKETDTD					
	70	80	90	100	110	120
	120	130	140	150	160	170
g914.pep	-ELGFRLCFSLPDFPCIGFQTALEQCSCSADXSASTIFCTRGCRRTSSPVKWKYSPATP					
m914	TELGFRICFSLPDFPCIGFQTALEQCSCSADXSASTIFCTKGCRRTSSPVKWKYSPSTL					
	130	140	150	160	170	180
	180	190	200	210	220	230
g914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
m914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	190	200	210	220	230	240
	240					
g914.pep	LPRIX					
m914	LPRIX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2775>:

a914.seq

```

1  ATGAAAAAAT GTATTTTGGG CATTTTGACC GCGTGTGCCG CCATGCCTGC
51  ATTTGCCGAC AGAATCGGCG ATTTGGAAGC ACGTCTGGCG CAGTTGGAAC
101 ACCGTGTCGC CGTATTGGAA AGCGGCAGCA ATACCGTCAA AATCGACCTT
151 TCGGTTCAA ATTCCACCAT GTATGTATGC AGCGTTACGC CTTTTCAGAA
201 GACGTTTGAG GCAAGCGATC GGAATGAAGG CGTGGCGCGG CAGAAAGTGC
251 GTCAGGCGTG CAACCGCGAA ACTTCGGCAA TGTTTTGCGA AGATGAGGCA
301 ATCCGATGCA GAAAATTCGA TTGATGTATC GGTGGACGG ATAAAGAAAC
351 GGATACGGAG CTTGGCTTCC GTATCTGTTT TTCTCTGCCC GATTTTCCAT
401 GCATCGGGTT TCAGACGGCA TTGGAATGTC AGTCGTGTTC TGCCGATTCC
451 TAGGCTTCGA CGATTTTTTG CACCAAAGGA TGCCGGACAA CGTCTTCGCC
501 GGTAAGGTG TGGAAATACA GCCCTTCCAC GCCGTGCAGT TTCTCAGCG
551 CATCTTTTAA TCCCGATTG ATGTTTTTGG GCAGGTCGAT TTGGCTGGTG
601 TCGCCGGTAA TGACGGCTTT CGCGCCGAAG CCGATGCGGG TCAGGAACAT
651 TTTCATTTGT TCGGGCGTGG TGTTTTGCGC TTCGTCGAGG ATGATGTATG
701 CGCCGTTGAG CGTCTGCGG CGCATATAG
```

This corresponds to the amino acid sequence <SEQ ID 2776; ORF 914.a>:

a914.pep

```

1  MKKCILGILT ACAAMPAFAD RIGDLEARLA QLEHRVAVLE SGSNTVKIDL
51  FGSNSTMYVC SVTPFQKTFE ASDRNEGVAR QKVRQACNRE TSAMFCEDEA
101 ICRKFD*CI GWTDKETDTE LGFRICFSLP DFPCIGFQTA LECQSCSADS
151 *ASTIFCTKG CRTTSSPVKV WKYSPSTPCS FSRASFPDL MFLGRSIWLV
201 SPVMTAFAPK PMVRNIFIC SGVVFCASSR MMYAPLSVLP RI*
```

1311

m914/a914 98.4% identity in 244 aa overlap

	10	20	30	40	50	60
m914.pep	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLES	GGNTVKIDLF	GSNSTMYVC			
a914	MKKCILGILTACAAMPAFADRIGDLEARLAQLEHRVAVLES	GSNSTVKIDLF	GSNSTMYVC			
	70	80	90	100	110	120
m914.pep	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD					
a914	SVTPFQKTFEASDRNEGVARQKVRQACNRETSAMFCEDEAIRCRKFDXCIGWTDKETD--					
	130	140	150	160	170	180
m914.pep	TELGFRCIFSLPDPFCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTL					
a914	TELGFRCIFSLPDPFCIGFQTALECSADXSASTIFCTKGCRTTSSPVKVKYSPSTP					
	190	200	210	220	230	240
m914.pep	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
a914	CSFSRASFPDLMFLGRSIWLVSPVMTAFAPKPMVRNIFICSGVVFCASSRMMYAPLSV					
	120	130	140	150	160	170
	180	190	200	210	220	230
m914.pep	LPRIX					
a914	LPRIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2777>:

g915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCagcg gaAGaggcac cgccgCCTTT ACCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGGCGGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2778; ORF 915.ng>:

g915.pep

```

1  MKKTLAIVA VFALSACRQA EEAPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMGAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2779>:

m915.seq

```

1  ATGAAGAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGC.tg
51  CCGGCAGGCG GAAGAGGGAC CGCCGCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TtTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG

```



1312

451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2780; ORF 915>:

m915.pep

1 MKKTLAIVA VSALSXRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP  
51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT  
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK  
151 VVGFDMPDT YIFK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 915 shows 97.0% identity over a 164 aa overlap with a predicted ORF (ORF 915.ng) from *N. gonorrhoeae*:

m915/g915

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g915	MKKTLAIVAVFALSACRQAEAPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					
	:					
g915	DQPVWFSTVQMFYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m915.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	:					
g915	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2781>:

a915.seq

1 ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTCCGCCT TAAGTGCCTG  
51 CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC  
101 GTTCGGTCCG AACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC  
151 AAAGCCAGA TTTTCTTGAA CGGCAACCC GATCAGCCCG TTTGTTCTC  
201 CACCATCAAG CAGATGTTTC GCTATACCAA GCTGCCCGAA GAGCCTAAAG  
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG  
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT  
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT  
401 TCGGCAACAA AGAGCAGGCT GAGAAATTG CAAAGGATAA AGGCGGTAAG  
451 GTTGTGCGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA

This corresponds to the amino acid sequence <SEQ ID 2782; ORF 915.a>:

a915.pep

1 MKKTLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP  
51 KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT  
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK  
151 VVGFDMPDT YIFK\*

m915/a915 99.4% identity in 164 aa overlap

	10	20	30	40	50	60
m915.pep	MKKTLAIVAVSALSXRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
a915	MKKTLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m915.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					
a915	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNVTDWTNPNADTEWMDAKKAFYVIDS					

1313

	70	80	90	100	110	120
	130	140	150	160		
m915.pcp	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
a915	GFIGGMGAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2783>:

g917.seq

```

1  ATGGTCAAac atctgccact cgcCGTcctg actgctTtgc tgcttgacgc
51  gtgcGGCGGT Tcggacaaac cgcctgccga Aaaaccggca ccggcgGaAA
101  accaaAacgt atTgaAAATT TataACTGGT CGGAATACGT CGATCCGGAA
151  ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGTTA CTTATGATGT
201  GTACGACAGT GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAAATCCG
251  GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAg
301  GCAGGTGCGT ATCAGAAAAT CGATAAGTCG ATGATTCCCA ATTATAAACA
351  TCTCAACCCCT GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGACCACG
401  AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451  GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501  GGATTGGTG TTCAACCCCG AATACACGTT CAAACTCAAA CAATGCGGCA
551  TCAGCTATTT GGACAGCGCG GCGGAAATTT ATCCCATGGT GTTGAACAT
601  TTGGGCAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651  GCCCTGCTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701  GCTTTATCGA TGATTGGCG CGCGCGGATA CCTGCGTAAC AATCGGTTTC
751  GCGCGAGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801  GGAAAAAATC CGCGTGATGA TGCCGAAAGA GGGCGTGGGG ATTTGGGTGG
851  ATTCTTTCTG GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901  TACATCAACG ACTTCTCTGA TCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951  cgttacCTAC GCGCCTTCGA GCAAGCCGGC GCGCGATTGT ATGGAGGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCGA GCGGGGAAGA TTTGAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCGGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CCGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2784; ORF 917.ng>:

g917.pep

```

1  MVKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51  TVADFEKKNQ IKVTYDVYDS DETLESKVLV GKSGYDIVAP SNAFVGRQIK
101  AGAYQKIDKS MIPNYKHLNP EMRLMDGVD PDHEYAVPFY WGTNTFAINT
151  ERVKKALGTD KLPDQWDLV FNPEYTFKLK QCGISYLDLS AEIYPMVLNY
201  LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251  GGDNLNIAKRR AEEAGGKEKI RVMMPKEGVG IWVDSFVIK DAKNVANAHK
301  YINDFLDPEV SAKNGNFVTY APSSKPARDL MEDEFKNDNT IFPSGEDLKN
351  SFIMVPIRPA ALKFMVRQWQ DVKAGK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2785>:

m917.seq

```

1  ATGACCAAAC ATCTGCCCCCT GGCCGTCCTG ACTGCTTTGC TGCTTGACGC
51  GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCA CCGGCGGAAA
101  ACCAAAACGT ATTGAAAATT TACAACTGGT CGGAATATGT CGATCCGGAA
151  ACCGTGCGCG ATTTTGAAAA GAAAAACGGC ATCAAGTTA CTTATGATGT
201  GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACA GGCAAGTCCG
251  GTTACGACAT TGTCGCGCCG TCCAATGCGT TTGTGGGCAG GCAGATTAAg
301  GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA
351  CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG
401  AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC
451  GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCACTG
501  GGATTGGTG TTCGACCCCG AATACACGTC CAAACTCAAG CAATGCGGCA
551  TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT
601  TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC
651  CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCCG
701  GCTTTATCGA TGATTGGCG CGCGCGGATA CCTGCGTAAC AATCGGTTTC

```

1314

```

751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CGGGCGGCAA
801 GGAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG
851 ATTCTTTCGT GATTCCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA
901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT
951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG
1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTGAAAAAAC
1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG
1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2786; ORF 917>:

m917.pep

```

1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENQNVLKI YNWSEYVDPE
51 TVADFEKNG IKVTYDVYDS DETLESKVLTKGSGYDIVAP SNAFVGRQIK
101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT
151 ERVKKALGTD KLDPNQWDLV FDPEYTSKLG QCGISYLD SA AEIYPMVLNY
201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF
251 GGDNLIAKRR AEEAGGKEKI RVMPKEGVG IWVDSFVIPK DAKNVANAHK
301 YINDFLDPEV SAKNGNFVTY APSSKPAREL MEDEFKNDNT IFPTEEDLKN
351 SFIMVPIQPA ALKFMVRQWQ DVKAGK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 917 shows 97.6% identity over a 376 aa overlap with a predicted ORF (ORF 917.ng) from *N. gonorrhoeae*:

m917/g917

m917.pep	10	20	30	40	50	60
	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
g917	MVKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKNG					
	10	20	30	40	50	60
m917.pep	70	80	90	100	110	120
	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
g917	IKVTYDVYDSDETLESKVLTKGSGYDIVAPSNFVGRQIKAGAYQKIDKSMIPNYKHLNP					
	70	80	90	100	110	120
m917.pep	130	140	150	160	170	180
	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFDPEYTSKLG					
g917	EMMRLMDGVDPDHEYAVPFYWGNTFAINTERVKKALGTDKLPDNQWDLVFNPEYTFKLK					
	130	140	150	160	170	180
m917.pep	190	200	210	220	230	240
	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					
g917	QCGISYLD SA AEIYPMVLNYLGKNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					
	190	200	210	220	230	240
m917.pep	250	260	270	280	290	300
	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
g917	RGDTCVTIGFGGDLNIAKRR AEEAGGKEKIRVMPKEGVGIWVDSFVIPKDAKNVANAHK					
	250	260	270	280	290	300
m917.pep	310	320	330	340	350	360
	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA					
g917	YINDFLDPEVSAKNGNFVTYAPSSKPARELMEDEFKNDNTIFPSGEDLKNSFIMVPIRPA					
	310	320	330	340	350	360

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m917.pep      ALKFMVRQWQDVKAGKX  
 |||||  
 g917          ALKFMVRQWQDVKAGKX  
 370

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2787>:

a917.seq  
 1 ATGACCAAAC ATCTGCCCTT GGCCGTCCTG ACTGCTTTGC TGCTTGCAGC  
 51 GTGCGGCGGT TCGGACAAAC CGCCTGCCGA AAAACCGGCG CCGGCGGAAA  
 101 ACCGAAACGT ATTGAAAATT TACAACTGGT CGGAATACGT CGATCCGGAA  
 151 ACCGTTGCCG ATTTTGAAAA GAAAAACGGC ATCAAGGTTA CTTATGATGT  
 201 GTACGACAGC GATGAAACGC TGGAAAGCAA GGTGCTGACC GGAAATCTGT  
 251 GTTACGACAT TGTGCGCGCG TCCAATGCGT TTGTGGGCAG GCAGATTAAG  
 301 GCAGGTGCGT ATCAGAAAAT CGATAAGTCG CTGATTCCCA ATTATAAACA  
 351 CCTCAACCCC GAAATGATGA GGCTGATGGA CGGGGTCGAT CCCGGCCACG  
 401 AATACGCCGT GCCGTTTTAT TGGGGGACAA ATACCTTCGC CATCAATACC  
 451 GAACGCGTGA AAAAGGCTTT GGGTACGGAC AAGCTGCCGG ACAACCAAGT  
 501 GGATTTGGTG TTCGACCCCG AATACACGTC CAACTCAAG CAATGCGGCA  
 551 TCAGCTATTT GGACAGCGCG GCGGAAATCT ATCCTATGGT GTTGAACAT  
 601 TTGGGTAAAA ACCCGAACAG CAGCAATACG GAAGACATCA GGGAGGCAAC  
 651 CGCCCTACTC AAGAAAAACC GCCCAATAT CAAACGCTTT ACTTCGTCGG  
 701 GCTTTATCGA TGATTGGCG CGCGGCGATA CCTGCGTAAC AATCGGTTTC  
 751 GCGGCGGATT TGAACATCGC CAAACGCCGT GCCGAAGAAG CCGGCGGCAA  
 801 GGAAAAAATC CGCGTGATGA TGCCCAAAGA GGGCGTGGGG ATTTGGGTGG  
 851 ATTCTTTCGT GATTCGAAA GATGCGAAAA ACGTCGCCAA CGCGCACAAA  
 901 TACATCAACG ACTTCCTCGA CCCGGAAGTG TCGGCGAAAA ACGGCAATTT  
 951 CGTTACTTAC GCGCCTTCGA GCAAGCCTGC GCGTGAGCTG ATGGAAGACG  
 1001 AATTTAAAAA CGACAATACG ATTTTCCCAA CCGAGGAGGA TTTGAAAAAC  
 1051 AGCTTTATCA TGGTGCCTAT CCAGCCGGCG GCATTGAAGT TTATGGTGCG  
 1101 CCAGTGGCAG GATGTGAAGG CGGGGAAATA A

This corresponds to the amino acid sequence <SEQ ID 2788; ORF 917.a>:

a917.pep  
 1 MTKHLPLAVL TALLLAACGG SDKPPAEKPA PAENRNVLKI YNWSEYVDPE  
 51 TVADFEKKNG IKVTYDVYDS DETLESKVL T GKSQYDIVAP SNAFVGRQIK  
 101 AGAYQKIDKS LIPNYKHLNP EMMRLMDGVD PGHEYAVPFY WGTNTFAINT  
 151 ERVKKALGTD KLPDQWDLV FDPEYTSKLK QCGISYLDSA AEIYPMVLNY  
 201 LGKNPNSSNT EDIREATALL KKNRPNIKRF TSSGFIDDLA RGDTCVTIGF  
 251 GGD LNIARR AEEAGGKEKI RVMPKPEGVG IWVDSFVIK DAKNVANAHK  
 301 YINDFLDPEV SAKNGNFVY APSSKPAREL MEDEFKNDNT IFPTEEDLKN  
 351 SFIMVPIQPA ALKFMVRQWQ DVKAGK\*

m917/a917 99.7% identity in 376 aa overlap

	10	20	30	40	50	60
m917.pep	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENQNVLKIYNWSEYVDPETVADFEKKNG					
a917	MTKHLPLAVLTALLLAACGGSDKPPAEKPAPAENRNVLKIYNWSEYVDPETVADFEKKNG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m917.pep	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
a917	IKVTYDVYDSDETLESKVLTKSGYDIVAPSNFVGRQIKAGAYQKIDKSLIPNYKHLNP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m917.pep	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLK					
a917	EMMRLMDGVDPGHEYAVPFYWGNTFAINTERVKKALGTDKLPDQWDLVFDPEYTSKLK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m917.pep	QCGISYLDAAEYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRF TSSGFIDDLA					

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a917      QCGISYLDAAEIYPMVLNLYLGNPNSSNTEDIREATALLKKNRPNIKRFSSGFIDDLA
           190      200      210      220      230      240

           250      260      270      280      290      300
m917.pep  RGDTCVTIGFGGDLNIAKRRAEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      RGDTCVTIGFGGDLNIAKRRAEAGGKEKIRVMPKKEGVGIWVDSFVIPKDAKNVANAHK
           250      260      270      280      290      300

           310      320      330      340      350      360
m917.pep  YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a917      YINDFLDPEVSAKNGNFVITYAPSSKPARELMEDEFKNDNTIFPTEEDLKNSFIMVPIQPA
           310      320      330      340      350      360

           370
m917.pep  ALKFMVRQWQDVKAGKX
           ||||||||||||||
a917      ALKFMVRQWQDVKAGKX
           370

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2789>:

```

g919.seq
1  ATGAAAAAAC ACCTGCTCCG CTCCGCCCTG TACGGcatCG CCGCCgccat
51  CctcgCCGCC TGCCAAAgca gGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCCG GACCGGCCGG CCGGCATCCC CGACCCCGCC
151 GGAACGACGG TTGCCGGCGG CGGGGCCGTC TATACCGTTG TGCCGCACCT
201 GTCCATGCCC CACTGGGCGG CGCaggATTT TGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG GCAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTGCAT TCCTTTCAGG CAAAGcGgTT
351 TTTTGAACGC TATTTACACG cgtGGCaggt tgcaggcaAC GGAAGcCTTG
401 Caggtagcgt TACCGGCTAT TACGAACCGG TGCTGAAGGG CGACGGCAGG
451 CGGACGGAAC GGGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCCGTCCCG CTGCCTGCCG GTTTGCGGGG CGGAAAAAAC CTTGTCCGCA
551 TCAGGCAGac ggGAAAAAAC AGCGGCACGA TCGACAATGC CGGCGGCACG
601 CATACGCGCG ACCTCTCCCG ATTCCCATC ACCGCGCGCA CAACGGcaat
651 caaaGGCAGG TTGAaggAA GCCGCTTCTT CCCTTACCAC ACGCGCAACC
701 AAAtcaacGG CGCGcggcTT GACGGCAAag cccCCATCCT CggttacgcC
751 GAagaccCcG tcgaacttTT TTTTCATGCAC AtccaaggCT CGGGCCGCTT
801 GAAAACCCcg tcgggcaaat acatCCGCaT cggaTacgcc gacAAAAACG
851 AACatccgTa tgtttccatc ggACGetaTA TGGCGGACAA AGGCTACCTC
901 AAGctcgggc agACCTCGAT GCAGGgcac aaagcCTATA TGCGGCAAAA
951 TCCGCAACGC CTCGCCGAAG TTTTGGGTCA AAACCCAGC TATATCTTTT
1001 TCCGCGAGCT TGCCGGAAGC GGCAATGAGG GCCCCGTCGG CGCACTGGGC
1051 ACGCCACTGA TGGGGGAATA CGCCGGCGCA ATCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTTT ACCCGCAAAG
1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CAGGCAGCGC GATCAAAGGC
1201 GCGGTGCGCG TGGATTATTT TTGGGGTTAC GGCGACGAAG CCGGCGAACT
1251 TGCCGGCAAA CAGAAAACCA CGGGATACGT CTGGCAGCTC CTGCCCAACG
1301 GCATGAAGCC CGAATACCGC CCGTGA

```

This corresponds to the amino acid sequence <SEQ ID 2790; ORF 919.ng>:

```

g919.pep
1  MKKHLRSAL YGIAAAILAA CQSRSIQTFP QPDSVINGP DRPAGIPDPA
51  GTTVAGGGAV YTVVPHLSMP HWAAQDFAKS LQSFRLGCAN LKNRQGWQDV
101 CAQAFQTPVH SFQAKRFFER YFTPWQVAGN GSLAGTVTGY YEPVLKGDGR
151 RTERARFPIY GIPDDFISVP LPAGLRGGKN LVRIQTGKN SGTIDNAGGT
201 HTADLSRFPI TARTTAIKGR FEGSRFLPYH TRNQINGGAL DGKAPILGYA
251 EDPVELFFMH IQSGRLKTP SGKYIRIGYA DKNEHPYVSI GRYMADKGYL
301 KLGQTSMQGI KAYMRQNPQR LAEVLGQNPS YIFFRELAGS GNEGVPVAGLG
351 TPLMGEYAGA IDRHYYTLGA PLFVATAHPV TRKALNRLIM AQDTGSAIKG
401 AVRVDYFWGY GDEAGELAGK QKTTGYVWQL LPNGMKPEYR P*

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1	ATGAAAAAAT	ACCTATTCCG	CGCCGCCCTG	TACGGCATCG	CCGCCGCCAT
51	CCTCGCCGCC	TGCCAAAGCA	AGAGCATCCA	AACCTTTCCG	CACCCGCACA
1 01	CATCCGTCAT	CAACGGCCCG	GACCGGCCCG	TCGGCATCCC	CGACCCCGCC
1 51	GGAACGACGG	TCGGCGGGCG	CGGGGCCGTC	TATACCGTTG	TACCGCACCT
2 01	GTCCTTGCCC	CACCTGGCCG	CGCAGGATTT	CGCCAAAAGC	CTGCAATCCT
2 51	TCCGCCTCGG	CTCGGCCAAT	TTGAAAAACC	GCCAGGCTG	GCAGGATGTG
3 01	TGCGCCCAAG	CCTTTCAAC	CCCGTCCAT	TCCTTTCAGG	CAAAACAGTT
3 51	TTTTGAACGC	TATTTACGCG	CTTGGCAGGT	TGCGGCAAC	GGAAAGCCTTG
4 01	CCGGTACGGT	TACCGGCTAT	TACGAACCGG	TGCTGAAGGG	CGACGACAGG
4 51	CGGACGGCAC	AAGCCCGCTT	CCCGATTTAC	GGTATTCCCG	ACGATTTTAT
5 01	CTCCGTCCCC	CTGCCTGCCG	GTTTGCGGAG	CGGAAAAGCC	CTTGTCGCGA
5 51	TCAGGCAGAC	GGGAAAAAAC	AGCGGCACAA	TCGACAATAC	CGGCGGCACA
6 01	CATACGCCCG	ACCTCTCCCG	ATTCCCCATC	ACCGCGCGCA	CAACAGCAAT
6 51	CAAAGGCGAG	TTTGAAGGAA	CGCGCTTCCT	CCCCATACCAC	ACGCGCAACC
7 01	AAATCAACGG	CGGCGCGCTT	GACGGCAAAG	CCCGCATACT	CGGTTACGCC
7 51	GAAGACCCTG	TCGAACTTTT	TTTTATGCAC	ATCCAAGGCT	CGGGCCGCTCT
8 01	GAAAACCCCG	TCCGGCAAT	ACATCCGCAT	CGGCTATGCC	GACAAAAACG
8 51	AACATCCyTA	CGTTTCCATC	GGACGCTATA	TGGCGGATAA	GGGCTACCTC
9 01	AAACTCGGAC	AAACCTCCAT	GCAGGGCATT	AAGTCTTATA	TGCGGCAAAA
9 51	TCCGCAACGC	CTCGCGGAAG	TTTTGGGTCA	AAACCCCAAG	TATATCTTTT
10 01	TCCCGGAGCT	TGCCGGAAGC	AGCAATGACG	GCCCTGTCGG	CGCACTGGGG
10 51	ACGCCGCTGA	TGGGGGAATA	TGCCGGCGCA	CTCGACCCGC	ACTACATTAC
11 01	CTTGGGTGCG	CCCTTATTTG	TCGCCACCGC	CCATCCGGTT	ACCCGCAAAAG
11 51	CCCTCAACCG	CCTGATTATT	GCGCAGGATA	CCGGCAGCGC	GATTAAAGGC
12 01	GCGGTGCGCG	TGGATTATTG	TTGGGGATAC	GGCGACGAAG	CCGGCGAACT
12 51	TCCGCGGCAA	CAGAAAACCA	CGGGATATGT	CTGGCAGCTC	CTACCCCAAG
GTATGAAGCC CGAATACGc CCGTAA					

m919.pep

1	<u>MKKYLFRAAL</u>	<u>YGIAAAILAA</u>	<u>CQSKSIQTFF</u>	<u>QPDTSVINGP</u>	<u>DRPVGIPDPA</u>
51	GTTVGGGGAV	YTVVPHLSLP	HWAQAQDFAKS	LQSFRLGCAN	LKNRQGWQDV
101	CAQAPQTPVH	SFQAKQFFER	YFTPWQVAGN	GSLAGTVTGY	YEPVLKGGDDR
151	RTAQARFFIY	GIPDDFISVP	LPAGLRSGKA	LVRIRQTGKN	SGTIDNTGGT
201	HTADLSRFFI	TARTTAIKGR	FEGSRFLPYH	TRNQINGGAL	DGKAPILGYA
251	EDPVELFFMH	IQSGRLKPT	SGKYIRIGYA	DKNEHPYVSI	GRYMAKGYL
301	KLQGTSMQGI	KSYMRRQNQR	LAELVLQONPS	YIFFRELGS	ANDGPVGALG
351	TPLMGEYAGA	VDRIYITLGA	PLFVATAHPV	TRKALNRLIM	SDQTGSAIKG
401	AVRVDYFWGY	GDEAGELAGK	QKTTGYVWOL	LPNGMKPEYR	P*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N.gonorrhoeae*  
ORF 919 shows 95.9 % identity over a 441 aa overlap with a predicted ORF (ORF  
919.ng) from *N. gonorrhoeae*:  
**m919/g919**

	10	20	30	40	50	60
m919.pep	MKKYLFRALYGIAAAAILAACQSKSIQTFFPQDTSVINGPDRPVGPDPAGTTVGGGAV					
	:   :   :                 :                     :             :					
g919	MKKHLLRSALYGIAAAAILAACQRSISQTFFPQDTSVINGPDRPAGIPDPAGTTVAGGGAV					
	:					
	10	20	30	40	50	60
	70	80	90	100	110	120
m919.pep	YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAQFQTPVHSFOAKQFFER					
	:   :					
g919	YTVVPHLSMPHWAAQDFAKSLQSFRLGCANLKNRQGWDVCAQAQFQTPVHSFOAKRFFER					
	:   :					
	70	80	90	100	110	120

1318

	130	140	150	160	170	180
m919.pap	YFTPWQVAGNGSLAGTVTGYEVLKGDGDRRTAQARFPIYGIPDDFISVPLPAGLRSGKA					
g919	YFTPWQVAGNGSLAGTVTGYEVLKGDGRRTERARFPIYGIPDDFISVPLPAGLRGGKN					
	130	140	150	160	170	180
	190	200	210	220	230	240
m919.pap	LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
g919	LVRIRQTGKNSGTIDNAGGTHTADLSRFPITARTTAIKGRFEGSRFLPYHTRNQINGGAL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m919.pap	DGKAPILGYAEDFVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
g919	DGKAPILGYAEDFVELFFMHIQSGRLKTPSGKYIRIGYADKNEHPYVSIGRYMADKGYL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m919.pap	KLGQTSMQGIKSYMRQNPQRLAEVLGQNPYSIYFFRELAGSSNDGPVAGALGTPLMGEYAGA					
g919	KLGQTSMQGIKAYMRQNPQRLAEVLGQNPYSIYFFRELAGSGNEGFPVAGALGTPLMGEYAGA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m919.pap	VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
	:					
g919	IDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVVDYFWGYGDEAGELAGK					
	370	380	390	400	410	420
	430	440				
m919.pap	QKTTGYVWQLLPNGMKPEYRFX					
g919	QKTTGYVWQLLPNGMKPEYRFX					
	430	440				

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2793>:

```

a919.seq
1  ATGAAAAAAT ACCTATTCCG CGCCGCCCTG TGCGGCATCG CCGCCGCCAT
51  CCTCGCCGCC TGCCAAAGCA AGAGCATCCA AACCTTTCCG CAACCCGACA
101 CATCCGTCAT CAACGGCCCG GACCGGCCGG TCGGCATCCC CGACCCCGCC
151 GGAACGACGG TCGCGGCCGG CGGGGCCGTT TATACCGTTG TGCCGCACCT
201 GTCCCTGCCC CACTGGGCGG CGCAGGATTT CGCCAAAAGC CTGCAATCCT
251 TCCGCCTCGG CTGCGCCAAT TTGAAAAACC GCCAAGGCTG CGAGGATGTG
301 TGCGCCCAAG CCTTTCAAAC CCCCGTCCAT TCCGTTCAAG CAAAACAGTT
351 TTTTGAACGC TATTTACGCG CGTGGCAGGT TGCAGGCAAC GGAAGCCTTG
401 CCGGTACGGT TACCGGCTAT TACGAGCCGG TGCTGAAGGG CGACGACAGG
451 CGGACGGCAC AAGCCCGCTT CCCGATTAC GGTATTCCCG ACGATTTTAT
501 CTCGTCCTCC CTGCTGCGG GTTTGCGGAG CGGAAAAGCC CTGTGTCGCA
551 TCAGGCAGAC GGGAAAAAAC AGCGGCACAA TCGACAATAC CGGCGGCACA
601 CATACCGCCG ACCTCTCCCA ATTCCCCTAT ACTGCGCGCA CAACGGCAAT
651 CAAAGGCAGG TTTGAAGGAA GCCGCTTCCT CCCCTACCAC ACGCGCAACC
701 AAATCAACGG CGGCGCGCTT GACGGCAAAG CCCCGATACT CGGTTACGCC
751 GAAGACCCCG TCGAACTTTT TTTTATGCAC ATCCAAGGCT CGGGCCGTCT
801 GAAAACCCCG TCCGGCAAAT ACATCCGCAT CGGCTATGCC GACAAAAACG
851 AACATCCCTA CGTTTCCATC GGACGCTATA TGGCGGACAA AGGCTACCTC
901 AAGCTCGGGC AGACCTCGAT GCAGGGCATC AAAGCCTATA TGCAGCAAAA
951 CCCGCAACGC CTCGCCGAAG TTTTGGGGCA AAACCCAGC TATATCTTTT
1001 TCCGAGAGCT TACCGGAAGC AGCAATGACG GCCCTGTCGG CGCACTGGGC
1051 ACGCCGCTGA TGGGCGAGTA CGCCGGCGCA GTCGACCGGC ACTACATTAC
1101 CTTGGGCGCG CCCTTATTTG TCGCCACCGC CCATCCGTTT ACCCGCAAAG

```

1319

1151 CCCTCAACCG CCTGATTATG GCGCAGGATA CCGGCAGCGC GATTAAAGGC  
 1201 GCGGTGCGCG TGGATTATTT TTGGGGATAC GCGGACGAAG CCGGCGAACT  
 1251 TGCCGCGAAA CAGAAAACCA CGGGATATGT CTGGCAGCTT CTGCCAACG  
 1301 GTATGAAGCC CGAATACCG CCGTAA

This corresponds to the amino acid sequence <SEQ ID 2794; ORF 919.a>:  
 a919.pep

```

      1  MKKYLFRAL  CGIAAAILAA  CQSKSIQTFP  QPDTSVINGP  DRPVGIPDPA
    51  GTTVGGGGAV  YTVVPHLSLP  HWAQDFAKS  LQSFRLGCAN  LKNRQGWQDV
   101  CAQAFQTPVH  SVQAKQFFER  YFTPWQVAGN  GSLAGTVTGY  YEPVLKGDGR
   151  RTAQARFPIY  GIPDDFISVP  LPAGLRSGKA  LVRIRQTGKN  SGTIDNTGGT
   201  HTADLSQFPI  TARTTAIKGR  FEGRFLPYH  TRNQINGGAL  DGKAPILGYA
   251  EDPVELFFMH  IQSGRLKTP  SGKYIRIGYA  DKNEHPYVSI  GRYMADKGYL
   301  KLGQTSMQGI  KAYMQONPQR  LAEVLGQNPS  YIFFRELTGS  SNDGPVGALG
   351  TPLMGEYAGA  VDRHYITLGA  PLFVATAHPV  TRKALNRLIM  AQDTGSAIKG
   401  AVRVDYFWGY  GDEAGELAGK  QKTTGYVWQL  LPNGMKPEYR  P*

m919/a919  98.6% identity in 441 aa overlap
      10      20      30      40      50      60
m919.pep  MKKYLFRALYGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          |||||  |||||  |||||  |||||  |||||  |||||
a919      MKKYLFRALCGIAAAILAACQSKSIQTFPQPDTSVINGPDRPVGIPDPAGTTVGGGGAV
          10      20      30      40      50      60

      70      80      90     100     110     120
m919.pep  YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCQAQFQTPVHVSQAKQFFER
          |||||  |||||  |||||  |||||  |||||  |||||
a919      YTVVPHLSLPHWAAQDFAKSLQSFRLGCANLKNRQGWQDVCQAQFQTPVHVSQAKQFFER
          70      80      90     100     110     120

      130     140     150     160     170     180
m919.pep  YFTPWQVAGNGSLAGTVTGYIEPVLKGDGRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
          |||||  |||||  |||||  |||||  |||||  |||||
a919      YFTPWQVAGNGSLAGTVTGYIEPVLKGDGRRTAQARFPIYGIPDDFISVPLPAGLRSGKA
          130     140     150     160     170     180

      190     200     210     220     230     240
m919.pep  LVRIRQTGKNSGTIDNTGGTHTADLSRFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
          |||||  |||||  |||||  |||||  |||||  |||||
a919      LVRIRQTGKNSGTIDNTGGTHTADLSQFPITARTTAIKGRFEGRFLPYHTRNQINGGAL
          190     200     210     220     230     240

      250     260     270     280     290     300
m919.pep  DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          |||||  |||||  |||||  |||||  |||||  |||||
a919      DGKAPILGYAEDPVELFFMHIIQSGRLKTPSGKYIRIGYADKNEHPYVSI GRYMADKGYL
          250     260     270     280     290     300

      310     320     330     340     350     360
m919.pep  KLGQTSMQGIKSYMQRNPORLAEVLGQNPSYIFFRELAGSSNDGPVGALGTPLMGEYAGA
          |||||  |||||  |||||  |||||  |||||  |||||
a919      KLGQTSMQGIKAYMQONPQORLAEVLGQNPSYIFFRELTGSSNDGPVGALGTPLMGEYAGA
          310     320     330     340     350     360

      370     380     390     400     410     420
m919.pep  VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          |||||  |||||  |||||  |||||  |||||  |||||
a919      VDRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
          370     380     390     400     410     420

      430     440
m919.pep  QKTTGYVWQLLPNGMKPEYRPX
          |||||  |||||
a919      QKTTGYVWQLLPNGMKPEYRPX
          430     440

```



Expression of ORF 919

The primer described in Example 1 for ORF 919 was used to locate and clone ORF 919. This sequence was purified and expressed in *E. coli* as provided in Figure 1 #. The hydrophilicity plots, antigenic index, and amphipathic regions of ORF 919 is provided in Figure 5 #. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 919 is provided in Exhibit C #.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2795>:

```
g920.seq (partial)
1  ..ccgatgcagc tggttaccga aaaAGGTAAG GAAAACATGA TTCAACGCGG
51  CACATACAAC TACCAATACC GCAGCAACCG TCCCGTCAAA GACGGCAGCT
101 ACCTCGTTAC CGCGAATAT CAGCCTACTT TCCCGTCAAA AAACAAAGCA
151 GGCTGGAAAC AGGCTGGCAT CAAAGAAATG CCTGACGCAA GCTATTGCGA
201 ACAAACCCGT ATGTTCCGTA AAAACATTGT CAACGTGGGA CACGAAAGCG
251 CGGACACCGC CATCATCACC AAACCGGTCG GACAAAACCTT GGAAATCGTC
301 CCGCTGGACA ATCcgccgca caTTCACgtg ggctaacgCt tcaaaGTccg
351 cgttCtgttc cgtGGCgaac cgCTGcccaa tgccACCgtt accgCtacAT
401 TTGacggctt cGAcaccagc gaccgcagca aaacgcacaa Aaccgaagcc
451 caagcctTCT ccgacaccac cgacggcgaa ggcgaagtgg acatcatCCC
501 CTTGCGccaa GGCTTttgga aAgcGAGTGT CGAATAcaaa gccgAtttcc
551 CCGATcaaAG CCTGTGccga AAACAggcga ACTACaCaac TTtaaccttc
601 caaatcgccc attctCacca tTAa
```

This corresponds to the amino acid sequence <SEQ ID 2796; ORF 920.ng>:

```
g920.pep (partial)
1  ..PMQLVTEKGK ENMIQRGTYN YQYRSNRPVK DGSYLVTAEY QPTFRSKNKA
51  GWKQAGIKEM PDASYCEQTR MFGKNIVNVG HESADTAIIT KPVGQNLEIV
101 PLDNPAIDHV GXRFKVRVLF RGEPLPNATV TATFDGFDTS DRSKTHKTEA
151 QAFSDTTDGE GEVDIIPLRQ GFWKASVEYK ADFPDQSLCR KQANYTTTLTF
201 QIAHSHH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2797>:

```
m920.seq
1  ATGAAGAAAA CATTGACACT GCTCTCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGmGTCT GGGTCGAAAC CGCCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAAACA TGATTCAACG CGGCACATAC AACTACCACT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAwACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTCTG
401 GCAAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAArCCGG TCGGACAAAA CTTGGAAATC GTCCCCTGCG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCGT TTCCGTGGCG
551 AACCCTGCTC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTCGACACC
601 AGCGACCGCA GCAAAACGCA CAAwmCCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CmCCTTGCGC CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA
```

This corresponds to the amino acid sequence <SEQ ID 2798; ORF 920>:

```
m920.pep
1  MKKTLTLLSV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKKK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
```

g920/m920

```

g920.pep      10          20          30
               PMQLVTEKGKENMIQRGTYNQYQRSNRPVK
               |||||
m920          GGEYLKADLGYGFEFLEPIAKDRLHIFSKPMQLVTEKGKENMIQRGTYNQYQRSNRPVK
              40          50          60          70          80          90

              40          50          60          70          80          90
g920.pep      DGSYLVTAEQPTFRSKNKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
               |||||
m920          DGSYLVIAEQPTFWSSKKAGWKQAGIKEMPDASYCEQTRMFGKNIVNVGHESADTAIIT
              100         110         120         130         140         150

              100         110         120         130         140         150
g920.pep      KPVGQNLEIVPLDNPAIHVGXRFKVRVLFRGEPLPNATVTATFDGFDTSDRSKTHKTEA
               |||||
m920          KPVGQNLEIVPLDNPANIHVGERFKVRVLFRGEPLPNATVTATFDGFDTSDRSKTHXXEA
              160         170         180         190         200         210

              160         170         180         190         200
g920.pep      QAFSDTTDGEGEVDIIPLRQGFVKASVEYKADFDPQSLCRKQANYTTLTFQIAHSHHX
               |||||
m920          QAFSDSTDKEGEVDIIIXLRQGFVKANVEHKTDFFDPQSVCQKQANYSTLTFQIGHSHHX
              220         230         240         250         260

```

```

a920.seq
1  TGAAGAAGAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCGCATC
51  CGCCCACGCC CACCGCGTGT GGGTCGAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCCAG ACTCGAACC
151 ATCGCCAAAG ACCGCTTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGCGGG
351 CATCAAAACA ATGCCTGACG CAAGCTATTG GCACAAACCT CGAATGTTCT
401 GCAAAACAT CGTCAACGTC GGACACGAAA CGCGGCACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAATC GTCCCCTGG ACAATCCCGC
501 CAACATTGCC GTAGGCGAAC GCTTCAAAGT CCGCGTTCGT TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG TCTTCGACAC
601 AGCGACCGCA GCAAAACGCA GAAACCGAA CGACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGT CAAGGCTTCT
701 GGAAAGCCAA TGTCGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCAATAA

```

a920.pap

1	*KKTLLTLLAV	<u>SALFAASAHA</u>	HRVWVETAHT	HGGEYLKADL	GYGEFPELEP
51	IAKDRLLHIFS	KPMQLVTEKG	KENMIQRGTY	NYQYRSNRPV	KDGSYLVIAE
101	YQPTFWSKNK	AGWKQAGIKQ	MPDASYCEQT	RMFGKNIVNV	GHSADTAII
151	TKPVGQNLEI	VPLDNPNANH	VGERFKVRVL	FRGEPLPNAT	VTATFDGFDT
201	SDRSKTHKTE	AQAFSDSTDD	KGEVDIIPLR	QGFVKANVEH	KADFPDQSVC
251	QKQANYSTLT	FOIGHSHH*			

m920/a920 97.0% identity in 267 aa overlap

1322

	10	20	30	40	50	60
m920.pep	MKKTLTLLSVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGFEFPELEPIAKDRLHIFS					
a920	XKKTLLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGFEFPELEPIAKDRLHIFS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m920.pep	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKXKAGWKQAGIKE					
a920	KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m920.pep	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
a920	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m920.pep	FRGEPLPNATVTATFDGFDTSDRSKTHXKEAQAFSDSTDDKGEVDIIXLRQGFWKANVEH					
a920	FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH					
	190	200	210	220	230	240
	250	260	269			
m920.pep	KTDFFDQSVQCQKQANYSTLTFQIGHSHHX					
a920	KADFFDQSVQCQKQANYSTLTFQIGHSHHX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2801>:

g920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCcggtt TcCGCACTAT TTGCCACATc
51  cgCaCACCCC CACCgCGTCT GGGTCGAAAC CgcccACACg cAcgGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGccAAAG ACCgccTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGT AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAT
251 ACCGCAGCAA CCGTCCCCTC AAAGACGGCA GCTACCTCGT TACCGCCGAA
301 TATCAGCCTA CTTTCCGGTC AAAAAACAAA GCAGGCTGGA AACAGGCTGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGTATGTTG
401 GTAAAAACAT TGTCAACGTG GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTACG GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCTA CATTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCCCAAGCCT TCTCCGACAC
651 CACCGACGGC AAAGGCGAAG TGGACATCAT CCCCTTGGCG CAAGGCTTTT
701 GGAAAGCGAG TGTGGAATAC AAAGCGGATT TCCCGATCA AAGCCTGTGC
751 CAAAACAGG CGAACTACAC AACTTTAACC TTCCAAATCG GCCATTCTCA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2802; ORF 920-1.ng>:

g920-1.pep

```

1  MKKTLTLLAV SALFATSAHP HRVWVETAHT HGGEYLKADL GYGFEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVTAE
101 YQPTFRSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFD
201 SDRSKTHKTE AQAFSDTTDG KGEVDIIPLR QGFWKASVEY KADFFDQSLC
251 KQQANYTTLT FQIGHSHH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2803>:

m920-1.seq

```

1  ATGAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCCACATC
51  CGCCCACGCC CACCGCTCT GGGTCGAAAC CGCCACACG CACGGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTCCCCGA ACTCGAACCC
151 ATCGCCAAAG ACCGCCTGCA CATCTTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAGT
251 ACCGAAGCAA CCGTCCCCTT AAGGACGGCA GTTACCTCGT CATCGCCGAA

```

```

301 TAATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAAGAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAACCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GTCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2804; ORF 920-1>:

m920-1.pep

```

1 MKKTLTLLAV SALFATSAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51 IAKDRLHIFS KPMQLVTERG KENMIQRTGY NYQYRSNRPV KDGSYLVIAE
101 YQPTFWSKNK AGWKQAGIKE MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKPVGQNLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDT
201 SDRSKTHKTE AQAFSDSTDD KGEVDIPLR QGFWKANVEH KTDFFDQSVK
251 QKQANYSTLT FQIGHSHH*

```

m920-1/g920-1 96.3% identity in 268 aa overlap

m920-1.pep	10	20	30	40	50	60
	MKKTLTLLAVSALFATSAHAHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
g920-1	MKKTLTLLAVSALFATSAHPRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS					
m920-1.pep	70	80	90	100	110	120
	KPMQLVTERGKENMIQRTGYNYQYRSNRPVKDGSYLVIAEYQPTFWSKNKAGWKQAGIKE					
g920-1	KPMQLVTERGKENMIQRTGYNYQYRSNRPVKDGSYLVIAEYQPTFRSKNKAGWKQAGIKE					
m920-1.pep	130	140	150	160	170	180
	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
g920-1	MPDASYCEQTRMFGKNIVNVGHESADTAITKPVGQNLEIVPLDNPANIHVGERFKVRVL					
m920-1.pep	190	200	210	220	230	240
	FRGEPLPNATVTATFDGFDTSRDRSKTHKTEAQAFSDSTDDKGEVDIPLRQGFWKANVEH					
g920-1	FRGEPLPNATVTATFDGFDTSRDRSKTHKTEAQAFSDTDGKGEVDIPLRQGFWKASVEY					
m920-1.pep	250	260	269			
	KTDFFDQSVKQKQANYSTLTTFQIGHSHHX					
g920-1	KADFFDQSLCQKQANYTTLTFQIGHSHHX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2805>:

a920.seq

```

1 TGAAAGAAAA CATTGACACT GCTCGCCGTT TCCGCCCTAT TTGCGGCATC
51 CGCCACAGCC CACCGCTCT GGTGCGAAAC CGCCACACAG CACGCGGCG
101 AATACCTTAA AGCCGACTTG GGCTACGGCG AATTTCCTGA ACTCGAACCC
151 ATCGCCAAAG ACCGCTGCA CATCTCAGC AAACCGATGC AGCTGGTTAC
201 CGAAAAAGGC AAGGAAAACA TGATTCAACG CGGCACATAC AACTACCAAGT
251 ACCGAAGCAA CCGTCCCGTT AAGGACGGCA GTTACCTCGT CATCGCCGAA
301 TATCAGCCTA CTTTCTGGTC AAAAAACAAA GCAGGCTGGA AACAGGCGGG
351 CATCAACAAA ATGCCTGACG CAAGCTATTG CGAACAAACC CGAATGTTTCG
401 GCAAAACAT CGTCAACGTC GGACACGAAA GCGCGGACAC CGCCATCATC
451 ACCAAACCGG TCGGACAAAA CTTGGAAATC GTCCCGCTGG ACAATCCCGC
501 CAACATTCAC GTAGGCGAAC GCTTCAAAGT CCGCGTTCTG TTCCGTGGCG
551 AACCGCTGCC CAATGCCACC GTTACCGCCA CCTTTGACGG CTTGCACACC
601 AGCGACCGCA GCAAAACGCA CAAAACCGAA GCACAGGCTT TCTCCGACAG
651 CACAGACGAC AAAGGCGAAG TGGACATCAT CCCCTTGCGC CAAGGCTTCT
701 GGAAGCCAA TGTGGAACAC AAAGCCGACT TCCCCGATCA AAGCGTGTGC
751 CAAAACAGG CGAACTACTC GACTTTAACC TTCCAAATCG GCCATTGCGA
801 CCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 2806; ORF 920-1.a>:

```

a920.pep
1  *KKTLTLLAV SALFAASAHA HRVWVETAHT HGGEYLKADL GYGEFPELEP
51  IAKDRLHIFS KPMQLVTEKG KENMIQRGTY NYQYRSNRPV KDGSYLVAIE
101 YQP TFWSKNK AGWKQAGIKQ MPDASYCEQT RMFGKNIVNV GHESADTAII
151 TKP VQONLEI VPLDNPANIH VGERFKVRVL FRGEPLPNAT VTATFDGFDI
201 SDRSKTHKTE AQAFSDSTDD KGEVDIIPLR QGFWKANVEH KADFPDQSVC
251 QKQANYSTLT FQIGHSHH*

m920-1/a920 98.9% identity in 267 aa overlap

      10      20      30      40      50      60
m920-1.pep MKKTLTLLAVSALFATSAAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
a920      XXXKTLTLLAVSALFAASAHHRVWVETAHTHGGEYLKADLGYGEFPELEPIAKDRLHIFS
      10      20      30      40      50      60

      70      80      90     100     110     120
m920-1.pep KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKE
a920      KPMQLVTEKGKENMIQRGTYNQYRSNRPVKDGSYLVAIEYQPTFWSKNKAGWKQAGIKQ
      70      80      90     100     110     120

      130     140     150     160     170     180
m920-1.pep MPDASYCEQTRMFGKNIVNVGHESADTAITKPVQONLEIVPLDNPANIHVGERFKVRVL
a920      MPDASYCEQTRMFGKNIVNVGHESADTAITKPVQONLEIVPLDNPANIHVGERFKVRVL
      130     140     150     160     170     180

      190     200     210     220     230     240
m920-1.pep FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
a920      FRGEPLPNATVTATFDGFDTSDRSKTHKTEAQAFSDSTDDKGEVDIIPLRQGFWKANVEH
      190     200     210     220     230     240

      250     260     269
m920-1.pep KTDFFPDQSVCCQKQANYSTLTFQIGHSHHX
a920      KADFPDQSVCCQKQANYSTLTFQIGHSHHX
      250     260

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2807>:

```

g921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTCC TTTCCGggtG
51  Ccagtctatt tatGtgccca cattgacggA aatccccgTg aatccccatca
101 ataCCgtcaa aacggaagCA CCTGCAAAAG GTTTTCGCCT CGCCCCTTCG
151 CATTGGGCGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGcgGCG CAATATCTGA
251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG
301 TATGAAATCT ACCTGCGTTC GCGGTAGAC AGCCAGCGCG GCGAAATCAA
351 TACGGAACAG TCCAAGCTGT ATATCGAGAA TGCCTTGCGC GGCTGGCAGC
401 AGCGTtggaA AAATATGGAT GCCAAACCCG ATAATCCCCG ATTTACCAAC
451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 2808; ORF 921.ng>:

```

g921.pep
1  MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLAPS
51  HWADVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM
101 YEIYLRSAVD SQRGEINTEQ SKLYIENALR GWQQRWKNMD AKPDNPFTN
151 FLMEVMKMQP LK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2809>:

```

m921.seq
1  ATGAAAAAAT ACCTTATCCC TCTTTCCATT GCGGCAGTTC TTTCCGGCTG
51  CCACTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA
101 ATACCGTCAA AACGGAAGCA CCTGCAAAAG GTTTCCGCCT TGCCTCTTCG
151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA
201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA

```

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251 A CAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 T ATGAAATCT ACCTGCGTTC GCGATAGAC AGCCAGCGGG GCGCAATCAA  
 351 T ACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC  
 401 A GCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC  
 451 T TTTTGATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2810; ORF 921>:

m921.pep

1 MKKYLIPLSI AAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS  
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM  
 101 YEIYLRSAID SQRGAINTAQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
 151 FLMEVMKMQP LK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 921 shows 95.7% identity over a 162 aa overlap with a predicted ORF (ORF 921.ng) from *N. gonorrhoeae*:

m921/g921

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
g921	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLAPSHWADVAKISD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m921.pep	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTAQ					
g921	EATRLGYQVGIGKMTKVQAAQYLNFRKRLVGRNAVDDSMYEIYLRSAVDSQRGEINTAQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.pep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFLMEVMKMQPLKX					
g921	SKLYIENALRGWQQRWKNMDAKPDNPAFTNFLMEVMKMQPLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2811>:

a921.seq

1 ATGAAAAAAT ACCTTATCCC TCTTTCCATT GTGGCAGTTC TTTCCGGCTG  
 51 CCAGTCTATT TATGTGCCCA CATTGACGGA AATCCCCGTG AATCCTATCA  
 101 ATACCGTCAA AACGGAAGCA CCTGCAAAG GTTCCCGCT TGCCTCTTCG  
 151 CATTGGACGG ATGTTGCCAA AATCAGCGAT GAAGCGACGC GCTTGGGCTA  
 201 TCAGGTGGGT ATCGGTAAAA TGACCAAGGT TCAGGCGGCG CAATATCTGA  
 251 ACAACTTCAG AAAACGCCTG GTCGGACGCA ATGCCGTCGA TGACAGTATG  
 301 TATGAAATCT ACCTGCGTTC GCGATAGAC AGCCAGCGGG GCGCAATCAA  
 351 TACGGAACAG TCCAAGCTGT ATATCCAGAA TGCCTTGCGC GGCTGGCAGC  
 401 AGCGTTGGAA AAATATGGAT GTCAAACCCA ACAACCCCGC ATTTACCAAC  
 451 TTTTGTATGG AAGTGATGAA GATGCAGCCC TTGAAATGA

This corresponds to the amino acid sequence <SEQ ID 2812; ORF 921.a>:

a921.pep

1 MKKYLIPLSI VAVLSGCQSI YVPTLTEIPV NPINTVKTEA PAKGFRLASS  
 51 HWTDVAKISD EATRLGYQVG IGKMTKVQAA QYLNFRKRL VGRNAVDDSM  
 101 YEIYLRSAID SQRGAINTAQ SKLYIQNALR GWQQRWKNMD VKPNNPAFTN  
 151 FLMEVMKMQP LK\*

m921/a921 99.4% identity in 162 aa overlap

	10	20	30	40	50	60
m921.pep	MKKYLIPLSIAAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
a921	MKKYLIPLSIVAVLSGCQSIYVPTLTEIPVNPINTVKTEAPAKGFRLASSHWTDVAKISD					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m921.p ep	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
a921	EATRLGYQVGIGKMTKVQAAQYLNNFRKRLVGRNAVDDSMYEIYLRSAIDSQRGAINTEQ					
	70	80	90	100	110	120
	130	140	150	160		
m921.p ep	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFMLEVMKMQLKX					
a921	SKLYIQNALRGWQQRWKNMDVKPNNPAFTNFMLEVMKMQLKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2813>:

g922.seq

```

1  ATGGAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CCCGCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAC CGGTATCCGA CAGCGGGTTT GCCGCCAATG CAAATGTCCG
201 CCGTTTTGTG GACGATGAAG TCGGGAAGG GGATTTTTC CAGGCGGAAT
251 GGCAGGATTT TTTGACAAA GCGGCTTACA AGGCGGACAT CGTCAAGATT
301 ATGCACCGAC CCTCCACATC GCGTCCGTGG TATGtgttcc gCacggGAAa
351 tt cGGgcagg gcgaaAtttc ACggcgCGCG Caggttttat GcggaaAacc
401 gcgcggttat cgatgatgtg gcgCAAAa acggcgGCC TGCCGAGCTT
451 ATCGTGGCGA TTATCGGGAT TGAAACGAAT TACGGCAAAA ATACGGGCAG
501 TTTCCGTGTG GCGGACGCAT TGGCGACTTT AGGCTTTGAT TATCCCCGCC
551 GCGCCGGGTT TTCCAAAAA GAATTGGTCG AGCTTTTAAA GCTGGCAAAA
601 GAAGAAGGCG GTGATGTTTT CGCCTTTAAG GGCagcTATG CGGGTGCAAT
651 GGGTATGCCG CAATTTATGC CTTGAGCTA CCGGAAATGG GCGGTGGATT
701 ATGAcgggga cggacatCGG GATATAtggg GCAACGTcgg tgatgtcgcg
751 gcatcggTTG CCAATTat at gaagCAGCAC GGTGGCGCA CgggcggtAA
801 AATGTTGGTG TCGGCGAcgt tggcgccggg tgcggATGTT CaggcAATCA
851 TTGGCGAAAA AACCGCCCTG ACGCGGACGG TGGCGGATT GAaggCGTAc
901 ggcacatccc ccggggaaac GCTCGCAGAT GATGAAAAGg cgTTTTTGT
951 CAAACTGGAA ACCGCACCCG GCGTGTGTTGA ATATTATTG GGCTTGAACA
1001 ATTTTATAC GGTATGGCAG TACAACCACA GCCGGATGTA TGTAAACGgcg
1051 gtcaggGACA TTGCAATTC GCTCGCGCGC CCGGGATTGT Aa

```

This corresponds to the amino acid sequence <SEQ ID 2814; ORF 922.ng>:

g922.p ep

```

1  MEKRKILPLA ICLAALSACT AMEARTPRAN EAQAPRADEM KESRPAFDA
51  AAVPVSDSGF AANANVRRFV DDEVKGDFS QA EWQDFDK AAYKADIVKI
101 MHRPSTSRPW YVFR TGNSGR AKFHGARRFY AENRAIDDV AQKYGPael
151 IVAIIGIETN YGNTGSFRV ADALATLGF YPRRAGFFQK ELVELLKLAK
201 EEGGDVFAFK GSYAGAMGMP QFMPSSYRKW AVDYDGDGHR DIWGNVGDVA
251 ASVANYMKQH GWRTGGKMLV SATLAPGADV QAIIGETAL TRTVADLKAY
301 GIIPGETLAD DEKAVLFKLE TAPGVFEYYL GLNNFYTVWQ YNHSRMVTA
351 VRDIANSLGG PGL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2815>:

m922.seq

```

1  ATGAAAAAGA GAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCCTGTACG GCGATGGAGG CACGCCACACC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGTGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 GCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTCCCG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCGTGGTA
351 TGTGTTCCGC ACGGAAATT CCGGCAAGGC GAAATTTCCG GCGCGCGGCC
401 GGTTTTATGC GGAAAACCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CGCAAAAAT ACGGCAGTT TCCGTGTGGC GGACGATTG GCGACCTTAG
551 GCTTTGATTA CCCCCCGCGC GCCGGGTTTT TCCAAAAAGA ATTGGTCGAG

```

```

601 CTTTAAAGC TGGCAAAGA AGAAGGCGC GATGTTTCG CCTTAAAGG
651 CAGCTATGCG GCGCAATGG GGATGCCGA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGATTAT GACGGGACG GACATCGGA CATATGGGGC
751 AACGTCGGCG ATGTCGCGG ATCGGTTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GCGGGAAAA TGCTGGTGTC TGCAACATTG GCGCCGGGTG
851 CCGATGTTCA GGCAATCATT GCGGAAAAA CCGCCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCCC GCGGAAGAGC TTGCAGATGA
951 TGAAAAGGCG GTTTTGTTCA AACTGGAAAC CGCACCGGCG GTGTTTGAAT
1001 ATTATTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAACCACAGC
1051 CCGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCCC
1101 GGGATTGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2816; ORF 922>:

m922.pep

```

1 MKKRKILPLA ICLAALSACT AMEARPPRAN EAQAPRAVEM KKERPAFDA
51 AAVFDAAAVP VSDSGFAANA NVRRFVDEV GKGDfsRAEW QDFDKAAYK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRFYAENR ALIDDVAQKY
151 GVPaelIVAV IGIETNYGKN TGSFRVADAL ATLGFDYPRR AGFFQKELVE
201 LLKLAKKEGG DVFAFKGSYA GAMGMPQFMP SSYRKWAVDY DGDGHRDIWG
251 NVGDVAASVA NYMKQHGWR TGGKMLVSATL APGADVQAI GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFEYLLGLNN FYTVWQYNHS
351 RMYVTAVRDI ANSLGGPGL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 922 shows 95.9% identity over a 369 aa overlap with a predicted ORF (ORF 922.ng) from *N. gonorrhoeae*:

m922/g922

m922.pep	10	20	30	40	50	60
	MKKRKILPLAICLAALSACTAMEARPPRANEAQAPRAVEMKKERPAFDA					
	:					
g922	10	20	30	40	50	
	MEKRKILPLAICLAALSACTAMEARTPRANEAQAPRADEMKKERPAFDAA-----AVP					
m922.pep	70	80	90	100	110	120
	VSDSGFAANANVRRFVDEVGKGDfsRAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
	:					
g922	60	70	80	90	100	110
	VSDSGFAANANVRRFVDEVGKGDfsQAEWQDFDKAAYKADIVKIMHRPSTSRPWYVFR					
m922.pep	130	140	150	160	170	180
	TGNSGKAKFRGARRFYAENRALIDDVAQKYGVPaelIVAVIGIETNYGKNTGSFRVADAL					
	: :					
g922	120	130	140	150	160	170
	TGNSGRAKFGARRFYAENRAVIDDVAQKYGVPaelIVAIIGIETNYGKNTGSFRVADAL					
m922.pep	190	200	210	220	230	240
	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
	:					
g922	180	190	200	210	220	230
	ATLGFDYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY					
m922.pep	250	260	270	280	290	300
	DGDGHRDIWGNVGDVAASVANYMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
	:					
g922	240	250	260	270	280	290
	DGDGHRDIWGNVGDVAASVANYMKQHGWR TGGKMLVSATLAPGADVQAI IGEKTALTRTV					
m922.pep	310	320	330	340	350	360
	ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					
	:					
g922	ADLKAYGIIPGETLADDEKAVLFKLETAPGVFEYLLGLNNFYTVWQYNHSRMYVTAVRDI					



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	300	310	320	330	340	350
	370					
m922.pep	ANSLGGPGLX					
g922	ANSLGGPGLX					
	360					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2817>:

```
a922.seq
1  ATGAAAAACA GAAAAATACT GCCGCTGGCA ATTTGTTTGG CGGCTTTGTC
51  TGCTGTACG GCGATGGAGG CACGCCCGCC CCGGGCAAAT GAAGCCCAAG
101 CCCCCCGCGC GGATGAAATG AAAAAAGAAA GCCGCCCGC GTTTGACGCG
151 CCAGCCGTAT TTGACGCGGC AGCCGTACCG GTATCCGACA GCGGGTTTGC
201 CGCCAATGCA AATGTCCGCC GTTTTGTGGA CGATGAAGTC GGGAAAGGGG
251 ATTTTTCCTG GCGGAATGG CAGGATTTT TTGACAAAGC GGCTTACAAG
301 GCGGACATCG TCAAGATTAT GCACCGCCCC TCCACATCGC GTCCGTGGTA
351 TGTGTTCCGC ACGGGAATT CCGGCAAGGC GAAATTTTCG GCGCGCGGCC
401 GGTTTTATGC GGAACCCGC GCGCTTATCG ATGATGTGGC GCAAAAATAC
451 GCGGTGCCTG CCGAATTAT CGTGGCGGTT ATCGGGATTG AAACGAATTA
501 CCGCAAAAT ACGGGCAGTT TCCGTGTGGC GGACGCATTG GCGACCTTAG
551 GCTTTGATTA CCCCCGCCG GCCGGGTTT TCCAAAAGA ATTGGTCGAG
601 CTTTAAAGC TGGCAAAGA AGAAGGCGGC GATGTTTTCG CCTTTAAAGG
651 CAGCTATGCG GGCGCAATGG GGATGCCGCA ATTTATGCCT TCGAGCTACC
701 GGAAATGGGC GGTGGATTAT GACGGGGACG GACATCGGGA CATATGGGGC
751 AATGTTGGCG ATGTCGCGGC ATCGATTGCC AATTATATGA AGCAGCACGG
801 TTGGCGCACG GGCGGGAAAA TACTGGTGTC TGCAACATTG GCGCCGGGTG
851 CCGATGTTCA GGCAATCATT GGCGAAAAA CCGCCTGAC GCGGACGGTG
901 GCGGATTGTA AGGCGTACGG CATCATCCC GCGGAAGAGC TTGCCGATGA
951 TGAAGAGGCG GTTTTGTTC AACTGGAAC CGCACCCGGC GTGTTTGAAT
1001 ATTATTTGGG CTTGAACAAT TTTTATACGG TATGGCAGTA CAATCACAGT
1051 CCGATGTATG TAACGGCGGT CAGGGACATT GCCAATTCGC TTGGCGGCC
1101 GGGATTGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2818; ORF 922.a>:

```
a922.pep
1  MKNRKILPLA ICLAALSACT AMEARPPRAN EAQAPRADEM KKEsrPAFDA
51  AAVFDAAAVP VDSGFAANA NVRRFVDEV GKGDfSRAEW QDFFDKAAyK
101 ADIVKIMHRP STSRPWYVFR TGNSGKAKFR GARRfYAENR ALIDDVAQkY
151 GVPaelIVAV IGIETNYGKN TGSFRVADAL ATLGfDYPRR AGFFQkELVE
201 LLKLAKEEGG DVFAFKGSYA GAMGMPQfMP SsYRKWAVDY DGDGHRDIWG
251 NVGDVAASIA NYMKQHGwRT GgKILVSATL APGADVQAIi GEKTALTRTV
301 ADLKAYGIIP GEELADDEKA VLFKLETAPG VFeyYLGLNN FYTVWQYNhS
351 RMYVTAVRDI ANSLGGPGL*
```

m922/a922 98.9% identity in 369 aa overlap

	10	20	30	40	50	60
m922.pep	MKKRKILPLAICLAALSACTAMEARPPRANEQAQAPRAVEMKKESRPAPFDAAAVFDAAAVP					
	:					
a922	MKNRKILPLAICLAALSACTAMEARPPRANEQAQAPRADEMKKESRPAPFDAAAVFDAAAVP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m922.pep	VDSGFAANANVRRFVDEVGKGDfSRAEWQDFFDKAAyKADIVKIMHRPSTSRPWYVFR					
a922	VDSGFAANANVRRFVDEVGKGDfSRAEWQDFFDKAAyKADIVKIMHRPSTSRPWYVFR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m922.pep	TGNSGKAKFRGARRfYAENRALIDDVAQkYGVPaelIVAVIGIETNYGKNtGSFRVADAL					
a922	TGNSGKAKFRGARRfYAENRALIDDVAQkYGVPaelIVAVIGIETNYGKNtGSFRVADAL					
	130	140	150	160	170	180
	190	200	210	220	230	240

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```

m922.pep  ATLGFDPYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922       ATLGFDPYPRRAGFFQKELVELLKLAKKEGGDVFAFKGSYAGAMGMPQFMPSSYRKWAVDY
          190      200      210      220      230      240

          250      260      270      280      290      300
m922.pep  DGDGHRDIWGNVGDVAASVANYMKQHGWRGTGGKMLVSATLAPGADVQAIIGEKALTALTRTV
          ||||||||||||||||:||||||||||||||||||||||||||||||||||||
a922       DGDGHRDIWGNVGDVAASIANYMKQHGWRGTGGKILVSATLAPGADVQAIIGEKALTALTRTV
          250      260      270      280      290      300

          310      320      330      340      350      360
m922.pep  ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
a922       ADLKAYGIIPGEELADDEKAVLFKLETAPGVFEYYLGLNNFYTVWQYNHSRMYVTAVRDI
          310      320      330      340      350      360

          370
m922.pep  ANSLGGPGLX
          ||||||||
a922       ANSLGGPGLX
          370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2819>:

```

g923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACCGATG GCGTGTGCGG CATTTCGTGC
51  CGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTCCTGCCTG CCTTGTTCGG
201 CGGTTGGACG GGCGCATACT TGGGTAGTAG GATGTTTCAGG CATAAAACGG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCT GCATCCTGAT TGATTATTC GTTCCGCCCG AACTTTTGT
351 AAAACTCGGG CAACATCTCT GA

```

This corresponds to the amino acid sequence <SEQ ID 2820; ORF 923.ng>:

```

g923.pep
1  MKROAFFKPM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRAVR
51  GKRRIPRHRL LLPALFGGWT GAYLGSRMFR HKTAKKRFV LFRITVSGNV
101 LATCILIDYF VPPELFVKLG QHL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2821>:

```

m923.seq
1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTTCGTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTTGCACTT TACGGCATCG ACAAACGGTG CGCCATACGG
151 GGGCAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CATTGCTCGG
201 CGGCTGGGTG GGCGCGTATT TCGGCAGCAT GACATTCAAA CATAAGACAG
251 CGAAAAGCG TTTTGTGTG CTGTTCCGTC TGACTGTTTC AGGTAATGTC
301 TTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTAA ACCAGTACGG
351 CGTTGCCCTG CCTTGCCGTA CTATTGTAC TGTCTGCGGC TTCGTGCCT
401 TGTCTCTGATT TTGTTAATC CACTATAT.T ATTTTGTCCC GCCTGAATT
451 TTCGTAAAC TCGGCAGAA TACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2822; ORF 923>:

```

m923.pep
1  MKROAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRCAR
51  GQRRIPEHRL LLPALLGGWV GAYFGSMTFK HKTAKKRFV LFRITVSGNV
101 LATLILYSG LNLNQYGVAS PCRTICTVCG FVALS*FLLI HYXYFVPEF
151 FVKLGQNT*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 923 shows 68.8% identity over a 157 aa overlap with a predicted ORF (ORF 923.ng) from *N. gonorrhoeae*:

g923/m923

	10	20	30	40	50	60
g923.pep	MKRQAFFKPMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
m923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100		
g923.pep	LLPALFGGWTGAYLGSRMFRHKTAKKRFVVLFRFTVSGNVLATCILID-----					
m923	LLPALGGWVGAYFGSMTFKHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			110	120		
g923.pep	-----YFVPPELFFVKLGQHLX					
m923	PCRTICTVCGFVALSXFLLIHYIYFVPPEFFVKLGQNTX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2823>:

a923.seq

```

1  ATGAAGCGGC AGGCTTTCTT CAAACTGATG GCGTGTGCGG CATTCTCTGC
51  TGCCGTTTCG CTGCGCCTCC CCGTATTGGG CGCGTGTTAC GCAATATTGT
101 CCCTCTATGC GTTGCACCTT TACGGCATCG ACAACGCGCG TGCCGTGCGG
151 GGAAAACGCC GCATTCCCGA ACACCGCCTG CTGCTGCCTG CCTGTGTCGG
201 CGGTTGGGCG GCGGCATACT TGGGCAGCAG GATATTCAGG CATAAACCGG
251 CGAAAAAGCG TTTGTGTTGT CTGTTCCGTC TGACTGTTTC GGGCAATGTC
301 CTGGCGACCC TCATCCTGAT TTATAGTGGA TTAAATTAA ACCAGTACGG
351 CGTTGCCTCG CCTTA.GCTC AAAGAGAACG ATTCTCTAAG GTGCTGAAGC
401 ACCAAGTGAA TCGGTTCCGT ACTATTTGTA CTGTCTGCGG CTTCGTCGCC
451 TTGTCCTGAT TTTGTGTAAT CCACTAT.AT TATTTTGTCC CGCCTGAATT
501 TTTCGTAAAA CTCGGGCAGA ATACCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2824; ORF 923.a>:

a923.pep

```

1  MKRQAFFKLM ACAAFLSAVS LRLPVLGACY AILSLYAFAL YGIDKRRVR
51  GKRRRIPEHRL LLPALFGGWA GAYLGSRIFR HKTAKKRFVV LFRFTVSGNV
101 LATLILIIYSG LNLNQYGVAS PXAQRERFSK VLKHQVNRER TICTVCGFVA
151 LS*FLLIHYX YFVPPEFFVK LGQNT*

```

m923/a923 84.6% identity in 175 aa overlap

	10	20	30	40	50	60
m923.pep	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRCRAIRGQRRRIPEHRL					
a923	MKRQAFFKLMACAAFLSAVSLRLPVLGACYAILSLEYAFALYGIDKRRRAVRGKRRIPEHRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m923.pep	LLPALGGWVGAYFGSMTFKHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLNQYGVAS					
a923	LLPALFGGWAGAYLGSRIFRHKTAKKRFVVLFRFTVSGNVLATLILIIYSGNLNLNQYGVAS					
	70	80	90	100	110	120
			130	140	150	159
m923.pep	PC-----RTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
a923	PXAQRERFSKVLKHQVNRFTICTVCGFVALSXFLLIHYXYFVPPEFFVKLGQNTX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2825>:

```
g925.seq
1  ATGAAACAAA TGCTTTTGGC cgtcggcggtg ggcGCGGTGT TGGCGGGCTG
51  CGGCAaggat gcCGGCGGtt acgaggggtTA TTGGCGCGAA AAGTCGGACA
101 AAAAagaggG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2826; ORF 925.ng>:

```
g925.pep
1  MKQMLLAVGV GAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNYFLN
51  KI NVFTGKEE SLLLSEKDGA LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKCKGQT QAYLDARNAL PSNQTYYQRO AAIEQLKRRF
151 EAEFDELEKE IKCNKPTLL F*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2827>:

```
m925.seq (partial)
1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGCGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG TATGATTGCC GTCAAAAAAG AAAAAGGCAA TTACTTCCTT
.....
```

This corresponds to the amino acid sequence <SEQ ID 2828; ORF 925>:

```
m925.pep (partial)
1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGYFL..
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 925 shows 94.0% identity over a 50 aa overlap with a predicted ORF (ORF 925.ng) from *N. gonorrhoeae*:

m925/g925

	10	20	30	40	50
m925.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGYFL				
	:				
g925	MKQMLLAVGVGAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNYFLNKINVFTGKE				
	10	20	30	40	50
g925	ESLLLSEKDGA LSINTGIGEIPIKLSDDGKELYVERRRYVKTDAA MKDKIIAHQKCKGQT				
	60	70	80	90	100 110

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2829>:

```
g925-1.seq
1  ATGAAACAAA TGCTTTTGGC CGTCGGCGTG GCGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGCGCGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAAGAGGG CGTGATTGCC GTCAAAAAA AAGGCAATTA CTTCTTAAT
151 AAAATCAACG TGTTTACAGG CAAGGAGGAG TCTTTGCTTT TGTCTGAAAA
201 AGACGGCGCG CTTTCGATAA ACACGGGGAT AGGGGAAATC CCGATCAAAC
251 TTTCCGACGA CGGAAAGAG CTGTATGTCG AACGCAGGCG GTATGTGAAA
301 ACCGATGCGG CGATGAAGGA CAAATCATC GCCCACCAGA AAAAGTGCGG
351 ACAACGGCA CAGGCATACC TCGACGCGCG AAATGCGTTG CCGTCAAACC
401 AAACGTATCA GCAGCGTCAG GCGGCGATCG AGCAATTGAA ACGGCGGTTT
451 GAAGCCGAGT TTGACGAATT GGAAAAAGAA ATCAAATGCA ACGGCAAACC
501 GACATTGTTG TTTTAG
```

This corresponds to the amino acid sequence <SEQ ID 2830; ORF 925-1.ng>:

g925-1.pep

1332

```

1  MKQMLLAVGV AAVLAGCGKD AGGYEGYWRE KSDKKEGVIA VKKKGNVFLN
51  KINVFTGKEE SLLSEKDG LSINTGIGEI PIKLSDDGKE LYVERRRYVK
101 TDAAMKDKII AHQKKCGQT QAYLDARNAL PSNQTYQQRQ AAIEQLKRRF
151 EAEFDELEKE IKCNGKPTLL F*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2831>:

m925-1.seq

```

1  ATGAAACAAA TGCTTTTAGC CGTCGGCGTG GTGGCGGTGT TGGCGGGCTG
51  CGGCAAGGAT GCCGGCGGTT ACGAGGGTTA TTGGCGCGAA AAGTCGGACA
101 AAAAGAGAGG TATGATTGCC GTCAAAAAG AAAAAGGCAA TTAATTCCTT
151 AATAAATCC ACCTGGTTAC AGGCAAGGAA GAGTCCTTGC TTTTGTCTGA
201 AAAAGACGGC GCGCTTTCGA TAAACACAGG GATAGGGGAA ATCCCGATCA
251 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGTAG GCAGTATGTC
301 AAAACCGATG CCGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
351 CGGACAAACA GCACAGGCAT ACCGCGACGC GCGAAATGCG TTGCCGTCAA
401 ACCAGACGTA TCAGCAGCAT CTGGCGGCGA TCGAGCAATT GAAACGGCGG
451 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAG
501 AAGCCCGGCA TTGTTGCTTT AG

```

This corresponds to the amino acid sequence <SEQ ID 2832; ORF 925-1>:

m925-1.pep..

```

1  MKQMLLAVGV VAVLAGCGKD AGGYEGYWRE KSDKKEGMIA VKKEKGNVFL
51  NKIHVVTGKE ESLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
101 KTDAAAMKDKI IAHQKKCGQT AQAYRDARNA LPSNQTYQQH LAAIEQLKRR
151 FEAEFDELEK EIKCNGRSPA LLL*

```

m925/g925 92.5% identity in 173 aa overlap

	10	20	30	40	50	60
m925-1.pep	MKQMLLAVGVVAVLAGCGKDAGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKE					
g925-1	MKQMLLAVGVAAVLAGCGKDAGGYEGYWREKSDKKEGVIAVKK-KGNVFLNKINVFTGKE					
	10	20	30	40	50	

	70	80	90	100	110	120
m925-1.pep	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRQYVKTDAAMKDKIIAHQKKCGQT					
g925-1	ESLLSEKDGALSINTGIGEIPKLSDDGKELYVERRRYVKTDAAMKDKIIAHQKKCGQT					
	60	70	80	90	100	110

	130	140	150	160	170	
m925-1.pep	AQAYRDARNALPSNQTYQQHLAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX					
g925-1	AQAYLDARNALPSNQTYQQRAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX					
	120	130	140	150	160	170

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2833>:

a925-1.seq

```

1  AATAAATCA ACCTGTTTAC AGGTAAGGAA GAATCTATGC TTTTGTCTGA
51  AAAAGACGGC GCGCTTTCGA TAAACACGGG GATAGGGGAA ATCCCGATCA
101 AACTTTCCGA CGACGGGAAA GAGCTGTATG TCGAACGCAG GCAGTATGTC
151 AAAACCGATG CCGCGATGAA GGACAAAATC ATCGCCCATC AGAAAAAGTG
201 CGGACAAACG GCACAGGCAT ATCTCGACGC GCGAAATGCG TTGCCGTCAA
251 ACCAGACGTA TCAGCAGCAT CAGGCGGCGA TCGAGCAGTT GAAACGGCGG
301 TTTGAAGCCG AGTTTGACGA ATTGGAAAAA GAAATCAAAT GCAACGGCAA
351 ACCGACATTG TTGTTTTAG

```

This corresponds to the amino acid sequence <SEQ ID 2834; ORF 925-1.a>:

a925-1.pep

```

1  NKINVTGKE ESMLLSEKDG ALSINTGIGE IPIKLSDDGK ELYVERRQYV
51  KTDAAAMKDKI IAHQKKCGQT AQAYLDARNA LPSNQTYQQH QAAIEQLKRR
101 FEAEFDELEK EIKCNGKPTL LF*

```

a925-1/m925-1 92.7% identity in 123 aa overlap

		10	20	30		
a925-1.pep		NKINVTGKEESMLLSEKDGALSINTGIGE				
m925-1	AGGYEGYWREKSDKKEGMIAVKKEKGNVFLNKIHVVTGKEESLLSEKDGALSINTGIGE					
	30	40	50	60	70	80
	40	50	60	70	80	90

1333

```

a925-1.pep      IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKCKGQTAQAYLDARNALPSNQTYQQH
                  |||
m925-1          IPIKLSDDGKELYVERRQYVKTDAAAMKDKIIAHQKCKGQTAQAYRDARNALPSNQTYQQH
                  90      100      110      120      130      140

                  100      110      120
a925-1.pep      QAAIEQLKRRFEAEFDELEKEIKCNGK-PTLLFX
                  |||
m925-1          LAAIEQLKRRFEAEFDELEKEIKCNGRSPALLX
                  150      160      170

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2835>:

```

g926.seq (partial)
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCGGAAGGG CGGTTGGCAG TCAAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CGCCCGTGG AAACCATCAA
201 TATCAACACC CCTTTGGGCA GTACGCTCGG ACAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAGGT
301 ACGgaagact tGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCGGAAG GCAGGCGTGT GCGGCGCGC CCTtaccGCA
401 TCCGTTTCTAGA CGGCATATTG GAACAATAcg GttggACAAT cgggCagaac
451 tgCCGACAGT GGGGGGCaag tccgaacgtt gcaactGaa...

```

This corresponds to the amino acid sequence <SEQ ID 2836; ORF 926.ng>:

```

g926.pep (partial)
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAEQ
101 TEDLSRQLVG FKLPIQYLHI WAEGRRVAGA PYRIRSDGIL EQYGTWIGQN
151 CRQWGASPNV ATE...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2837>:

```

m926.seq
1  ATGAAACACA CCGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC
51 GCAATTACCT CAAATAACG AAAACCTGTG GCAGCCGTCC GAACACATCA
101 GCAGTTTTCG AGCAGAAGGG CGGTTGGCAG TGAAGCGGA AGGGAAGGT
151 TCGTATGCAA ATTTTCGATTG GACATACCAA CGCCCGTGG AAACCATCAA
201 TATCAATACC CCTTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG
251 ACGGCGCATT GGCAGTGGAC GGCAAAGGAA ATGTCTATCA GGCAGAAAGT
301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAACGTC CAATCCAATA
351 TCTGCATATC TGGGCAGATG GCAGGCGTGT GCGGCGCGC CCTTACCGCA
401 TCCGTCGCGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAAC
451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT
501 GAACATCAGG CTGGTTTTC ACGAAATCG TATGCCGTCT GAAACCGAAA
551 CCCCGGAACG CTGTGCGGCG CGCACGAGAT AA

```

This corresponds to the amino acid sequence <SEQ ID 2838; ORF 926>:

```

m926.pep
1  MKHTVSASVI LLLTACAQLP QNNENLWQPS EHISSFAAEG RLAVKAEGKG
51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES
101 AEELSRQLVG FKLPIQYLHI WADGRRVAGA PYRILPDGIL EQYGTWVGRT
151 ADSSGQVRTL QLNNGNLNIR LVFTEIGMPS ETETPERCAA RTR*

```

g926/m926 91.6% identity in 155 aa overlap

```

                  10      20      30      40      50      60
g926.pep      MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
                  |||
m926          MKHTVSASVILLTACAQLPQNNENLWQPSEHISSFAAEGRLAVKAEGKGSYANFDWTYQ
                  10      20      30      40      50      60

                  70      80      90      100     110     120
g926.pep      PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEGETEDLSRQLVGFKLPIQYLHI
                  |||
m926          PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAEAEELSRQLVGFKLPIQYLHI
                  70      80      90      100     110     120

                  130     140     150     160
g926.pep      WAEGRRVAGAPYRIRSDGILEQYGTWIGQNCRQWGASPNVATE

```

1334

m926  
 ||:||||||| |||||:|:|  
 WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS  
 130 140 150 160 170 180

## a926.seq

1 ATGAAACACA CTGTATCCGC ATCGGTCATC CTGCTTTTGA CCGCTTGCGC  
 51 GCAATTACCT CAAAATAACG AAAACCTGTG GCAGCCGTCC GAACACACCC  
 101 GCAGTTTCAC GCGGAAGGG CGGTGGCAG TGAAAGCGGA AGGGAAAGGT  
 151 TCGTATGCAA ATTTGATTG GACATACCAA CCGCCCGTGG AAACCATCAA  
 201 TATCAACACC CCTTGGGCA GTACGCTCGG GCAGTTGTGT CAAGACAGGG  
 251 ACGGCGCATT GGCAGTGGAC GGCAGAGGAA ATGTCTATCA GCGGAAAGT  
 301 GCGGAAGAAT TGAGCAGGCA GCTGGTCGGT TTCAAAGTGC CAATCCAATA  
 351 TCTGCATATC TGGGCAGATG GCAGGCCTGT GCGGGGCGCG CCTTACCGCA  
 401 TCCTGCCGGA CGGCATATTG GAACAATACG GTTGGACTGT CGGCAGAACC  
 451 GCCGACAGTG GGGGGCAAGT CCGAACGTTG CAACTGAATA ACGGAAATTT  
 501 GAACATCAGG CTGGTTTTCA CCGAGATTGG TATGCCGTCT GAAACCGAAA  
 551 CCCAAGAACA ATGCGCGGCA CGCATACAGT AA

## a926.pep

1 MKHTVSASVI LLLTACAQLP QNNENLWQPS EHTRSFTAEG RLAVKAEGKG  
 51 SYANFDWTYQ PPVETININT PLGSTLGQLC QDRDGALAVD GKGNVYQAES  
 101 AEELSRLVGF FKLPIQYLHI WADGRPVAGA PYRILPDGIL EQYGWTVGRT  
 151 ADSGGQVRTL QLNNGNLNR LVFTEIGMPS ETETQECCAA RIQ\*

m926/a926 96.9% identity in 191 aa overlap

	10	20	30	40	50	60
m926.pep	MKHTVSASVILLTACAQLPQNNENLWQPSSEHISFSAEGRRLAVKAEGKGSYANFDWTYQ					
a926	MKHTVSASVILLTACAQLPQNNENLWQPSSEHTRSFTAEGRLAVKAEGKGSYANFDWTYQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m926.pep	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRLVGFKLPIQYLHI					
a926	PPVETININTPLGSTLGQLCQDRDGALAVDGKGNVYQAESAELSRLVGFKLPIQYLHI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m926.pep	WADGRRVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
a926	WADGRPVAGAPYRILPDGILEQYGWTVGRTADSGGQVRTLQLNNGNLNIRLVFTEIGMPS					
	130	140	150	160	170	180
	190					
m926.pep	ETETPERCAARTRX					
a926	ETETQECCARIQX					
	190					

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2839>:

## g927.seq

1 atgaaaacct acGCacAggC ACTCTATacc GCAGCCCTGC TCACCGCCTG  
 51 CAGCCCcgca GCcgatTcaa accatCCGTC CGGAcAAaAT GCCCCGGCCA  
 101 ATACCGAATC cgacGgaaAA AACATtaccC TGctcaatgc cTcgtacgat  
 151 gtGACACGGT ATTTttacaa agaatacgac cacTtgtttg tcggaaCATA  
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAA TCCCACGGCG  
 251 GCTTCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCITCA AGCCGATGTC  
 301 GTAACCATGA ACCAATCTTC CGACATCGAC CTGCTCGAAA AAAA.GGACT  
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGATCACGCC GCACCCTACA

1335

401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCcaa ACAGAtccgC  
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAAGAC  
 501 CTCGGGCAAC GGACGCTACG CCTTCCTCGG CGCATACGGT TACGGTCTGA  
 551 AAGCCAACAA CGGcaaCGAG CAGGAAGCCC AAAAaCTCGT CGCATCCATC  
 601 CTCAAAAACA CACCCGTTTT TGAaaACGGC GGACGCGc.c CGCCGCCACC  
 651 ACCCTTCACAC AACGCAACAT CGGCGACGTA CTCATCACTT TTGAAAACga  
 701 agCcaactac gtCAGCAAAA AACTGA

This corresponds to the amino acid sequence <SEQ ID 2840; ORF 927.ng>:

g927.pep

1 MKTYAQALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD  
 51 VTRYFYKEYD HLFVGTQYSE HPGTSVSIQQ SHGGFSKQAL SVANGLQADV  
 101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR  
 151 DWNDLAKDGV NIVIAKTSNG GRYAFLGAYG YGLKANNGNE QEAQKLVASI  
 201 LKNTPVFENG GRXPPPPSH NATSATYSSL LTKPTTSAK N\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2841>:

m927.seq

1 ATGAAACCT ACGACCCGGC ACTCTATACC GCAGCCCTGC TCACCGCCTG  
 51 CAGCCCCGCA GCCGATTCAA ACCATCCGTC CGGACAAAAT GCCCCGGCCA  
 101 ATACCGAATC CGACGGAAAA AACATTACCC TGCTCAACGC CTCATACGAT  
 151 GTGGCAGGGG ATTTTACAA AGAATACAAC CCCTTATTTA TCAAAACATA  
 201 CCAATCCGAA CACCCCGGCA CATCCGTCAG CATCCAACAG TCCACGGCG  
 251 GCTCCAGCAA ACAGGCATTA TCCGTAGCCA ACGGCCTTCA AGCCGATGTC  
 301 GTAACCATGA ACCAATCCTC CGACATCGAC CTGCTCGAAA AAAAAGGACT  
 351 GGTAGAAAAA GGCTGGCAAC AAGCCCTCCC CGACCACGCC GCGCCCTACA  
 401 CCAGCACTAT GGTTCCTT GTCCGAAAA ACAACCCCAA ACAGATCCGC  
 451 GATTGGAACG ACCTTGCCAA AGACGGCGTT AACATCGTCA TCGCCAATCC  
 501 CAAAACCTCG GGCAACGGAC GCTACGCCTT CCTCGGCGCA TACGGTTACG  
 551 GTCTGAAAAA CACCAACGGC AACGAACAGG AAGCCCAAAA ACTCGTCGCA  
 601 TCATCCTCA AAAACACCCC CGTTTTTGA AAGGCGGAC GCKcGCCACC  
 651 ACCACCTTCA CACAACGCAA CATCGGCGAC GTACTCATCA CTTTGAAAA  
 701 CGAAGCCAAC TACGTCAGC AAAAActGA

This corresponds to the amino acid sequence <SEQ ID 2842; ORF 927>:

m927.pep

1 MKTYAPALYT AALLTACSPA ADSNHPSGQN APANTESDGK NITLLNASYD  
 51 VARDFYKEYN PLFIKTYQSE HPGTSVSIQQ SHGGSSKQAL SVANGLQADV  
 101 VTMNQSSDID LLEKKGLVEK GWQQALPDHA APYTSTMVFL VRKNNPKQIR  
 151 DWNDLAKDGV NIVIANPKTS GNGRYAFLGA YGYGLKTTNG NEQEAQKLVA  
 201 SILKNTPVFE NGGRXPPPS HNATSATYSS LLTKPTTSA KN\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 927 shows 94.2% identity over a 243 aa overlap with a predicted ORF (ORF 927.ng) from *N. gonorrhoeae*:

g927/m927

	10	20	30	40	50	60
g927.pep	MKTYAQALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVTRYFYKEYD					
	:       :					
m927	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60
	70	80	90	100	110	120
g927.pep	HLFVGTQYSEHPGTSVSIQQSHGGFSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	:					
m927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120
	130	140	150	160	170	
g927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIA--KTSNGRYAFLGA					
m927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGRYAFLGA					
	130	140	150	160	170	180



1336

	180	190	200	210	220	230
g927.pep	YGYGLKANNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTS					
	:					
m927	YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPP-SHNATSATYSSLLKTKPTTS					
	190	200	210	220	230	

	240
g927.pep	AKNX
m927	AKNX
	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2843>:

a927.seq

1	ATGAAAACCT	ACGCACCGGC	ACTCTATACC	GCAGCCCTGC	TCAGCGCCTG
51	CAGCCCCGCA	GCCGATTCAA	ACCATCCGTC	CGGACAAAAT	GCCCCGCCA
101	ATACCGAATC	CGACGGAAAA	AACATTACCC	TGCTCAACGC	CTCATACGAT
151	GTGGCACGGG	ATTTTACAA	AGAATACAA	CCCTTATTTA	TCAAAACATA
201	CCAATCCGAA	CACCCCGGCA	CATCCGTCAG	CATCCAACAG	TCCCACGGCG
251	GCTCCAGCAA	ACAGGCATTA	TCCGTAGCCA	ACGGCCTTCA	AGCCGATGTC
301	GTAACCATGA	ACCAATCCTC	CGACATCGAC	CTGCTCGAAA	AAAAAGGACT
351	GGTAGAAAAA	GGCTGGCAAC	AAGCCCTCCC	CGACCACGCC	GCGCCCTACA
401	CCAGCACTAT	GGTTTTCCTT	GTCCGAAAAA	ACAACCCCAA	ACAGATCCGC
451	GATTGGAACG	ACCTTGCCAA	AGACGGCGTT	AACATCGTCA	TCGCCAATCC
501	CAAAACCTCG	GGCAACGGAC	GCTACGCCTT	CCTCGGCGCA	TACGGTTACG
551	GTCTGAAAAC	CACCAACGGC	AACGAACAGG	AAGCCCAAAA	ACTCGTCGCA
601	TCCATCCTCA	AAAACACCCC	CGTTTTTGAA	AACGGCGGAC	GCGCGCCACC
651	ACCACCTTCA	CACAACGCAA	CATCGGCGAC	GTACTCATCA	CTTTTGAAAA
701	CGAAGCCAAC	TACGTCAGCA	AAAAACTGA		

This corresponds to the amino acid sequence <SEQ ID 2844; ORF 927.a>:

a927.pep

1	MKTYAPALYT	AALLSACSPA	ADSNHPSGQN	APANTESDGK	NITLLNASYD
51	VARDFYKEYN	PLFIKTYQSE	HPGTSVSIQQ	SHGGSSKQAL	SVANGLQADV
101	VTMNQSSDID	LLEKKGLVEK	GWQQALPDHA	APYTSTMVFL	VRKNNPKQIR
151	DWNDLAKDGV	NIVIANPKTS	GNGRYAFLGA	YGYGLKTTNG	NEQEAQKLVA
201	SILKNTVPFE	NGGRAPPPPS	HNATSATYSS	LLKTKPTTSA	KN*

m927/a927 99.2% identity in 242 aa overlap

	10	20	30	40	50	60
m927.pep	MKTYAPALYTAALLTACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	:					
a927	MKTYAPALYTAALLSACSPAADSNHPSGQNAPANTESDGKNITLLNASYDVARDFYKEYN					
	10	20	30	40	50	60

	70	80	90	100	110	120
m927.pep	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	:					
a927	PLFIKTYQSEHPGTSVSIQQSHGGSSKQALSVANGLQADVVTMNQSSDIDLLEKKGLVEK					
	70	80	90	100	110	120

	130	140	150	160	170	180
m927.pep	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA					
	:					
a927	GWQQALPDHAAPYTSTMVFLVRKNNPKQIRDWNDLAKDGVNIVIANPKTSNGNGRYAFLGA					
	130	140	150	160	170	180

	190	200	210	220	230	240
m927.pep	YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRXPPPPSHNATSATYSSLLKTKPTTSA					
	:					
a927	YGYGLKTTNGNEQEAQKLVASILKNTVPVFENGGRAPPPPSHNATSATYSSLLKTKPTTSA					
	190	200	210	220	230	240

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m927.pap KNX  
 |||  
 a927 KNX

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2845>:

g929.seq  
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG  
 51 CGCCCTGGTT TTGGCACTGC CCGTACccga CGGGGTCAAG CCTCAGGCTT  
 101 GGACGCTGCT GGCTATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG  
 151 GTTATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT  
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA  
 251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT  
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT  
 351 TATCGCCGTT TTTGGAAGAA AAACgctggg CATCGGTTAC AGTCTCGCTC  
 401 TTTCGGAAC GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC  
 451 GCGGCGATTA TACATCgaT TATGcagtcg attgCcgCA GttacggctC  
 501 caatCCCGCA AAAGGCACag aaggcaagat gggtaAATAT TtggcTTtgg  
 551 tc aattatCA TTCaaTCCC atttcgtcgg ctAtggctat taCTGcaact  
 601 gCCCCaaACC CTTTAATcgt caacttgatt gccGaaaaTt taggcagtag  
 651 tt tccgtCTT Tcttgggggg cgTGGGcgTg ggcaatGGCT Gttcccggcg  
 701 tt atcgcctt TttcgTTATG CTTTGATTTT TATATTTTTT GTATCCGCCT  
 751 GA AATTAAAG AAACGCCCAA TGCTGttcAA TTTGCCAAAG ACCGTCTGAG  
 801 CGAGATGGGT AAAATGtcgg CAGACGAAAT CATTATGGCG GTCATTTTCG  
 851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT  
 901 CA CGCTTTTA GTATCAacgc caccGCCACC GCATTATATCG GATTAAGCCT  
 951 GC TTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTTG AAAGAAAAAA  
 1001 GC GCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA  
 1051 TT TTTaAATA Aactcggact gattaaatGG TTCTCCGAG TGTGGCGGA  
 1101 Aa gtgtcggc GGT TTTGGCG TTAGCGGCAC GGCTCGGGC GTAATCCTCG  
 1151 TGCTTGctta TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT  
 1201 ATTACCGCTA TGTTCCGCGC ATTTCTCGCT GTCGCCGTTT CACTGAATGC  
 1251 CC CGGCGATG CCGACTGCGC TGATGATGGC GGCCGCATCC AACATTATGA  
 1301 TGACCCCTCAC TCATTATGCG ACCGGTACTT CACCTGTGAT TTTCGGCTCG  
 1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTTA TCATGAGCGT  
 1401 AGTCAATTTT CTGATTTTTT CCGTTATCGG CAGCATTTGG TGGAAAGTTC  
 1451 TGCGATATTG GTAA

This corresponds to the amino acid sequence <SEQ ID 2846; ORF 929.ng>:

g929.pap  
 1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK  
 51 VMPLGALSII AVGLVAVTV TADKPGAAMS DALSAFANPL IWLIAIAVMI  
 101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLLA PVTPSNTARG  
 151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMAITAT  
 201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP  
 251 EI KETPNAVQ FAKDRLSEMG KMSADEIIMA VIFGILLLLW ADVPALITGN  
 301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA  
 351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH  
 401 ITAMFGAFLA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS  
 451 GYTTMGEWWK AGFIMSVVNF LIFSVIGSIW WKVLGYW\*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2847>:

m929.seq  
 1 ATGAAATTGG GTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG  
 51 CGCCCTGGTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT  
 101 GGACGCTGCT GGCCATGTTT GTCGGTGTGA TTGCCGCCAT TATCGGCAAG  
 151 GCCATGCCGT TGGGCGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT  
 201 AACCGGCGTA ACCGCCGACA AACCGGGCGC GGCGATGAGC GATGCGTTGA  
 251 GTGCGTTTCG CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT  
 301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTTGTT  
 351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC  
 401 TTTCGGAAC GCTGCTGGCT CCCGTTACCC CTTCCAATAC CGCGCGCGGC

```

451 GGCGGCATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTCTGTCG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCGGCTTT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGGCG
701 TTATCGCCTT TTTCGTTATG CCTTTGATT TATATTWYT GTATCCGCCT
751 GAAATTAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGCT GCTGTTGTGG GCAGATGTTT CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGACTTGGGA CGATGTTTGT AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGAG TGTGGCGGA
1101 AAGTGTCCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCGCGCGATG CCGACCGCGC TGATGATGGC GCGCGCATCC AACATTATGA
1301 TGACCCTCAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTCCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGAAG GCGGGTTTA TCATGAGCGT
1401 AGTTCAATTT CTGATTTTTT TCGTTATCGG CAGCATTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2848; ORF 929>:

m929.pep

```

1 MKLGFKPIPL AIAAVLCALV LALPVPDGVK PQAWTLLAMF VGVIAAIIGK
51 AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTLGIGY SLALSELLA PVTSPNTARG
151 GGIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYXLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASSTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNF LIFFVIGSIW WKVLGYW*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 929 shows 98.8% identity over a 487 aa overlap with a predicted ORF (ORF 929.ng) from *N. gonorrhoeae*:

g929/m929

	10	20	30	40	50	60
g929.pep	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPKQAWTLLAMFVGVIAAIIGKVMPLGALSII					
m929	MKLGFKPIPLAIAAVLCALVLALPVPDGVKPKQAWTLLAMFVGVIAAIIGKAMPLGALSII					
	10	20	30	40	50	60
g929.pep	AVGLVAVTGVTTADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
m929	AVGLVAVTGVTTADKPGAAMSDALSAFANPLIWLIAIAVMISRGLLKTGLGMRIGYLFIAV					
	70	80	90	100	110	120
g929.pep	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
m929	FGRKTLGIGYSLALSELLAPVTSPNTARGGGIIHPIMQSIAGSYGSNPAKGTEGKMGKY					
	130	140	150	160	170	180
g929.pep	LALVNYHNPFISSAMAITATAPNPLIVNLIENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
m929	LALVNYHNPFISSAMFITATAPNPLIVNLIENLGSSFRLSWGAWAWAMAVPGVIAFFVM					
	190	200	210	220	230	240

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	190	200	210	220	230	240
	250	260	270	280	290	300
g929.pep	PLILYFLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
m929	PLILYXLYPPEIKETPNVQFAKDRLEMGKMSADEIIMAVIFGILLLLWADVLPALITGN					
	250	260	270	280	290	300
	310	320	330	340	350	360
g929.pep	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
m929	HAFSINATATAFIGLSLLLLSGVLTWDDVLKEKSAWDTIIWFGALIMMAAFNLKGLIKW					
	310	320	330	340	350	360
	370	380	390	400	410	420
g929.pep	FSGVLAESVGGGLGVSGTAAGVILVLAIFYAHYMFASSTAHITAMFGAFLAAVSLNAPAM					
m929	FSGVLAESVGGGLGVSGTAAGVILVLAIFYAHYMFASSTAHITAMFGAFAAAVSLNAPAM					
	370	380	390	400	410	420
	430	440	450	460	470	480
g929.pep	PTALMMAAASNIMMTLTHYATGTSPIVFGSGYTTMGEWWKAGFIMSVVNFLIFSVIGSIW					
m929	PTALMMAAASNIMMTLTHYATGTSPIVFGSGYTTMGEWWKAGFIMSVVNFLIFFVIGSIW					
	430	440	450	460	470	480
g929.pep	WKVLGYWX					
m929	WKVLGYWX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2849>:

a929.seq

```

1  ATGAAATTGG GTTTCAAACC GATACCCCTC GCCATTGCCG CAGTATTGTG
51  CGCCTTGTTT TTGGCACTGC CCGTACCCGA CGGGGTCAAG CCTCAGGCTT
101 GGACGCTGCT GGCCATGTTT ATCGGTGTA TTGCCGCCAT TATCGGCAAG
151 GCCATGCCGT TGGGTGCGCT GTCGATTATT GCCGTCGGGT TGGTCGCAGT
201 AACCGGCGTA ACCGCCGACA AACCGGGTGC GGCATGAGC GATGCGTTGA
251 GTGCGTTCGC CAATCCGTTG ATTTGGCTGA TTGCCATCGC AGTTATGATT
301 TCGCGCGGTT TGCTCAAAAC AGGGCTGGGG ATGCGTATCG GATATTGTTT
351 TATCGCCGTT TTTGGAAGAA AAACGCTGGG CATCGGTTAC AGTCTCGCTC
401 TTTCCGAAC TCTGCTGGCT CCGGTTACCC CTCCAATAC CGCGCGCGGC
451 GCGGCGATTA TACATCCGAT TATGCAGTCG ATTGCCGGCA GTTACGCTC
501 CAATCCCGCA AAAGGCACAG AAGGCAAGAT GGTAAATAT TTGGCTTTGG
551 TCAACTATCA TTCCAATCCC ATTTGCTCGG CTATGTTTAT TACTGCAACT
601 GCCCCCAACC CTTTAATCGT CAACTTGATT GCCGAAAATT TAGGCAGTAG
651 TTTCCGCTCT TCTTGGGGGG CGTGGGCGTG GGCAATGGCT GTTCCCGCGC
701 TTATCGCCTT TTTGCTTATG CCTTTGATTT TATATTTTTT GTATCCGCCT
751 GAAATTAAAG AAACGCCCAA TGCCGTTCAA TTTGCCAAAG ACCGTCTGAG
801 GGAGATGGGT AAAATGTCGG CAGACGAAAT CATTATGGCG GTCATTTTCG
851 GTATCTTGTT GCTGTTGTGG GCAGATGTC CCGCCCTTAT TACCGGCAAT
901 CACGCTTTTA GTATCAACGC CACCGCCACC GCATTATCG GATTAAGCCT
951 GCTTTTGCTT TCCGGTGTAT TGAATGGGA CGATGTTTTG AAAGAAAAAA
1001 GCGCGTGGGA TACGATTATT TGGTTTGGCG CATTGATTAT GATGGCCGCA
1051 TTTTAAATA AACTCGGACT GATTAAATGG TTCTCCGGAG TGTGCGGGA
1101 AAGTGTGCGC GGTGTTGGCG TTAGCGGCAC GGCTGCGGGC GTAATCCTCG
1151 TGCTTGCTTA TATGTATGCG CATTATATGT TTGCCAGTAC TACTGCACAT
1201 ATTACCGCTA TGTTCGGCGC ATTTTTCGCT GCTGCCGTTT CACTGAATGC
1251 CCCGGCGATG CCGACCGCGC TGATGATGGC GGCCGCATCT AACATTATGA
1301 TGACCCCTAC TCATTATGCG ACCGGTACTT CGCCTGTGAT TTTGCGTTTCG
1351 GGCTACACCA CAATGGGAGA ATGGTGGAAG GCGGGTTTTA TCATGAGCGT
1401 AGTCAATTTT CTGATTTTTT TCGTTATCGG CAGCATTTGG TGGAAAGTTC
1451 TGGGGTATTG GTAA

```

This corresponds to the amino acid sequence <SEQ ID 2850; ORF 929.a>:

```

a929.pep
1  MKLGFKPIPL AIAAVLCALV LALVPDGVK PQAWTLLAMF IGVIAAIIGK
51  AMPLGALSII AVGLVAVTGV TADKPGAAMS DALSAFANPL IWLIAIAVMI
101 SRGLLKTGLG MRIGYLFIAV FGRKTIGIGY SLALSELLLA PVTFSNTARG
151 GGIIHPIMQS IAGSYGSNPA KGTEGKMGKY LALVNYHNSP ISSAMFITAT
201 APNPLIVNLI AENLGSSFRL SWGAWAWAMA VPGVIAFFVM PLILYFLYPP
251 EIKETPNAVQ FAKDRLREMG KMSADEIIMA VIFGILLLLW ADVPALITGN
301 HAFSINATAT AFIGLSLLLL SGVLTWDDVL KEKSAWDTII WFGALIMMAA
351 FLNKLGLIKW FSGVLAESVG GLGVSGTAAG VILVLAYMYA HYMFASTTAH
401 ITAMFGAFFA AAVSLNAPAM PTALMMAAAS NIMMTLTHYA TGTSPVIFGS
451 GYTTMGEWWK AGFIMSVVNE LIFFVIGSIW WKVLGYW*

```

m929/a929 99.6% identity in 487 aa overlap

m929.pep	10	20	30	40	50	60
	MKLGFKPIPLAIAAVLCALV	LALVPDGVK	PQAWTLLAMF	IGVIAAIIGK	AMPLGALSII	
a929	MKLGFKPIPLAIAAVLCALV	LALVPDGVK	PQAWTLLAMF	IGVIAAIIGK	AMPLGALSII	
	10	20	30	40	50	60
m929.pep	70	80	90	100	110	120
	AVGLVAVTGV	TADKPGAAMS	DALSAFANPL	IWLIAIAVMIS	SRGLLKTGLG	MRIGYLFIAV
a929	AVGLVAVTGV	TADKPGAAMS	DALSAFANPL	IWLIAIAVMIS	SRGLLKTGLG	MRIGYLFIAV
	70	80	90	100	110	120
m929.pep	130	140	150	160	170	180
	FGRKTIGIGY	SLALSELLLA	PVTFSNTARG	GGIIHPIMQS	IAGSYGSNPA	KGTEGKMGKY
a929	FGRKTIGIGY	SLALSELLLA	PVTFSNTARG	GGIIHPIMQS	IAGSYGSNPA	KGTEGKMGKY
	130	140	150	160	170	180
m929.pep	190	200	210	220	230	240
	LALVNYHNSP	ISSAMFITAT	APNPLIVNLI	AENLGSSFRL	SWGAWAWAMA	VPGVIAFFVM
a929	LALVNYHNSP	ISSAMFITAT	APNPLIVNLI	AENLGSSFRL	SWGAWAWAMA	VPGVIAFFVM
	190	200	210	220	230	240
m929.pep	250	260	270	280	290	300
	PLILYXLYPP	EIKETPNAVQ	FAKDRLREMG	KMSADEIIMA	VIFGILLLLW	ADVPALITGN
a929	PLILYFLYPP	EIKETPNAVQ	FAKDRLREMG	KMSADEIIMA	VIFGILLLLW	ADVPALITGN
	250	260	270	280	290	300
m929.pep	310	320	330	340	350	360
	HAFSINATAT	AFIGLSLLLL	SGVLTWDDVL	KEKSAWDTII	WFGALIMMAA	FLNKLGLIKW
a929	HAFSINATAT	AFIGLSLLLL	SGVLTWDDVL	KEKSAWDTII	WFGALIMMAA	FLNKLGLIKW
	310	320	330	340	350	360
m929.pep	370	380	390	400	410	420
	FSGVLAESVG	GLGVSGTAAG	VILVLAYMYA	HYMFASTTAH	ITAMFGAFFA	AAVSLNAPAM
a929	FSGVLAESVG	GLGVSGTAAG	VILVLAYMYA	HYMFASTTAH	ITAMFGAFFA	AAVSLNAPAM
	370	380	390	400	410	420
m929.pep	430	440	450	460	470	480
	PTALMMAAAS	NIMMTLTHYA	TGTSPVIFGS	GYTTMGEWWK	AGFIMSVVNE	LIFFVIGSIW
a929	PTALMMAAAS	NIMMTLTHYA	TGTSPVIFGS	GYTTMGEWWK	AGFIMSVVNE	LIFFVIGSIW
	430	440	450	460	470	480
m929.pep	WKVLGYWX					

a929

WKVLGYWX

g930.seq not found yet

g930.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2851>:

m930.seq

```

1  ATGAACTTC CTTTATCCTA TTTGCCTAAT ATTGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAAACACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTTC TGCCATTAAAC GAAATGGTGT TGAAGGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG aAGCTTCAAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 2852; ORF 930>:

m930.pep

```

1  MKLPLSYLPN IRFLSWCCLL AGIIAPATLL ASPNP AEIRM QDIIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EWLGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGSFN *

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2853>:

g930-1.seq (partial)

```

1  GGC AAGTGC TGCATGCGGG CGACATTAAT CAAATCATGT CCTTAGCACA
51  AAA TGCTTTG ATCGGCAGGG GATATACCAC GACCCGTATC TTGGCTGCGC
101 CACAGGATT GAATAGTGGC AAGCTTCAAT TAACCTGAT GCCGGGCTAT
151 CTGCGCTCCA TACGAATCGA TCGGTCCAAC GATGATCAAA CCCATGCAAG
201 ACGTATTGCA GCATTCCAAA ACAAATTCC CACCGCTCG AACGATCTGT
251 TGAATCTGCG TGATTGGAA CAAGGACTGG AAAATCTCAA ATGTCTCCCG
301 ACTGCGGAAG CCGATCTCCA AATCGTTCCC GTAGAGAGAG AACCAAACCA
351 AAGTGATGTC GTGGTGCAAT GCGGTAACG TCTGCTGCCC TACTGTGTGA
401 GTGTGGGGAT GGATAATTCG GGTAGTGAGG CGACAGGAAA ATACCAAGGA
451 AATATCACTT TCTCTGCCGA CAATCCTTTT GGA CTGAGTG ATATGTTCTA
501 TGTAAATTAT GGACGTTCAA TTGGCGGTAC GCCCGATGAG GAAAATTTTG
551 ACGGCCATCG CAAAGAAGGC GGATCAAACA ATTACGCCGT ACATTATTCA
601 GCCCTTTTCG GTAATGGAC ATGGGCATTC AATCACAATG GCTACCGTTA
651 CCATAGGCG GTTCCGGAT TATCGGAAGT CTATGACTAT AATGGA AAAA
701 GTTACAACAC TGATTTCGGC TTCAACCGCC TGTGTATCG TGATGCCAAA
751 CGCAAAACCT ATCTCAGTGT AAACTGTGG ACGAGGGA AAAAAGTTA
801 CATTGATGAT GCCGAACCTA CTGTACAACG GCGTAAAC ACAGGTTGGT
851 TGGCAGAACT TTCCACAAA GGATATATCG GTCGCAGTAC GGCAGATTTT
901 AAGTTGAAAT ATAAACACGG CACCGCATG AAAGATGCTC TGCGCGCGCC
951 TGAAGAAGCC TTTGGCGAAG GCACGTCACG TATGAAAATT TGGACGGCAT
1001 CGGCTGATGT AAATACTCCT TTCAAATCG GTAACAGCT ATTTGCCTAT
1051 GACACATCCG TTCATGCACA ATGGAACAAA ACCCGCTAA CATCGCAAGA
1101 CAAACTGGCT ATCGGCGGAC ACCACACCGT ACGTGGCTTC GACGGTGA
1151 TGAGTTTGCC TGCCGAGCGG GGATGGTATT GCGCAACGA TTTGAGCTGG
1201 CAATTTAAAC CAGGCCATCA GCTTTATCTT GGGGCTGATG TAGGACATGT
1251 TTCAGGACAA TCCGCCAAAT GGTATCGGG CCAAACCTA GCCGCGACAG
1301 CAATTGGGAT ACGCGGCGAG ATAAAGCTTG GCGGCAACCT GCATTACGAT
1351 ATATTACCG GCCGTGCATT GAAAAGCCC GAATATTTT AGACGAAGAA
1401 ATGGGTAACG GGGTTTCAGG TGGTTATTC GTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2854; ORF 930-1.ng>:

g930-1.pep (partial)

```

1  GKCLHAGDIN QIMSLAQNAL IGRGYTTTRI LAAPDLNSG KLQLTLMPGY
51  LRSIRIDRSN DDQTHAGRIA AFQNKFPTRS NDLLNLRDLE QGLENLKCLP
101 TAEADLQIVP VEREPNQSDV VVQWR*RLLP YCVSVGMDNS GSEATGKYQG
151 NITFSADNPF GLSDMEFYVNY GRSIGGTPDE ENFDGHRKEG GSNNYAVHYS
201 APFGKWTWAF NHNGYRYHQA VSGLSEVYDY NGKSYNTDFG FNRLLYRDAK
251 RKTYLSVKLW TRETKSYIDD AELTVQRRKT TGWLAELSHK GYIGRSTADF
301 KLYKHGTGM KDALRAPEEA FEGTSRMKI WTASADVNTF FQIGKQLFAY
351 DTSVHAQWNK TPLTSQDKLA IGGHHTVRGF DGEMSLPAER GWYWRNDLSW
401 QFKPGHQLYL GADVGHVSGQ SAKWLSGQTL AGTAIGIRGO IKLGGNLHYD

```

451 IFTGRALKKP EYFQTKKWT GFQVGYSF\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2855>:

m930-1.seq

```
1  ATGAACTTC CTTATCCTA TTTGCCTAAT ATTCGCTTTT TGTCTTGGTG
51  CTGCTTATTG GCAGGTATCA TTGCTCCTGC TACTTTGTTG GCCTCCCCCA
101 ACCCTGCCGA AATCCGTATG CAGCAAGATA TTCAGCAACG CCAACGCGAA
151 GAGCAGTTGC GCCAAACCAT GCAGCCTGAA AGCGATGTGC GTTTGCATCA
201 AAAAACCACG GGGGAAACGG TTAATCAGTT GATGGGCGAT GACAGCAGCC
251 AACCGTGTGT TGCATTAAAC GAAAGTGGTG TGGAAAGCGA ACACCATGCT
301 CGGTTTCAGT TTGCCCTAAA ACGTGCCTTG CGCGAAACGG GTTTTCAGGC
351 TGGCAAGTGT CTGCATGCGG GCAACATTAA TCAAATCATG TCCTTAGCAC
401 AAAATGCTTT GATCGGCAGG GGATATACCA CGACCCGTAT CTTGGCTGCG
451 CCACAGGATT TGAATAGTGG CAAGCTTCAA TTAACCTGTA TACCGAGCTA
501 TCTGCGCTCC ATACGAATCG ATCGGTCTAA CGATGATCAA ACCCATGCAG
551 GACGTATTGC AGCATTCCAG AACAAATTTC CCACCCGCTC GAACGATCTG
601 TTGAATCTGC GTGATTGGGA ACAAGGACTG GAAAATCTCA AACGTCTCCC
651 GACTGCCGAA GCCGATCTCC AAATCGTTCC CGTAGAGGGA GAACCAACCC
701 AAAGTGATGT CGTGGTGCAA TGGCGGCAAC GTCTGCTGCC CTACCGTGTG
751 AGTGTGGGGA TGGATAATTC GGGTAGTGAG GCGACAGGAA AATACCAAGG
801 AAAATATCACT TTCTCTGCCG ACAATCCTTT GGGACTGAGT GATATGTTCT
851 ATGTAATAAT TGGACGTTCC ATTGGCGGTA CGCCCGATGA GGAAGTTTTT
901 GACGGCCATC GCAAAGAAGG CGGATCAAAC AATTACGCCG TACATTATTC
951 AGCCCTTTTC GGTAAATGGA CATGGGCATT CAATCACAAT GGCTACCGTT
1001 ACCATCAGGC AGTTTCCGGA TTATCGGAAG TCTATGACTA TAATGGAAAA
1051 AGTTACAATA CTGATTTCGG CTTCAACCGC CTGTTGTATC GTGATGCCAA
1101 ACGCAAAACC TATCTCGGTG TAAACTGTG GATGAGGGAA ACAAAAAGTT
1151 ACATTGATGA TGCCGAACCT ACTGTACAAC GGCCTAAAAC TCGCGGTTGG
1201 TTGGCAGAAA TTTCCACAAA AGAATATATC GGTGCGAGTA CGGCAGATTT
1251 TAAGTTGAAA TATAAACGCG GCACCGGCAT GAAAGATGCT CTGCGCGCGC
1301 CTGAAGAAGC CTTTGGCGAA GGCACGTCAC GTATGAAAT TGGACGGCA
1351 TCGGCTGATG TAAATACTCC TTTTCAAATC GGTAACAGC TATTTGCCTA
1401 TGACACATCC GTTCATGCAC AATGGAACAA AACCCCGCTA ACATCGCAAG
1451 ACAAACGGC TATCGGCGGA CACCACACCG TACGTGGCTT CGACGGTGAA
1501 ATGAGTTTGT CTGCCGAGCG GGGATGGTAT TGGCGCAACG ATTTGAGCTG
1551 GCAATTTAAA CAGGCCATC AGCTTTATCT TGGGGCTGAT TAGGACATG
1601 TTTCAGGACA ATCGGCCAAA TGGTTATCGG GCCAACTCT AGTCGGCACA
1651 GCAATTGGGA TACGCGGGCA GATAAAGCTT GCGGCAAC TGCATTACGA
1701 TATATTACC GCGCGGCAT TGA AAAAGCC CGAATTTTC CAATCAAGGA
1751 AATGGGCAAG CGGTTTCAG GTAGGCTATA CGTTTTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2856; ORF 930-1&gt;:

m930-1.pep

```
1  MKLPLSYLPN IRFLSWCCLL AGIIPATLL ASPNPAEIRM QQDIQQRQRE
51  EQLRQTMQPE SDVRLHQKNT GETVNQLMGD DSSQPCFAIN EVVLEGEHHA
101 RFQFALKRAL RETGFQAGKC LHAGNINQIM SLAQNALIGR GYTTTRILAA
151 PQDLNSGKLQ LTLIPSYLRS IRIDRSNDDQ THAGRIAAFQ NKFPTRSNDL
201 LNLRLDLEQL ENLKRLLPTAE ADLQIVPVEG EPNQSDVVVQ WRQRLPYRV
251 SVGMDNSGSE ATGKYQGNIT PSADNPLGLS DMFYVNYGRS IGGTPDEESF
301 DGHRKEGGSN NYAVHYSAPP GKWTWAFNHN GYRYHQAVSG LSEVYDYNK
351 SYNTDFGFNR LLYRDAKRKT YLGVKLWMRE TKSVIDDAEL TVQRRKTAGW
401 LAELSHKEYI GRSTADFKLK YKRGTMKDA LRAPEEAFGE GTSRMKIWTA
451 SADVNTPFQI GKQLFAYDTS VHAQWNKTP L TSQDKLAIGG HHTVRGFDGE
501 MSLSAERGWY WRNDSLWQFK PGHQLYLGLAD VGHVSGQSAK WLSGQTLVGT
551 AIGIRGQIKL GGNLHYDIFT GRALKKPEFF QSRKWASGFQ VGYTF*
```

m930-1/g930-1 95.4% identity in 478 aa overlap

	90	100	110	120	130	140
m930-1.pep	AINEVVLEGEH	HARFQFALKRAL	RETGFQAGKCL	HAGNINQIMSLA	QNALIGRGYTT	TRI
g930-1.pep				GKCLHAGDINQIM	SLAQNALIGRGY	TTTRI
				10	20	30
	150	160	170	180	190	200
m930-1.pep	LAAPQDLNSGKL	QLTLIPSYLRS	IRIDRSNDDQ	THAGRIAAFQ	NKFPTRSNDL	LNLRDLE
g930-1.pep	LAAPQDLNSGKL	QLTLMPGYLRS	IRIDRSNDDQ	THAGRIAAFQ	NKFPTRSNDL	LNLRDLE
	40	50	60	70	80	90
	210	220	230	240	250	260
m930-1.pep	QGLENLKRLPTA	EADLQIVPVEG	EPNQSDVVVQ	WRQRLPYRV	SVGMDNSGSEAT	GKRYQG

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```

g930-1.pep  QGLENLKCLPTAEADLQIVPVEREPNQSDVVVQWRXRLLPYCVSVGMDNSGSEATGKYQG
              100      110      120      130      140      150
m930-1.pep  270      280      290      300      310      320
NITFSADNPLGLSDMFYVNYGRSIGGTPDEESFDGHRKEGGSNNYAVHYSAPFGKWTWAF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NITFSADNPFGLSDMFYVNYGRSIGGTPDEENFDGHRKEGGSNNYAVHYSAPFGKWTWAF
              160      170      180      190      200      210
m930-1.pep  330      340      350      360      370      380
NHNGYRYHQAVSGLSEVYDNGKSYNTDFGNRLLYRDAKRKTYLGVKLMWRETKSYIDD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  NHNGYRYHQAVSGLSEVYDNGKSYNTDFGNRLLYRDAKRKTYLSVKLWTRETKSYIDD
              220      230      240      250      260      270
m930-1.pep  390      400      410      420      430      440
AELTVQRRKTAGWLAELSHKEYIGRSTADFKLKYKRGTGMKDALARPEEAFGEGTSRMKI
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  AELTVQRRKTTGWLAELSHKGYIGRSTADFKLKYKHGTGMKDALARPEEAFGEGTSRMKI
              280      290      300      310      320      330
m930-1.pep  450      460      470      480      490      500
WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLSAER
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  WTASADVNTPFQIGKQLFAYDTSVHAQWNKTPLTSQDKLAIGGHHTVRGFDGEMSLPAER
              340      350      360      370      380      390
m930-1.pep  510      520      530      540      550      560
GWYWRNDSLWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLVGTAIGIRGQIKLGGNLHYD
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  GWYWRNDSLWQFKPGHQLYLGADVGHVSGQSAKWLSGQTLGTAIGIRGQIKLGGNLHYD
              400      410      420      430      440      450
m930-1.pep  570      580      590
IFTGRALKKPEFFQSRKWASGFQVGYTF
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g930-1.pep  IFTGRALKKPEYFQTKKWVTGFQVGYSTFX
              460      470

```

a930-1.seq not yet found

a930-1.pep not yet found

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2857>:

```

g931.seq
1   ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCGCGTCCT GATGGAACCC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCTCCAAAAC CGTTGCCAAT
151 TTCTGTCGCT ATGCCCGAAA AGGCTTTTAC GACAACACGA TTTTCCACCG
201 CGTcatCGGC GGCTTCGTCA TCCAAGGCGA CGGATTGACC GAGGACTTGG
251 TGCAAAAGGC AACCGATAAG GCCGTTGCCA ACGAATCCGG caacgGCTTG
301 AAAAACACCG TCGGCACCAT CGCAATGGCG CGGACGGCAG CCCCCGATTC
351 CGCCGCGGCC CAATTCTTTA TCAATCTGGC GGACAACGGT TCGCTCGACT
401 ACAAACACCG ACAATACGGC TACACCGTTT TCGGCAGGGT AGAAAGCGGA
451 ATGGACACCG TTTCCAAAT  CGCCCGCTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG
551 GGCAGTAACA CGCAGACAGA CGTTCAGACG GCGTCGCCCG TTTCCCAAAA
601 AACGCCGTTT AA

```

This corresponds to the amino acid sequence <SEQ ID 2858; ORF 931.ng>:

```

g931.pep
1   MKPKFKTVLT ALLLAVSLPS MAATRVLMET DMGNIRLVLD ESKASKTVAN
51  FVRYARKGFY DNTIFHRVIG GFVIQDGLT EDLVQKATDK AVANESGNGL
101 KNTVGTIAMA RTAAPDSAAA OFFINLADNG SLDYKNGQYG YTVFGRVESG
151 MDTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*

```



The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2859>:

```
m931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCTAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACGACACCG TTTTTCACCG
201 CGTTATCGAC GGTTTTGTTA TCCAGGGCGG TGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACCG CCGGCACCAT CGCCATGGCG CGGACGACAG CCCCCGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGC GGACCA.kCT TCGCTCGACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT
501 TTATCAAAAC GTACCCGTAC AGCCCGTCAA AATCCGTGCG GTTGTGTGCG
551 GGCAGTAA
```

This corresponds to the amino acid sequence <SEQ ID 2860; ORF 931>:

```
m931.pep..
1  MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN
51  FVRYARKGFY DDTVFHRVID GFVIQGGGLT EDLAQKASDK AVANESGNGL
101 KNTAGTIAMA RTTAPDSATS QFFINLADXX SLDYKNGQYG YTVFGRVESG
151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 931 shows 91.9% identity over a 185 aa overlap with a predicted ORF (ORF 931.ng) from *N. gonorrhoeae*:

g931/m931

	10	20	30	40	50	60
g931.pep	MKPKFKTVLTALLLAVSLPSMAATRVLMETDMGNIRLVLDISKASKTVANFVRYARKGFY					
m931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLDISKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	DNTIFHRVIGGFVIQGDGLTEDLVQKATDKAVANESGNGLKNTVGTIAMARTAAPDSAAA					
m931	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
	70	80	90	100	110	120
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPQPVKIRR					
	130	140	150	160	170	180
g931.pep	QFFINLADNGSLDYKNGQYGYTVFGRVESGMDTVSKIARVKTATRGFYQNPVPQPVKIRR					
m931	QFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNPVPQPVKIRR					
	130	140	150	160	170	180
g931.pep	VVVGQX					
m931	VVVGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2861>:

```
a931.seq
1  ATGAAACCCA AATTCAAAC CGTTTTAACC GCGCTGCTTT TGGCGGTTTC
51  CCTGCCGTCT ATGGCGGCAA CCCATGTTTT GATGGAAACC GATATGGGCA
101 ATATCCGTTT GGTTTTGGAC GAATCCAAAG CCCCCAAAAC CGTTGCCAAT
151 TTCGTGCGCT ATGCCCGAAA AGGCTTTTAC GACAATACGA TTTTTCACCG
201 CGTCATCGGC GGCTTCGTTA TCCAAGGCGG CGGATTGACC GAGGACTTGG
251 CACAAAAGGC AAGCGATAAG GCCGTTGCCA ACGAATCCGG CAACGGCTTG
301 AAAAACACTG TCGGCACCAT CGCCATGGCG CGGACGGCCG ATCCGGATTC
351 CGCCACCAGC CAATTCTTTA TCAATCTGGT GGACAATGAT TCGCTCAACT
401 ACAAAAACGG ACAATACGGC TATACCGTTT TCGGCAGGGT CGAAAGCGGC
```

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451 ATGAACACCG TTTCCAAAT CGCCCGCGTC AAAACCGCCA CGCGCGGCTT  
 501 TTATCAAAC GTACCCGTAC AGCCCGTCAA AATCCGTCGC GTTGTGTGCG  
 551 GGCAGTAA

This corresponds to the amino acid sequence <SEQ ID 2862; ORF 931.a>:

a931.pep  
 1 MKPKFKTVLT ALLLAVSLPS MAATHVLMET DMGNIRLVLD ESKAPKTVAN  
 51 FVRYARKGFY DNTIFHRVIG GFVIQGGGLT EDLAQKASDK AVANESGNGL  
 101 KNTVGTIAMA RTADPDSATS OFFINLVDND SLNYKNGQYG YTVFGRVESG  
 151 MNTVSKIARV KTATRGFYQN VPVQPVKIRR VVVGQ\*

m931/a931 94.6% identity in 185 aa overlap

	10	20	30	40	50	60
m931.pep	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
a931	MKPKFKTVLTALLLAVSLPSMAATHVLMETDMGNIRLVLD ESKAPKTVANFVRYARKGFY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m931.pep	DDTVFHRVIDGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTAGTIAMARTTAPDSATS					
a931	DNTIFHRVIGGFVIQGGGLTEDLAQKASDKAVANESGNGLKNTVGTIAMARTADPDSATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m931.pep	OFFINLADXXSLDYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
a931	OFFINLVDNDSLNYKNGQYGYTVFGRVESGMNTVSKIARVKTATRGFYQNVVPVQPVKIRR					
	130	140	150	160	170	180
m931.pep	VVVGQX					
a931	VVVGQX					

g932.seq not found yet

g932.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2863>:

m932.seq  
 1 ATGAAATATA TCGTATCAAT CTCTCTGGCT ATGGGATTGG CTGCCTGTTC  
 51 GTTTGGGGGA TTAAACCAA ATCCGTGGGA CGCCGCGTCA TTTTGGGAAT  
 101 TGAAAAATTA CGCAATCCC TATCCGGGAT CAGCCTCGGC GGCACCTGAC  
 151 CAATATCCAT CGAAAGCAAG ACGAAGGCAA CTGAAAGACA TGCAAGAGTG  
 201 CGGCTATGAC CCAATAGACG GCGGAAAGTC TGAAGCAGAT GCCTGCCTGA  
 251 GGAAAAAAGG CTGGTGTCGT AAGGGTTTCG ACCCTTATCC CGAAAAACAA  
 301 AAATACGAAT GGCTCGAGA AGAAGGAAAA ACAAAATGA

This corresponds to the amino acid sequence <SEQ ID 2864; ORF 932>:

m932.pep  
 1 MKYIVSISLA MGLAACFSGG FKPNPWAAS FWELKNYANP YPGSASAALD  
 51 QYPSKARRRQ LKDMQECGYD PIDGGKSEAD ACLRKKGWCR KGFDYPYENK  
 101 KYEWPREEGK TK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 932 shows \_\_\_% identity over a \_\_\_ aa overlap with a predicted ORF (ORF 932.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2865>:

g934.seq  
 1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTGC CACTCACCGC

q934.ppt

```

1  MKKIIASALI  ATFALTACQD  DTQARLERQQ  KQIEALQQQL  AQQADDTVYQ
51  LT  PEAVKDTI  PAQAQANGNN  GQPVTKKRR  AVYLREIDRK  LAAAKPDWRG
101 GR  RYVRQRAG  KQIHDTGGQR  QPRRPSRAC  LPSVRTPQCA  HQQGFEHAQP
151 P  CKTTGGGA  ALPPDNAPR  KLPSPRYAF  RQKAVNPARQ  CRLKGFQTAF
201 LY  LLGALLCC  RLIFRRHFVS  KRLMSGWQF*

```

m934.seq (partial)

51	CGGCTCGAAC	AGCAGCAGAA	ACAGATTGAA	GCCCTGCAAC	AGCAGCTCGC
51	ACACGAGGCA	GACGATACGG	TTTACCAACT	GACTCCCGAA	GCAGTCAAAG
101	ACACCATTCC	TGCCGAAAGCA	CAGGCAAAACG	GCAACAACgG	GCAACC CGTT
151	ACCGGTAA .A	GCAGGGGCAGC	AGTATATTTA	CGACCAATCG	ACAGGAAGCT
201	GGCTGCTGCA	AAGCCTGGTC	GGCGCGGCGG	CAGGCGCGTT	TATCGGCAAC
251	GCGCTGGCAA	ACAAATTAC	ACGGGCAGGC	AACCAAGACA	GTCCCGTCGC
301	CCGGCGCGCG	CGTGCAGCCT	ACCATCAGTC	CGCAGCGCCC	AATGGCGCGA
351	yCAGCAGGGA	TTTGAACACG	CGCAGCCTCC	GTGCAAAAAC	ACAGGCGCGG
401	CAKGGCGAGC	GTTACCGCCC	GACAACGCGC	CGCs CGCs CA	ATTACCGCCG
451	CCCCGCTATG	CGCGGTTTCG	GCAGGAGGCG	GTAACCCCGG	CGCGCCAATG
501	CCGTCTGAAG	AGCTTTTCAGA	CGGCATTThT	GCATTGTGTA	GGGACATTGT
551	TATGTTGCCG	TTTGATTTTC	AGACGGCATT	TTGTTTCCAA	GCGTTTGATG
601	TCGGGATGGC	AATTCTGA			

m934.pep (partial)

```

1      .RLEQQQKQIE ALQQQLAQQA DDTVYQLTPE AVKDTIPAEA QANGNNGQPV
51     TGXRRRAAVYL RPIDRKLAAA KPGRRGRRV YRQRAGKQIH TGRQPRQSR
101    PARACSLPSV RTPQCAHQQG FEHAQPPCKT TGGAXAALPP DNAPXRQLPP
151    PRYARFRQEA VNPARQCRLK SFQTAFXHLL GTLLCCRLIF RRHFVSKRLM
201    SGWQF*

```

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 934 shows 91.7% identity over a 205 aa overlap with a predicted ORF (ORF 934.ng) from *N. gonorrhoeae*:

m934/q934

```
m934.pep                                     10      20      30  
RLEQQQKQIEALQQLAQQADDTVYQLTPEAVKDIT  
|||:|||||  
g934    MKKIIASALIATFALTACQDDTQARLERQQKQIEALQQLAQQADDTVYQLTPEAVKDIT  
          10      20      30      40      50      60  
  
m934.pep          40      50      60      70      80      90  
PAEAQANGNNGQPVTGXRRAAVYLRLPIDRKLAAAKPGRRGRRVYRQRAGKQIHTGROPR  
||:|||||  
g934    PAQAQANGNNGQPVTGKRRAAVYLRLPIDRKLAAAKPDWRGGRRVYRQRAGKQIHTGGQPR  
          70      80      90     100     110     120  
  
          100     110     120     130     140     150
```

```
a934.s.eq
1 ATGAAAAAAA TCATCGCCTC CGCGCTTATC GCAACATTCC CACTCGCCGC
51 CTGCCAAGAC GACGCGCAGG CGCGGCTCGA ACAGCAGCAG AAACAGATTG
1 01 AAGCCCTGCA ACAGCAGCTC GCACAGCAGG CACAGCAGATC GGGTTTACCAA
1 51 CTGACTCCCG AAGCAGTCAA AGACACCAAT CCTGCCGAAG CACAGGCAAA
2 01 CGGCAACAAC GGGCAACCCG TTACCGG.TA AAGACGGGCA GCAGTATATT
2 51 TACGACCAAT CGACATGAGG CTGGCTGCTG CAAAGCCTGG TCGGCGCGGC
3 01 GGCAGGCGCG TTTATCGGCA ACGCGCTGGC AAACAAATTG ACACGGGCAG
3 51 GCAACCAAGA CAGTCCCGTC GCGCGGCGCG CGCCTGCCGC CTACCATCAG
4 01 TCCGCACATC CCAATGCGCG CACCAGCAGG GATTTGAACA CGCGCAGCCT
4 51 CCGTGCAAAA CAACAGGCGG CGCAGGCGCA GCGTTACCGC CCGACAACGC
5 01 GCCCGCCCGC CAATTACCGC CGCCCCGCCA TGCGGGTTT CCGCAGAAGG
5 51 CGGTAAATCC GGCCTGCCAA TGCCGTCTGA AGGGCTTTCA GACGGCATT
6 01 TTGTATTGTG TAGGGACATT GTTATGTTCG CGTTTGATT TTAGACGGCA
6 51 TTTTGTTCCT AAGAGTTTGA GTTCGGGATG GCAATTCTGA
```

a934.pap

1	<u>MKKIIASALI</u>	<u>ATFALAACQD</u>	DAQARLEQQQ	KQIEALQQQL	AQQADDTVYQ
51	LTPEAVKDTI	PAAEQANGNN	GQPVTX*RRR	AVYLRPIDRK	LAAAKPGRRG
1 01	GRVYRQQRAG	KQIHTGRQPR	QSRPPARACR	LPSVRTSQCA	HQQGFEHAQP
1 51	PCKTTGGAGA	ALPPDNAPAR	QLPPPRHARF	RQKAVNPACQ	CRLKGFQTAF
2 01	<u>LYLLGTLLCC</u>	<u>RLIFRRHFVS</u>	<u>KSLMSGWQF*</u>		

```

m934.pep                                10          20          30
                                         RLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
                                         |||
a934      MKKIIASALIATFALAACQDDAQRLEQQQKQIEALQQQLAQQADDTVYQLTPEAVKDTI
              10          20          30          40          50          60

              40          50          60          70          80          90
m934.pep      PAEAQANGNNGQPVTGXRRAAVYLRPIDRKLAAPGRRGGRRVYRQRAGKQIHTGRQPR
              |||
a934      PAEAQANGNNGQPVTXXRRAAVYLRPIDRKLAAPGRRGGRRVYRQRAGKQIHTGRQPR
              70          80          90          100         110         120

              100         110         120         130         140         150
m934.pep      QSRRPARACSLPSVRTPQCAHQQGFEHAQPPCKTTGGAXAALPPDNAPXRQLPPPRYARF
              |||
a934      QSRRPARACRLPSVRTSQCAHQQGFEHAQPPCKTTGGAGAALPPDNAPARQLPPPRHARF
              130         140         150         160         170         180

              160         170         180         190         200
m934.pep      RQEAVNPARQCRLKSFQTAFXHLLGTLCCRLIFRRHFVSKRLMSGWQFX
              |||
a934      RQKAVNPACQCRLKGFQTAFLYLLGTLCCRLIFRRHFVSKSLMSGWQFX
              190         200         210         220         230

```

g935.seq not found yet

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```

601 AATAGAAATG CCAATAATGC CGCGCCGCGAG TATTGCCGGC AAAACGGAGG
651 CCGGCAGATA TGCAGTGTCA GCCGGGCGGA GCGGGCGGCA GGCTTGAATT
701 ATGAAATCGA GCGCGAAAAA CTGACGGCGT TGGCAGATAA TCATTATTGT
751 TTGTTCCGTT CCAATATCGG CGGCACGAGC TATTATTCA GTAAAAATC
801 AGCTTATGAC GACGGGTTTC GCAGAGCGTA TTTGGGTTGG CAGTATAAAA
851 ATGCACGGCA GACGGCGGGG ATTTTGCCGT TTTATCAGGT GCAGTTGTCC
901 GGCAGCGACG GCTTTGATGC GAAAACAAA CGGGTAAACA ACCGCCGCCT
951 GCCGCCGTAT ATGCTGGCGC ACGGAGTCGG CGTGCAGTTG TCCCATACTT
1001 ACCGCCCAA CCCGGGATGG CAATTTTCGG TCGCGCTGGA ACATTACCGC
1051 CAACGCTACC GCGAACAGGA TAGGGCGGAA TACAATAACG GTCGGCAGGA
1101 CGGGTTTTAT GTTTCGTCGG CAAAACGTTT GGGCGAATCG GCAACTGTGT
1151 TCGGCGGCTG GCAGTTTGTG CGGTTGTGC CGAAACGCGA AACGGTGGGC
1201 GCGCGCGTCA ATAATGCCGC CTACGGCGC AACGGTGGT ATGCCGGCTG
1251 GCGCGAGGAG TGGCGGCAGT TGGGCGGTTT GAACAGTCGG GTTCCCGCT
1301 CTTATGCCCG CCGCAACTAT AAGGGCGTTG CGGCTTTCTC GACAGAGGCG
1351 CAACGCAACC GCGAATGGAA TGTCTCGCTG GCTTTGAGCC ACGACAAGTT
1401 GTCGTACAAA GGTATCGTGC CCGCGTTGAA TTATCGTTT GGCAGGACGG
1451 AAAGTAATGT GCCGTATGCG AAACGCCGCA ACAGCGAGGT GTTGTGTGCG
1501 GCGGATTGGC GGTTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 2874; ORF 935.a>:

```

a935.pep
1  MLYFRYGLV VWCAAGVSAA YGADAPAILD DKALLQVQRS VSDKWAESDW
51  KVDNDAPRVV DGDFLLAHPK MLEHSLRDVL NGNQADLIAS LADLYAKLPD
101 YDAVLYGRAR ALLAKLAGRP AEAVARYREL HGENAADERI LLDLAAAEFD
151 DFRKLSAERH FAEAEKLDLP APVLENVGRF RKKAEGLTGW RFGGISPAV
201 NRNANNAAPQ YCRQNGGRQI CSVSRAERAA GLNYEIEAEK LTALADNHYL
251 LFRSNIGGTS YYFSKKSAYD DGFGRAYLGW QYKNARQTAG ILPFYQVQLS
301 GSDGFDATK RVNNRRLPPY MLAGVGVQL SHTYRPNPGW QFSVALEHYR
351 QRYREQDRAE YNNGRQDGFY VSSAKRLGES ATVFGGWQFV RFVPKRETVG
401 GAVNNAAYRR NGVYAGWAQE WRQLGGLNSR VSASYARRNY KGVAAFSTEA
451 QRNREWNVSL ALSHDKLSYK GIVPALNYRF GRTESNVPIYA KRRNSEVFFV
501 ADWRF*

```

m935/a935 98.8% identity in 505 aa overlap

	10	20	30	40	50	60
m935.pep	MLYFRYGLVWVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVENDAPRVV					
a935	MLYFRYGLVWVWCAAGVSAAYGADAPAILDDKALLQVQRSVSDKWAESDWKVDNDAPRVV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m935.pep	DGDFLLAHPKMLEHSLRDALNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
a935	DGDFLLAHPKMLEHSLRDVLNGNQADLIASLADLYAKLPDYDAVLYGRARALLAKLAGRP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m935.pep	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAAKLDLPAPVLENVGRF					
a935	AEAVARYRELHGENAADERILLDLAAAEFDDFRKLSAERHFAEAEKLDLPAPVLENVGRF					
	130	140	150	160	170	180
	190	200	210	220	230	240
m935.pep	RKKTEGLTGWRFGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
a935	RKKAEGLTGWRFGGISPAVNRNANNAAPQYCRQNGGRQICSVSRAERAAGLNYEIEAEK					
	190	200	210	220	230	240
	250	260	270	280	290	300
m935.pep	LTPLADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
a935	LTALADNHYLLFRSNIGGTSYYFSKKSAYDDGFGRAYLGWQYKNARQTAGILPFYQVQLS					
	250	260	270	280	290	300

g935.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2871>:

m935.seq

```

1  A T G T T G T A T T   T C A G A T A C G G   C T T T T T G G T T   G T T T G G T G T G   C G G C A G G T G T
51  T T C T G C C G C C   T A T G G G G C G G   A T G C G C C C G C   G A T T T T G G A T   G A C A A G G C A T
101 T G T T G C A G G T   G C A G C G G T C G   G T G T C G G A T A   A G T G G G C G G A   A T C A G A T T G G
151 A A A G T T G A A A   A T G A T G C C C C   G C G C G T G G T T   G A C G G G G A T T   T T T T G T T G G C
201 G C A T C C G A A A   A T G T T G G A A C   A T A G T T T G C G   C G A C G C G C T C   A A C G G C A A T C
251 A G G C G G A A T T   A A T C G C T T C G   T T G G C G G A T T   T G T A T G C C A A   G C T G C C G G A T
301 T A T G A C G C G G   T T T T G T A C G G   C A G G G C G C G G   G C T T T G C T G G   C G A A A T T G G C
351 G G G A A G G C C G   G C G G A G G C G G   T G G C G C G G T A   T C G G G A A C T G   C A C G G G G A A A
401 A T G C G G C A G A   C G A G C G G A T T   T T G C T G G A T T   T G G C G G C G G C   G G A G T T T G A C
451 G A T T T C C G G C   T G A A G T C G G C   A G A A A G G C A T   T T T G C G G A G G   C G G C A A A A T T
501 G G A T T T G C C G   G C A C C G G T T T   T G G A A A A T G T   G G G G C G T T T T   C G G A A A A A A A
551 C G G A G G G G C T   G A C G G G C T G G   C G T T T T T C G G   G C G G C A T C A G   T C C G G C G G T C
601 A A T A G A A A T G   C C A A T A A T G C   C G C G C C G C A A   T A T T G C C G G C   A A A A C G G A G G
651 C C G G C A G A T A   T G C A G T G T C A   G C C G G G C G G A   G C G G G C G G C A   G G G T T G A A T T
701 A T G A A A T C G A   G G C G A A A A G   C T G A C G C C G T   T G G C A G A T A A   T C A T T A T T T G
751 T T G T T C C G T T   C C A A T A T C G G   C G G C A C G A G C   T A T T A T T T C A   G T A A A A A A T C
801 A G C T T A T G A T   G A C G G G T T C G   G C A G G G C G T A   T T T G G G T T G G   C A G T A T A A A A
851 A T G C A C G G C A   G A C G G C G G G G   A T T T T G C C G T   T T T A T C A G G T   G C A G T T G T C G
901 G G C A C G A C G   G C T T T G A T G C   G A A A A C A A A A   C G G G T A A A C A   A C C G C C G C C T
951 G C C G C C G T A T   A T G C T G G C G C   A C G A G T C G G   C G T G C A G C T G   T C C C A T A C T T
1001 A C C G C C C A A A   C C C G G G A T G G   C A A T T T T C G G   T C G C G C T G G A   A C A T T A C C G C
1051 C A A C G C T A C C   G C G A A C A G G A   T A G G G C G G A A   T A C A A T A A C G   G C A G G C A G G A
1101 C G G G T T T T A T   G T T C G T C G G   C A A A A C G T T T   G G G C G A A T C G   G C A A C T G T G T
1151 T C G G C G G C T G   G C A G T T T G T G   C G G T T T G T G C   G A A A A C G C G A   A A C G G T G G G C
1201 G G C G C G G T C A   A T A A T G C C G C   C T A C C G G C G C   A A C G G T G T T T   A T G C C G G T T G
1251 G G C G C A G G A G   T G G C G G C A G T   T G G G C G G T T T   G A A C A G T C G G   G T T T C C G C G T
1301 C T T A T G C C C G   C C G C A A C T A T   A A G G G C A T T G   C G G C T T T C T C   G A C A G A G G C G
1351 C A A C G C A A C C   G C G A A T G G A A   T G T C T C G C T G   G C T T T G A G C C   A C G A C A A G T T
1401 G T C G T A C A A A   G G T A T C G T G C   C G G C G T T G A A   T T A T C G T T T C   G G C A G G A C G G
1451 A A A G T A A T G T   G C C G T A T G C G   A A A C G C C G C A   A C A G C G A G G T   G T T T G T G T C G
1501 G C G G A T T G G C   G G T T T T G A

```

This corresponds to the amino acid sequence &lt;SEQ ID 2872; ORF 935&gt;:

m935.pep

```

1  M L Y F R Y G F L V   V W C A A G V S A A   Y G A D A P A I L D   D K A L L Q V Q R S   V S D K W A E S D W
51  K V E N D A P R V V   D G D F L L A H P K   M L E H S L R D A L   N G N Q A D L I A S   L A D L Y A K L P D
101 Y D A V L Y G R A R   A L L A K L A G R P   A E A V A R Y R E L   H G E N A A D E R I   L L D L A A A E F D
151 D F R L K S A E R H   F A E A A K L D L P   A P V L E N V G R F   R K K T E G L T G W   R F S G G I S P A V
201 N R N A N N A A P Q   Y C R O N G G R Q I   C S V S R A E R A A   G L N Y E I E A E K   L T P L A D N H Y L
251 L F R S N I G G T S   Y Y F S K K S A Y D   D G F G R A Y L G W   Q Y K N A R Q T A G   I L P F Y Q V Q L S
301 G S D G F D A K T K   R V N N R R L P P Y   M L A H G V G V Q L   S H T Y R P N P G W   Q F S V A L E H Y R
351 Q R Y R E Q D R A E   Y N N G R Q D G F Y   V S S A K R L G E S   A T V F G G W Q F V   R F V P K R E T V G
401 G A V N N A A Y R R   N G V Y A G W A Q E   W R Q L G G L N S R   V S A S Y A R R N Y   K G I A A F S T E A
451 Q R N R E W N V S L   A L S H D K L S Y K   G I V P A L N Y R F   G R T E S N V P Y A   K R R N S E V F V S
501 A D W R F *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2873>:

a935.seq

```

1  A T G T T G T A T T   T C A G A T A C G G   T T T T T T G G T T   G T T T G G T G T G   C G G C A G G T G T
51  T T C T G C C G C C   T A T G G G G C G G   A T G C G C C C G C   G A T T T T G G A T   G A C A A G G C A T
101 T G T T G C A G G T   G C A G C G G T C G   G T G T C G G A T A   A G T G G G C G G A   A T C G G A T T G G
151 A A A G T T G A C A   A T G A T G C C C C   G C G C G T G G T T   G A C G G G G A T T   T T T T G T T G G C
201 G C A T C C G A A A   A T G T T G G A A C   A T A G T T T G C G   C G A C G T G C T C   A A C G G C A A T C
251 A G G C G G A T T T   G A T C G C T T C G   T T G G C G G A T T   T G T A T G C C A A   G C T G C C G G A T
301 T A T G A C G C G G   T T T T G T A C G G   C A G G G C G C G G   G C T T T G C T G G   C G A A A T T G G C
351 G G G A A G G C C G   G C G G A G G C G G   T G G C G C G G T A   T C G G G A A C T G   C A C G G G G A A A
401 A T G C G G C A G A   C G A G C G G A T T   T T G C T G G A T T   T G G C G G C G G C   G G A G T T T G A C
451 G A T T T C C G G C   T G A A G T C G G C   A G A A A G G C A T   T T T G C C G A G G   C G G A A A A A T T
501 G G A T T T G C C G   G C G C C G G T T T   T G G A A A A T G T   G G G G C G T T T T   C G G A A A A A A G
551 C G G A G G G G C T   G A C G G G C T G G   C G T T T T T C G G   G C G G C A T C A G   T C C G G C G G T C

```

1350

	310	320	330	340	350	360
m935.pep	GSDGFDATKRVNNRRLPPYMLAHGVQVLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
a935	GSDGFDATKRVNNRRLPPYMLAHGVQVLSHTYRPNPGWQFSVALEHYRQRYREQDRAE					
	310	320	330	340	350	360
	370	380	390	400	410	420
m935.pep	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
a935	YNNGRQDGFYVSSAKRLGESATVFGGWQFVRFPKRETVGGAVNNAAYRRNGVYAGWAQE					
	370	380	390	400	410	420
	430	440	450	460	470	480
m935.pep	WRQLGGLNSRVSASYARRNYKGIAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
a935	WRQLGGLNSRVSASYARRNYKGVAAFSTEAQRNREWNVSLALSHDKLSYKGIVPALNYRF					
	430	440	450	460	470	480
	490	500				
m935.pep	GRTESNVFYAKRRNSEVFVSADWRFX					
a935	GRTESNVFYAKRRNSEVFVSADWRFX					
	490	500				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 2875>:

g936.seq

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51  CCTTGCCCTC GCGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGcgcgAACCA CCGcgcgcga AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TGCGGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCaccgT CGGCGTACAA AAAGTCATTA CCCTTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2876; ORF 936.ng>:

g936.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51  NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2877>:

m936.seq (partial)

```

1  ATGAAACCCA AACCACACAC CGTCCGCACC CTGATTGCCG CCATTTCAG
51  CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCCGAACCA CCGCGCGCA AACCAGCAGC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCC...

```

This corresponds to the amino acid sequence <SEQ ID 2878; ORF 936>:

m936.pep (partial)

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51  NVMALRIETT ARSYLRONNQ TKGYTPQISV VGYNRHLLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVNYIT VASLPRTA...

```

ORF 936 shows 93.8% identity over a 128 aa overlap with a predicted ORF (ORF 936.ng) from *N. gonorrhoeae*:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2879>:

This corresponds to the amino acid sequence <SEQ ID 2880; ORF 936.a>:

m936/a936 95.3% identity in 128 aa overlap

		10	20	30	40	50	60
m936.pep		MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSAVD	RRTTGAQTDDNV	MALRIETT			
			::   :	:			
a936		MKPKPHTVRTLTAAVLSLALGGCVSAVVGGA	AVGAKSAVD	RRTTGAQTDDNV	MALRIETT		
		10	20	30	40	50	60
		70	80	90	100	110	120
m936.pep		ARSYL	RNNQTKGYTPQISV	VGYNRHLL	LLGQVATEGEKQFV	GQIARSEQAAEGV	NYIIT
a936		ARSYL	RNNQTKGYTPQISV	VGYNRHLL	LLGQVATEGEKQFV	GQIARSEQAAEGV	NYIIT
		70	80	90	100	110	120
m936.pep	VASLPRTA						



1352

```

          |||||
a936      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
          130      140      150      160      170      180

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2881>:

g936-1.seq

```

1  ATGAAACCCA AACACACAC CGTCCGCACC CTGATTGCCG CCGTCCTCAG
51 CCTTGCCCTC GCGGGCTGCT TCAGCGCAGT CGTCGGCGGG GCCGCCGTCG
101 GCGCAAAATC CGTCATCGAC CGccgAACCA CCGgcgcgca AACCGATGac
151 aACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ACCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTATACAA
351 CTACATTACC GTCGCCTCCC TGCCGCGCAC TCGGGCGGAC ATCGCCGGCG
401 ACAC TTGGAA CACGTCCAAA GTCCGCGCca cgCTGCTGGG CATCAGCCCC
451 GCTACACAGG CGCGCGTCAA AATCATTACC TACGGCAATG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCAccgT CGGCGTACAA AAAGTCATTA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2882; ORF 936-1.ng>:

g936-1.pep

```

1  MKPKPHTVRT LIAAVLSLAL GGCFSAVVGG AAVGAKSVID RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2883>:

m936-1.seq

```

1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGATTGCCG CCATTTTCAG
51 CCTTGCCCTT AGCGGCTGCG TCAGCGCAGT AATCGGAAGC GCCGCCGTCG
101 GCGCGAAATC CGCCGTCGAC CGCGGAACCA CCGCGCGGCA AACCGACGAC
151 AACGTTATGG CGTTGCGTAT CGAAACCACC GCCCGTTCCT ATCTGCGCCA
201 AAACAACCAA ACCAAAGGCT ACACGCCCCA AATCTCCGTC GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAAAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCGCCGAAG GCGTGTACAA
351 CTATATTACC GTCGCCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACAC TTGGAA CACATCCAAA GTCCGCGCCA CGCTGTGGG CATCAGCCCC
451 GCCACACAGG CGCGCGTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCACCACCGT CGGCGTACAA AAAGTCATCA CCCTCTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2884; ORF 936-1>:

m936-1.pep

```

1  MKPKPHTVRT LIAAIFSLAL SGCVSAVIGS AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AAEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIIV YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVTILYQNYV
201 QR*

```

m936-1/g936-1 95.5% identity in 202 aa overlap

	10	20	30	40	50	60
m936-1.pep	MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAKSVD RRTTGAQTDDNVMALRIETT					
	:     :     :     :     :     :     :     :     :					
g936-1	MKPKPHTVRTLIAAVLSLALGGCFSAVVGGAAVGAKSVID RRTTGAQTDDNVMALRIETT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m936-1.pep	ARSYLRQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	:     :     :     :     :     :     :     :					
g936-1	ARSYLRQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m936-1.pep	VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT					
	:     :     :     :     :     :     :     :					

1353

```

g936-1      VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIITYGNVTYVMGILTPEEQAQIT
              130      140      150      160      170      180
              190      200
m936-1.pep  QKVSTTVGVQKVITLYQNYVQRX
              |||||
g936-1      QKVSTTVGVQKVITLYQNYVQRX
              190      200

```

The following g partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2885>:

```

a936-1.seq
1  ATGAAACCCA AACCGCACAC CGTCCGCACC CTGACTGCCG CCGTCCTCAG
51 CCTTGCCTCT GCGCGCTGCG TCAGCGCAGT CGTCGGCGGC GCGGCGGTCTG
101 GCGCGAAATC CGCGCTCGAC CGCCGAACCA CCGGCGCGCA AACCGACGAC
151 AACGTAATGG CGCTGCGTAT CGAAACCACC GCCCGCTCCT ATCTGCGCCA
201 AAAAACCACC ACCAAGGCT ACACGCCCCA AATCTCCGTT GTCGGCTACA
251 ACCGCCACCT GCTGCTGCTC GGACAAGTCG CCACCGAAGG CGAGAAACAG
301 TTCGTCGGTC AGATTGCACG TTCCGAACAG GCCCGCGAAG GCGTGTACAA
351 CTACATTACC GTGCGCTCCC TGCCGCGCAC TGCCGGCGAC ATCGCCGGCG
401 ACACTTGGAA CACATCCAAA GTCCGCGCCA CGCTGTTGGG CATCAGCCCC
451 GCCACACAGG CGCGCTCAA AATCGTTACC TACGGCAACG TAACCTACGT
501 TATGGGCATC CTCACCCCGG AAGAACAGGC GCAGATTACC CAAAAAGTCA
551 GCAACACCGT CGGCGTACAA AAAGTCATCA CCCTTACCA AACTACGTC
601 CAACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2886; ORF 936-1.a>:

```

a936-1.pep
1  MKPKPHTVRT LTAAVLSLAL GGCVS AVVGG AAVGAKSAVD RRTTGAQTDD
51 NVMALRIETT ARSYLRQNNQ TKGYTPQISV VGYNRHLLL GQVATEGEKQ
101 FVGQIARSEQ AEGVYNYIT VASLPRTAGD IAGDTWNTSK VRATLLGISP
151 ATQARVKIVT YGNVTYVMGI LTPEEQAQIT QKVSTTVGVQ KVITLYQNYV
201 QR*

a936-1/m936-1 97.0% identity in 202 aa overlap

m936-1.pep      10      20      30      40      50      60
MKPKPHTVRTLIAAIFSLALSGCVSAVIGSAAVGAASVDRRTTGAQTDDNVMALEIET
|||||
a936-1          10      20      30      40      50      60
MKPKPHTVRTLTAAVLSLALGGCVSAVVGGAAGAKSAVDRRTTGAQTDDNVMALEIET

m936-1.pep      70      80      90      100     110     120
ARSYLRQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT
|||||
a936-1          70      80      90      100     110     120
ARSYLRQNNQTKGYTPQISVVGYNRHL LLLGQVATEGEKQFVGQIARSEQAAEGVYNYIT

m936-1.pep      130     140     150     160     170     180
VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT
|||||
a936-1          130     140     150     160     170     180
VASLPRTAGDIAGDTWNTSKVRATLLGISPATQARVKIVTYGNVTYVMGILTPEEQAQIT

m936-1.pep      190     200
QKVSTTVGVQKVITLYQNYVQRX
|||||
a936-1          190     200
QKVSTTVGVQKVITLYQNYVQRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2887>:

```

g937.seq
1  atGAAAAATA TTCTCTTagt ATTGTTAGC TTTGTGCCAT TATGTGTCCG
51 CACTGATCTG CCGCTGAata tCGAAGACAT AATGaccgAC AAGGGAAAAT
101 GGAAactGGA AACTTccctt acctacctga acaGCGAAAA cagCCGCGCC
151 GCACTTGCCT CACCGGTTTA CATTCAGACC GGCTCGCTT CCTTTATCCC
201 CGTCCCGACC GAAATTCAGG AAAACGGCAG CAATACCGAT ATGCTCGCCG
251 GCACGCTCGG TTTGCGCTAC GGACTGaccg GCAataccga CATTTACGGC
301 AGCGGCAGCT ATCTGTGGCA CGAAGAACGC AAATCGaccg GCAACGGCAA

```

g937.pap

1 MKNILLVFVS FVPLCVRTDL PLNIEDIMTD KGKWKLETSL TYLNSSENSRA  
51 ALASPVYIQT GSASFIPVPT EIQENGSTND MLAGTLGLRY GLTGNTDIYG  
101 SG SYLWHEER KLDGNGKTRN KRMSDISAGI SHTFLKDGKN PALIAFLEST  
151 VYEKSRNKAS SGKSWLGAT TYKAIDPIVL SLTAAyrING SKTSLDDVKY  
201 KAGNYWMLNP NISFAANDRI SLTGGIQWLQ QKPDRIHGKK ESARNTSTYA  
251 HFGAGFGFTK TAALNASARF NVSGQSSSEL KLGVOHTF\*

m937.seq

51	ATGAAGCGCA	TCTTTTGGCC	CGCCTTGCCC	GCCATCCTGC	CTTTATCCAC
101	TTATGCCGAC	CTGCCCTTGA	CGATTGAAGA	CATAATGACC	GACAAGGGAA
151	AA TGGAAACT	GGAAACTTCC	CTTACCTACC	TGAACAGCGA	AAACAACCGC
201	GC CGAACTTG	CCGCACCGGT	TTACATTCAA	ACCGGCGCAA	CCTCGTTTAT
251	CC CCATTCCG	ACCGAAATCC	AAGAAAA CGG	CAGCAATACC	GATATGCTCG
301	TCGGCAGCGT	CGGTTTGGCG	TACggATCGA	CCGGGAATAC	CGACATTTTAC
351	GGCAGCGGCA	GCTATCTGTG	GCACGAAGAA	CGCAAACCTG	ACGGCAACAG
401	CAAAACCCGC	AACAAACGGA	TGTCCGACGT	ATCCCTCGGC	ATCAGCCACA
451	CTTTCCTTAA	AGACGACAAA	AACCCCGCCC	TAATCAGCTT	TCTTGAAGAG
501	ACGGTTTACG	AAAAATCGCG	CAACAAAGCC	TCGTCGGGAA	AATCCTGGGT
551	CA TCGGCGCC	ACCACCTACA	AGGCCATAGA	TCCGATTGTC	CTTTCCTCTA
601	CCGCGCGCTA	CCGCATCAAC	GGCAGCAAAA	CCCTTTTCAGA	CGGCATCCGC
651	TACAAATCGG	GCAACTACCT	GCTGCTCAAC	CCCAACATCT	CATTTGCTGC
701	CAACGACAGA	ATCAGCCTGA	CCGGAGGCAT	CCAATGGCTG	GGCAGGCAGC
751	CCGACCGGAC	GGACGGCAAA	CGGGAATCCT	CCAGAAACAC	ATCCACCTAC
801	GCCCATTTTC	GCGCAGGTTT	CGGTTTCACC	AAAACCACGG	CTTTAAACGC
851	ATCCGACAGT	TTCACCGTTT	CAGGGCAAAG	CAGTTCGGAA	CTGAAATTTC
	CGGTACAGCA	TACATTTTAA			

m937.pcp..

```

1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSNNR
51  AELAAPVYIQ TGATSFIPPI TEIQENGSTNT DMLVGTGLRL YGLTGNTDIY
101 GSGSYLWHEE RKLDSGSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLDGIR
201 YKSGNYLLLN PNISFAANDR ISLTGGIQWL GROPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSSE LKFGVQHTF*

```

**Homology with a predicted ORF from *N. gonorrhoeae***

g937/m937

	10	20	30	40	50	59
g937.pep	MKNILL-VFVSFVPLCVRTDLPLNIEDIMTDKGKWKLETSLTYLNSENSRAALASPVYIQ					
	:  :: :    : :   :     :     :     :     :     : :    :					
m937	MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ					
	10	20	30	40	50	60
	60	70	80	90	100	119
q937.pep	TGSASFIPVPTEIQENGSTNDMLAGTLGLRYGLTGNTDIYGGGSYLWHEERKLDGNKTR					

m937	1	70	80	90	100	110	120
	20	30	40	50	60	70	80
	90	100	110	120	130	140	150
	160	170	180	190	200	210	220
	230	240	250	260	270	280	290
	300	310	320	330	340	350	360
	370	380	390	400	410	420	430
	440	450	460	470	480	490	500
	510	520	530	540	550	560	570
	580	590	600	610	620	630	640
	650	660	670	680	690	700	710
	720	730	740	750	760	770	780
	790	800	810	820	830	840	850
	860	870	880	890	900	910	920
	930	940	950	960	970	980	990
	1000	1010	1020	1030	1040	1050	1060
	1070	1080	1090	1100	1110	1120	1130
	1140	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260	1270
	1280	1290	1300	1310	1320	1330	1340
	1350	1360	1370	1380	1390	1400	1410
	1420	1430	1440	1450	1460	1470	1480
	1490	1500	1510	1520	1530	1540	1550
	1560	1570	1580	1590	1600	1610	1620
	1630	1640	1650	1660	1670	1680	1690
	1700	1710	1720	1730	1740	1750	1760
	1770	1780	1790	1800	1810	1820	1830
	1840	1850	1860	1870	1880	1890	1900
	1910	1920	1930	1940	1950	1960	1970
	1980	1990	2000	2010	2020	2030	2040
	2050	2060	2070	2080	2090	2100	2110
	2120	2130	2140	2150	2160	2170	2180
	2190	2200	2210	2220	2230	2240	2250
	2260	2270	2280	2290	2300	2310	2320
	2330	2340	2350	2360	2370	2380	2390
	2400	2410	2420	2430	2440	2450	2460
	2470	2480	2490	2500	2510	2520	2530
	2540	2550	2560	2570	2580	2590	2600
	2610	2620	2630	2640	2650	2660	2670
	2680	2690	2700	2710	2720	2730	2740
	2750	2760	2770	2780	2790	2800	2810
	2820	2830	2840	2850	2860	2870	2880
	2890	2900	2910	2920	2930	2940	2950
	2960	2970	2980	2990	3000	3010	3020
	3030	3040	3050	3060	3070	3080	3090
	3100	3110	3120	3130	3140	3150	3160
	3170	3180	3190	3200	3210	3220	3230
	3240	3250	3260	3270	3280	3290	3300
	3310	3320	3330	3340	3350	3360	3370
	3380	3390	3400	3410	3420	3430	3440
	3450	3460	3470	3480	3490	3500	3510
	3520	35					

```

a937.seq
1 ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTTC CTTACCTACC TGAACACGCA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGCGT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACTCG ACGGCAACGG
351 CAAAACCCGA ACAAAACGGA TGTCCGAGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCCGCCC TTCTCAGCTT TCTTGAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCGTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAG CAACACAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CTTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GCGAAGCAGC
701 CGGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTCCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGACGCT TTCAACGTTT CAGGGCAAAG CAGTTCGGAA CTGAAATTG
851 GCGTACAGCA TAGCTTTTAA

```

a937.pep

1	MKRIFLPALP	AILPLSAYAD	LPLTIEDIMT	DKGKWKLETS	LTYLNSENNRR
51	AELAAPVYIQ	TGATSFIPIP	TEIQENGST	DMLVGTGLLR	YGLTGNTDIY
101	SGSGYLWHEE	RKLDGNGKTR	NKRMSDVSIG	ISHTFLKDDK	NPALISFLES
151	TVYEKSRNKA	SSGKSWLIGA	TTYKAIDPVV	LSLTAAYRIN	GSKTLLSNNTK
201	YKAGNYWMLN	PNISFAANDR	ISLTGGIQWL	GKQPDRLDGK	KESARNTSTY
251	AHEGAGFGFT	KTTALNASAR	FNVSGQSSE	LKFGVQHTF*	

```

      10      20      30      40      50      60
m937.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          |||||:|||||
a937      MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNRAELAAPVYIQ
          10      20      30      40      50      60

      70      80      90      100     110     120
m937.pep  TGATSFIPPIPTIEIQENGSNTDMLVGTGLGLRYGLTGNTDIYSGGSYWLWHEERKLDGNSKTR
          |||||:|||||
a937      TGATSFIPPIPTIEIQENGSNTDMLVGTGLGLRYGLTGNTDIYSGGSYWLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

1356

	130	140	150	160	170	180
m937.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a937	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m937.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a937	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m937.pep	RESSRNTSTYAHFGAGFGFTKTTALNASARENVSGQSSSELKFGVQHTFX					
a937	KESARNTSTYAHFGAGFGFTKTTALNASARENVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

g939.seq not found yet

g939.pep not found yet

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 2893>:

m939.seq (partial)

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCCTCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAATATCGG
201 CATCCGCGAC GTAAACGCAC CC...
```

This corresponds to the amino acid sequence &lt;SEQ ID 2894; ORF 939&gt;:

m939.pep (partial)

```

1  MKRLTLIAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD VNAP...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2895>:

a939.seq

```

1  ATGAAACGAT TGACTTTATT GGCCTTTGTT TTGGCTGCCG GTGCGGTTTC
51  CGCATCTCCC AAAGCAGACG TGGAAAAAGG CAAACAGGTT GCCGCAACGG
101 TTTGTGCGGC TTGCCATGCA GCAGACGGTA ACAGCGGCAT TGCATGTAT
151 CCGCGTTTGG CGGCACAGCA TACTGCTTAC ATCTATCATC AAACATCGG
201 CATCCGCGAC GGTAAACGCA CCCACGGTTC GGCAGCTGTG ATGAAACCGG
251 TGGTAATGAA TTTGAGCGAT CAGGATATTT TGAACGTATC CGCATTCTAT
301 GCCAAACAGC AGCCCAAATC CGGTGAAGCC AATCCTAAGG AAAATCCCGA
351 ATTGGGTGCG AAAATCTATC GCGGCGGTTT GAGCGATAAA AAAGTGCCGG
401 CGTGATGTC CTGCCACGGT CCGAGCGGTG CGGGTATGCC GGGGGGCGGA
451 AGCGAAATTC AGGCTTATCC GCGTTTGGGC GGTCAGCATC AGGCATATAT
501 TGTGAACAG ATGAATGCCT ACAAGTCCGG TCAGCGTAAA AATACCATCA
551 TGAAGATAT TGCAAACCGT ATGTCTGAAG AAGATTTGAA AGCGTCGCC
601 AACTTTATCC AAGGTTTGCG TTAA
```

This corresponds to the amino acid sequence &lt;SEQ ID 2896; ORF 939.a&gt;:

a939.pep

```

1  MKRLTLIAFV LAAGAVSASP KADVEKGKQV AATVCAACHA ADGNSGIAMY
51  PRLAAQHTAY IYHQTIGIRD GKRTGSAAV MKPVVMNLSQ QDILNVSAFY
101 AKQPKSGEA NPKNPELGA KIYRGLSDK KVPACMSCHG PSGAGMPGGG
151 SEIQAYPRLG GQHQAIVEQ MNAYKSGQRK NTIMEDIANR MSEDILKAVA
201 NFIQGLR*
```

m939/a939 100.0% identity in 70 aa overlap

	10	20	30	40	50	60
m939.pep	MKRLTLIAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					
a939	MKRLTLIAFVLAAGAVSASPKADVEKGKQVAATVCAACHAADGNSGIAMYPRLAAQHTAY					

1357

```

              10      20      30      40      50      60
              70
m939.p<ep    IYHQTIGIRDVNAP
              |||||
a939         IYHQTIGIRDGKRTHGSAAVMKPVVMNLSDDILNVSAFYAKQPKSGEANPKENPELGA
              70      80      90      100     110     120

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2897>:

```

g950.seq
1  ATGAACAAAA ATATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTCT
51 GGC CGCCGGC GCCGTTGCCG CCCACAAACC GGCAAGCAAC GCAACAGGCG
101 TTC AAAAATC CGCCCAAGGC TCTTGCGGCG CATCCAAATC TGCCGAAGGT
151 TCG TGCGGCG CATCCAAATC TGCCGAAGGT TCGTGCGGCG CGGCTGCTTC
201 TAA AGCAGGC GAAGGCAAAT GCGGCGAGGG CAAATGCGGT GCAACTGTAA
251 AAA AAGCCCA CAAACACACC AAAGCATCTA AAGCCAAAGC CAAATCTGCC
301 GAA GGCAAT GCGGCGAAGG CAAATGCGGT TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2898; ORF 950.ng>:

```

g950.pep
1  MNKNIAAALA GALSLSLAAG AVAAHKPASN ATGVOKSAQG SCGASKSAEG
51 SCGAASKAEG SCGAAASKAG EGKCGEGKCG ATVKKAHKHT KASKAKAKSA
101 EGKCGEGKCG SK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2899>:

```

m950.seq
1  ATGAACAAAA ACATTGCTGC CGCTCTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGC CGCCGGT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTC ATAAATC CGCCCATGCG TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCG TGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAA ATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2900; ORF 950>:

```

m950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKSANG SCGASKSAEG
51 SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 950 shows 86.6% identity over a 112 aa overlap with a predicted ORF (ORF 950) from *N. gonorrhoeae*

m950/g950 86.6% identity in 112 aa overlap

```

              10      20      30      40      50
m950.pep    MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKSANGSCGASKSAEGSCGA-----
              |||||
g950         MNKNIAAALAGALSLSLAAGAVAANKPASNATGVOKSAQSGCGASKSAEGSCGASKSAEG
              10      20      30      40      50      60

              60      70      80      90     100
m950.pep    -----AGSKAGEGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
              |||||
g950         SCGAAASKAGEGKCGEGKCGATVKKKAHKHTKASKAKAKSAEGKCGEGKCGSKX
              70      80      90     100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2901>:

```

a950.seq
1  ATGAACAAAA ACATTGCTGC CGCACTCGCC GGTGCTTTAT CCCTGTCTTT
51 GGCCGCGGCT GCAGTTGCTG CCAACAAACC GGCAAGCAAC GCAACAGGCG
101 TTCATAAATC CGCCCATGCG TCTTGCGGCG CGTCCAAATC TGCCGAAGGT
151 TCGTGCGGCG CGGCTGGTTC TAAAGCAGGC GAAGGCAAAT GCGGCGAGGG
201 CAAATGCGGT GCGACCGTAA AAAAAACCCA CAAACACACC AAAGCATCTA
251 AAGCCAAGGC CAAATCTGCC GAAGGCAAAT GCGGCGAAGG CAAATGCGGT
301 TCTAAATAA

```

1358

This corresponds to the amino acid sequence <SEQ ID 2902; ORF 950.a>:

```
a950.pep
1  MNKNIAAALA GALSLSLAAG AVAANKPASN ATGVHKS AHG SCGASKSAEG
51  SCGAAGSKAG EGKCGEGKCG ATVKKTHKHT KASKAKAKSA EGKCGEGKCG
101 SK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 950 shows 100.0% identity over a 102 aa overlap with a predicted ORF (ORF 950) from *N. meningitidis*

a950/m950 100.0% identity in 102 aa overlap

```

      10      20      30      40      50      60
a950.pep  MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHG SCGASKSAEGSCGAAGSKAG
          |||
m950      MNKNIAAALAGALSLSLAAGAVAANKPASNATGVHKS AHG SCGASKSAEGSCGAAGSKAG
          |||
      70      80      90     100
a950.pep  EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSKX
          |||
m950      EGKCGEGKCGATVKKTHKHTKASKAKAKSAEGKCGEGKCGSK
          |||
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2903>:

```
g951.seq
1  ATGATTATGT TACCCGCCCG TTCTACTATT TTATCTGTCC TCGCAGCAGC
51  CCTGCTTGCC GGACAGGCGT ATGCTGCCCG CGCGGCGGAT GTGGAGCTGC
101 CGAAGGAAGT CGGAAGGTT TTAAGGAAAC ATCGGCGTTA CAGCGAGGAA
151 GAAATCAAAA ACGAACGCGC ACGGCTTGCG GCAGTGGGCG AACGGGTCAA
201 CAGGGTGTTT ACGCTGTTGG GCGGTGAAAC GGCTTTGCAG AAAGGGCAGG
251 CGGGAACGGC TCTGGCAACC TATATGCTGA TGTGGAACG CACAAAATCC
301 CCCGAAGTCG CCGAACGCGC CTTGGAATG GCCGTGTGCG TGAACGCGTT
351 TGAACAGGCG GAAATGATTT ATCAGAAATG GCGGCAGATC GAGCCTATAC
401 CGGGTGAGGC GCAAAAACGG GCGGGGTGGC TCGGGAACGT ATTGAGGGAA
451 GGGGGAATC AGCATCTGGA CGGGTGGAAG GAGGTGCTGG CGCAATCGGA
501 CGATGTGCAA AAACGCGAGG TATTTTGCT GCTGGTGCAA GCCGCCGTGC
551 AGCAGGGTGG GTTGGCTCAA AAAGCATCGA AAGCGGTTTC CCGTGGCGCG
601 TTGAAGTATG AACATCTGCC CGAAGCGGCG GTTGCCGATG CGGTGTTCCG
651 CGTACAGGGA CGCGAAAAGG AAAAGGCAAT CGAAGCTTTG CAGCGTTTGG
701 CGAAGCTCGA TACGGAATA TTGCCCCCA CTTTAATGAC GTTGCGTCTG
751 ACTGCACGCA AATATCCCGA AATACTCGAC GGCTTTTTCG AGCAGACAGA
801 CACCCAAAC CTTTCGGCGG TCTGGCAGGA AATGGAATT ATGAATCTGG
851 TTTCCTCGC TAAGCCGGAT GATGCCTATG CGCGTTTGAA CGTGCTGTTG
901 GAACACAACC CGAATGCAAA CTTGTATATT CAGGCGGCGA TATTGGCGGC
951 AAACCGAAAA GAAGGTGCGT CCGTTATCGA CCGGTACGCC GAAAAGGCAT
1001 ACGGCAGGGG GACGGGGGAA CAGCGGGGCA GGGCGGCAAT GACGGCGGCG
1051 ATGATATATG CCGACCGCAG GGATTACGCC AAAGTCAGGC AGTGTTGAA
1101 AAAAGTGTCG GCGCCGGAAT ACCTGTTTCA CAAAGGCGTG CTGGCGGCTG
1151 CGGCGGCTGC CGAATTGGAC GGAGGCGGGG CGGCTTTGCG GCAGATCGGC
1201 AGGGTGCGGA AACTTCCCGA ACAGCAGGGG CGGTATTTTA CGGCAGACAA
1251 TTTGTCCAAA ATACAGATGC TCGCCCTGTC GAAGCTGCCC GACAAACGGG
1301 AAGCCCTGAT CGGGCTGAAC AACATCATCG CCAAACTTTC GGGCGCGGGA
1351 AGCACGGAAC CTTTGCGCGA AGCATTGGCA CAGCGTTTCA TTATTACGA
1401 ACAGTTTCGGC AAACGGGGAA AAATGATTGC CGACCTGAA ACCGCGCTCA
1451 AACTTACGCG CGATAATGCA CAAATTATGA ATAATCTGGG CTACAGCCTG
1501 CTTTCCGATT CCAAACTTTT GGACGAGGGT TTCGCCCTGC TTCAGACGGC
1551 ATACCAAACT AACCCGGACG ATACCGCCGT TAACGACAGC ATAGGCTGGG
1601 CGTATTACCT GAAAGGCGAC GCGGAAAGCG CGCTGCCGTA TCTGCGGTAT
1651 TCGTTTGAAA ACGACCCCGA GCCCGAAGTT GCCGCCATT TGGGCGAAGT
1701 GTTGTGGGCA TTGGGCGAAC GCGATCAGGC GGTGACGTA TGGACGACGG
1751 CGGCACACCT TAGGGGAGAC AAGAAAATAT GCGGGGAGAC GCTCAAACGC
1801 TACGGAATCG CCTTGCCCGA GCCTTCCCGA AAACCCCGGA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 2904; ORF 951.ng>:

```
g951.pep
1  MIMLPARFTI LSVLAAALLA GOAYAAGAAD VELPKEVGKV LRKHRRYSEE
```

```

51  EIKNERARLA AVGERVNRVF TLLGGETALO KQOAGTALAT YMLMLERTKS
101 PEVAERALEM AVSLNAFEQA EMIYQKWRQI EPIPGEAQKR AGWLRNVLRE
151 GGNQHLDGLE EVLAQSDDDVQ KRRIFLLLVQ AAVQGGVQAQ KASKAVRRRAA
201 LKYEHLPEAA VADAVFGVQG REKEKAIEAL ORLAKLDTEI LPPTLMTLRL
251 TARKYPEILD GFFEQTDTQN LSAVWOEMEI MNLVSLRKPD DAYARLNVLL
301 EHNENANLYI QAAILAANRK EGASVIDGYA EKAYGRGTGE QRGRAAMTAA
351 MIYADRRDYA KVRQWLKKS APEYLFDKGV LAAAAAELD GGRAALRQIG
401 RVRKLPEQQG RYFTADNLSK IQMLALSCLP DKREALIGLN NIIAKLSAAG
451 STEPLAEALA QRSIIYEQFG KRGKMIADLE TALKLTPDNA QIMNNLGYSL
501 LSDSKRLDEG FALLQYAYOI NPDDTAVNDS IGWAYYLLKGD AESALPYLRY
551 SFENDPEPEV AAHLGEVLWA LGERDQAVDV WTQAAHLRGD KKIWRETLKR
601 YGIALPEPSR KPRK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2905>:

m951.seq

```

1  ATGATTATGT TACCTAACCG TTCAAAATG TTAAGTGTGT TGACGGCAAC
51  CTTGATTGCC GGACAGGTAT CTGCCGCCG AGGCGGTGCG GGGGATATGA
101 AACAGCCGAA GGAAGTCGGA AAGGTTTCA GAAAGCAGCA GCGTTACAGC
151 GAGGAAGAAA TCAAAACGA ACGCGCACGG CTTGCGGCAG TGGGCGAGCG
201 GGTTAATCAG ATATTACGT TGCTGGGAGG GAAACCGGCC TTGCAAAAGG
251 GGCAGGCGGG AACGGCTCTG GCAACCTATA TGCTGATGTT GGAACGCACA
301 AAATCCCCCG AAGTCGCCGA ACGCGCCTTG GAAATGGCCG TGTCGCTGAA
351 CGCGTTTGAA CAGGCGGAAA TGATTATCA GAAATGGCCG CAGATTGAGC
401 CTATACCGGG TAAGGCGCAA AAACGGGCGG GGTGGCTGCG GAACGTGCTG
451 AGGGAAAGAG GAAATCAGCA TCTGGACGGA CTGGAAGAAG TGCTGGCTCA
501 GCGCGGACGAA GGACAGAACC GCAGGCTGTT TTTATTGTTG GCACAGCCG
551 CCGTGCAACA GCAGGGGTTG GCGCAAAAG CATCGAAAGC GGTTCGCCGC
601 CCGGCGTTGA AATATGAACA TCTGCCGAA GCGGCGGTTG CCGATGTGGT
651 GTTCAGCGTA CAGGACGCG AAAAGGAAA GGCAATCGGA GCTTTGCAGC
701 GTTTGGCGAA GCTCGATACG GAAATATTGC CCCCACCTT AATGACGTTG
751 CGTCTGACTG CACGCAATA TCCCGAATA CTCGACGGCT TTTTCGAGCA
801 GACAGACACC CAAACCTTT CGGCCGCTG GCAGGAATG GAAATTATGA
851 ATCTGTTTTC CCTGCACAGG CTGGATGATG CCTATGCCG TTTGAACGTG
901 CTGTTGGAAC GCAATCCGAA TGCAGACCTG TATATTCAGG CAGCGATATT
951 GGCGGCAAAC CGAAAAGAAG GTGCTTCCGT TATCGACGGC TACGCCGAAA
1001 AGGCATACGG CAGGGGGACG GAGGAACAGC GGAGCAGGGC GCGGCTAACG
1051 GCGGCGATGA TGTATGCCGA CCGCAGGGAT TACGCCAAG TCAGGCAGTG
1101 GCTGAAAAAA GTATCCGCGC CGGAATACCT GTTCGACAAA GGTGTGCTGG
1151 CGGCTGCGGC GGCTGTCGAG TTGGACGGCG GCAGGGCGGC TTTGCGGCAG
1201 ATCGGCAGGG TGCGGAAACT TCCGAAACAG CAGGGGCGGT ATTTTACGGC
1251 AGACAATTG TCCAAAATAC AGATGCTCGC CCTGTCGAAG CTGCCCGATA
1301 AACGGGAGGC TTTGAGGGGG TTGGACAAGA TTATCGAAAA ACCGCTTGCC
1351 GGCAGTAATA CAGAGTTACA GGCAGAGGCA TTGTACAGC GGTCAAGTGT
1401 TTACGATCGG CTTGGCAAGC GAAAAAAT GATTTCAGAT CTTGAAAGGG
1451 CGTTACAGCT TGCACCCGAT AACGCTCAGA TTATGAATA TCTGGGCTAC
1501 AGCCTGCTGA CCGATTCCAA ACGTTTGAC GAAGGTTTCG CCCTGCTTCA
1551 GACGGCATAC CAATCAACC CGGACGATAC CGCTGTCAAC GACAGCATAG
1601 GCTGGGCGTA TTACCTGAAA GCGGACGCGG AAAGCGCGCT GCCGTATCTG
1651 CCGTATTCGT TTGAAAACGA CCCCAGAGCC GAAGTTGCCG CCCATTGCGG
1701 CGAAGTGTG TGGCATTGG GCGAACGCGA TCAGGCGGTT GACGTATGGA
1751 CGCAGGCGGC ACACCTTACG GGAGACAAGA AAATATGGCG GGAAACGCTC
1801 AAACGTCACG GCATCGCATT GCCCAACCT TCCGAAAAAC CTCGGAAATA
1851 A

```

This corresponds to the amino acid sequence <SEQ ID 2906; ORF 791>:

m951.pep

```

1  MIMLPNRFKM LTVLTATLIA QVSAAGGGA GDMKQPEVG KVFRKQORYS
51  EEEIKNERAR LAAVGERVNO IFTLLGETA LQKQAGTAL ATYMLMLERT
101 KSPEVAERAL EMAVSLNAFE QAEMIYQKWR QIEPIPGKAQ KRAGWLRNVL
151 RERGNQHLDG LEEVLAQADE GQNRVFLLL AQAAVQDGL AQKASKAVRR
201 AALKYEHLPE AAVADVFSV QGREKEKAIG ALQRLAKLDT EILPPTLMTL
251 RLTAARKYPEI LDGFFEQTDT QNLSAVWQEM EIMNLVSLHR LDDAYARLNV
301 LLERNPNADL YIQAILAAN RKEGASVIDG YAEKAYGRGT EEQRSRAALT
351 AAMMYADRRD YAKVRQWLKK VSAPEYLFDK GVLAATAAVE LDGGRALRQ
401 IGRVRKLPEQ QGRYFTADNL SKIQMLALS LDPKREALRG LDKIIEKPPA
451 GSNTELQAEA LVQSVVYDR LGKRKMKISD LERAFRLAPD NAQIMNNLGY
501 SLLTDSKRLD EGFALLQYAI QNPDDTAVN DSIWAYYLLK GDAESALPYL
551 RYSFENDPEP EVAHLGEVL WALGERDQAV DVWTQAAHLT GDKKIWRETL
601 KRHGIALPQP SRKPRK*

```

Computer analysis of this amino acid sequence gave the following results:



Homology with a predicted ORF from *N. gonorrhoeae*

ORF 951 shows 88.6% identity over a 616 aa overlap with a predicted ORF (ORF 951) from *N. gonorrhoeae*

m951/g951 88.6% identity in 616 aa overlap

m951.pep	10	20	30	40	50	60
	MIMLPNRFKMLTVLTATLIAGQVSAAGGGAGDMKQPKVGVFRKQORYSEEEIKNERAR					
g951	10	20	30	40	50	
	MIMLPARFTILSVLAAALLAGQAYAA--GAADVLPKEVGVKVLKHHRYSEEEIKNERAR					
m951.pep	70	80	90	100	110	120
	LAAVGERVNIQFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
g951	60	70	80	90	100	110
	LAAVGERVNRVFTLLGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE					
m951.pep	130	140	150	160	170	180
	QAEMIQKWRQIEPIPGKAQKRAGWLRNVLRERGNQHLGLEEVLAQADEGQNRVFLLL					
g951	120	130	140	150	160	170
	QAEMIQKWRQIEPIPGEAQKRAGWLRNVLRERGNQHLGLEEVLAQSDDVQKRIFLL					
m951.pep	190	200	210	220	230	240
	AQAAVQQDGLAQKASKAVRRAALKYEHLPAAVADVFSVQGREKEKAIGALQRLAKLDT					
g951	180	190	200	210	220	230
	VQAAVQQGGVAQKASKAVRRAALKYEHLPAAVADVFGVQGREKEKAIEALQRLAKLDT					
m951.pep	250	260	270	280	290	300
	EILPPTLMTLRLTARKYPEILDGFEQTDTONLSAVWQEMEIMNLVSLHRLDDAYARLNV					
g951	240	250	260	270	280	290
	EILPPTLMTLRLTARKYPEILDGFEQTDTONLSAVWQEMEIMNLVSLRKPDDAYARLNV					
m951.pep	310	320	330	340	350	360
	LLERNPNADLYIQAILAANRKEGASVIDGYAEKAYGRGTEEQRSRAALTAAMMYADRRD					
g951	300	310	320	330	340	350
	LLEHNPANLYIQAILAANRKEGASVIDGYAEKAYGRGTGEQGRAMTAAMIYADRRD					
m951.pep	370	380	390	400	410	420
	YAKVRQWLKKSVAPEYLFDKGVLAATAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
g951	360	370	380	390	400	410
	YAKVRQWLKKSVAPEYLFDKGVLAATAAELDGGRAALRQIGRVKRLPEQQGRYFTADNL					
m951.pep	430	440	450	460	470	480
	SKIQMLALSCLPKREALRGLDKIIEKPPAGSNTLQAEALVQRSVVYDRLGKRKKMISD					
g951	420	430	440	450	460	470
	SKIQMLALSCLPKREALIGLNIIAKLSAAGSTEPLAEALAQRSIIYEQFGKRKGMID					
m951.pep	490	500	510	520	530	540
	LERAFRLAPDNAQIMNNGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
g951	480	490	500	510	520	530
	LETALKLTPDNAQIMNNGYSLLTDSKRLDEGFALLQTAYQINPDDTAVNDSIGWAYYLK					
m951.pep	550	560	570	580	590	600
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLTGDKKIWRETL					
g951	540	550	560	570	580	590
	GDAESALPYLRYSFENDPEPEVAHLGEVLWALGERDQAVDVWTQAAHLRGDKKIWRETL					
m951.pep	610					
	KRHGIALPQPSRKPRK					
g951	600	610				
	KRYGIALPEPSRKPRKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2907>:

```
a951.seq
1  ATGTTACCCG CCCGTTTCAC CATTATCT GTGCTCGCGG CAGCCCTGCT
51  TGC CGGGCAG GCGTATGCCG CCGCGCGGCG GGTATGCGAAG CCGCCGAAGG
101 AAG TCGGAAA GGTTTTCAGA AAGCAGCAGC GTTACAGCGA GGAAGAAATC
151 AAA AACGAAC GCGCAGCGCT TCGGCACTG GCGGAGCGGG TTAATCAGAT
201 ATT TACGTTG CTGGGAGGGG AAACCGCCTT GCAAAAGGGG CAGGCGGGAA
251 CGG CTCTGGC AACCTATATG CTGATGTTGG AACGCACAAA ATCCCCCGAA
301 GTC GCCGAAC GCGCCTTGA AATGGCCGTG TCGCTGAACG CGTTTGAACA
351 GGC GGAATG ATTTATCAGA AATGGCGGCA GATTGAGCCT ATACCGGGTA
401 AGG CGCAAAA ACGGGCGGGG TGGCTGCGGA ACGTGCTGAG GGAAGAGGA
451 AAT CAGCATC TAGACGGACT GGAAGAAGTG CTGGCTCAGG CGGACGAAGG
501 ACA GAACCGC AGGGTGT TTTTATTGTTG CAAAGCCGCC GTGCAACAGG
551 ACG GGTGGC GCAAAAAGCA TCGAAAGCGG TTCGCCGCGC GGCCTTGAGA
601 TAT GAACATC TGCCCGAAGC GCGCGTTGCC GATGTGGTGT TCAGCGTACA
651 GGG ACGCCAA AAGGAAAAGG CAATCGGAGC TTGCGAGCGT TTGGCGAAGC
701 TCG ATACGGA AATATTGCCC CCCACTTTAA TGACGTTGCG TCTGACTGCA
751 CGC AATATC CCGAAATACT CGACGGCTTT TTCGAGCAGA CAGACACCCA
801 AAA CCTTTGC GCGCTCTGGC AGGAAATGGA AATTATGAAT CTGGTTTCCC
851 TGC ACAGGCT GGATGATGCC TATGCGCGTT TGAACGTGCT GTTGGAAACG
901 AAT CCGAATG CAGACCTGTA TATTCAGGCA GCGATATTGG CGGCAAAACCG
951 AAA AGAAGGT GCTTCCGTTA TCGACGGCTA CGCCGAAAAG GCATACGGCA
1001 GGG GGCAGG GGAACAGCGG GGCAGGGCGG CAATGACGGC GCGCATGATA
1051 TAT GCCGACC GAAGGGATTA CACCAAAGTC AGGCAGTGGT TGAAAAAAGT
1101 GTC CGCGCCG GAATACCTGT TCGACAAAGG TGTGCTGGCG GCTGCGGCGG
1151 CTG TCGAGTT GGACGGCGGC AGGGCGGCTT TCGGCGAGAT CGGCAGGGTG
1201 CGGAAACTTC CCGAACAGCA GGGCGGTAT TTTACGGCAG ACAATTGTG
1251 CAA AATACAG ATGTTCCGCC TGTCGAAGCT GCCCGACAAA CGGAGGCTT
1301 TGA GGGGTTT GGACAAGATT ATCGAAAAAC CGCTGCCCG CAGTAATACA
1351 GAGTTACAGG CAGAGGCATT GGTACAGCGG TCAGTTGTTT ACGATCGGCT
1401 TGG CAAGCGG AAAAAATGA TTTCAGATCT TGAAGGGCG TTCAGGCTTG
1451 CAC CCGATAA CGCTCAGATT ATGAATAATC TGGGCTACAG CTGCTTTCC
1501 GAT TCCAAAC GTTTGGACGA AGGCTTCGCC CTGCTTCAGA CGGCATACCA
1551 AAT CAACCG GACGATACCG CTGTCAACGA CAGCATAGGC TGGGCGTATT
1601 ACC TGAAGG CGACGCGGAA AGCGCGTGC CGTATCTCG GTATTCTGTT
1651 GAA AACGACC CCGAGCCCGA AGTTGCCGCC CATTGGGCG AAGTGTGTG
1701 GGC ATTGGGC GAACGCGATC AGGCGGTTGA CGTATGGACG CAGGCGGCAC
1751 ACC TTACGGG AGACAAGAAA ATATGGCGGG AAACGCTCAA ACGTCACGGC
1801 ATCGCATTGC CCCAACCTTC CCGAAACCT CCGAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 2908; ORF 951.a>:

```
a951.pep
1  MLPARFTILS VLAAALLAGQ AYAAGAADAK PPKEVGKVF R KQORYSEEEI
51  KNERARLAAY GERVNQIFTL LGGETALQKG QAGTALATYM LMLERTKSPE
101 VAERALEMAV SLNAFEQAEM IYOKWROIEP IPGKAOKRAG WLRNVLRERG
151 NQHL DGL EEV LAQADEGQNR RVFLLLAQAA VQDGLAQKA SKAVRRAALR
201 YEHLPEAAVA DVVFSVQGRE KEKAIGALQR LAKLDTEILP PTLMLRLTA
251 RKYPEILDGF FEQTDTONLS AVWQEMEIMN LVSLHRLDDA YARLNVLLER
301 NPNADLYIQ AILAA NRKEG ASVIDGYAEK AYGRGTGEQR GRAAMTAAMI
351 YADRRDYTKV RQWLK KVSAP EYLFDKGVLA AAAVELDGG RAALRQIGRV
401 RKLPEQGRY FTADNLSIQ MFALSKLPDK REALRGLDKI IEKPPAGSNT
451 ELQAEALVQR SVYDRLGKR KKMISDLERA FRLAPDNAQI MNNLGYSLLS
501 DSKRLDEGFA LLQYAYQINP DDTAVNDSIG WAYYLGDAE SALPYLRYSF
551 ENDP EPEVAA HLGEVLWALG ERDQAVDVT QAAHLTGDKK IWRETLKRHG
600 IALPQPSRKP RK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 951 shows 96.4% identity over a 614 aa overlap with a predicted ORF (ORF 951) from *N. meningitidis*

a951/m951 96.4% identity in 614 aa overlap

```
a951.pep      10      20      30      40      50
               MLPARFTILSVLAAALLAGQAYAG--AADAKPPKEVGKVF RKQORYSEEEIKNERAR
               ||| || :|:|:|:|:|:|:| ||| :| | | | | | | | | | | | | | | | | | |
m951          10      20      30      40      50      60
               MIMLPNRFKMLTTLTATLIAGQVSAAGGGAGDMKQPKVEVGKVF RKQORYSEEEIKNERAR
               ||| || :|:|:|:|:|:|:| ||| :| | | | | | | | | | | | | | | | | | |
a951.pep      60      70      80      90     100     110
               LAAVGERVNQIFTL LGGETALQKGQAGTALATYMLMLERTKSPEVAERALEMAVSLNAFE
```

q952.seq (partial)

9552.864 (p. 10)

1	TTGTCTTATC	GTTTGAATGC	TGCACCGATG	TTTAAACGATA	ATCCTGTTGT
51	TTACGGAAAA	ATCAAATTGC	AGAGTTGGAA	AGCGCGGCGG	GATTTCAAAT
101	TTGTAAGACA	GGATTGGAT	TTTTCTCTCG	GGCGCGCTTC	GGTGGCGACG
151	CTTTTGAACA	ATTTTACGG	GCAAAAGCTG	ACGGAAGAAG	AAGTGTGGGA
201	AAAAC TGGGT	AAGGAACAGA	TGCGCGCGTC	GTTTGAGGAT	ATGCGGCGCA
251	TTATGCCCGA	TTTGGGTTTT	GAGCGAAGAT	GCTATGCCCT	GTCPTTCCGAA
301	CAGCTCGCG	AGTTGAAAA	CCCCGTCATC	GTGTATCTGA	AATACCCGAA
351	AGACGACCAT	TTTTCGGTAT	TCCGCGGAGT	GGATGGCAAT	ACGGTTTTGC
401	TTGCCGACCC	GTCGCCGGGT	CATGTTTCGA	TGAGCAGGGC	GCAGTTTTTG
451	GAGGCTTGGC	AAACCCGTGA	GGGAAATTTG	GCAGGCCAAA	TTTTGGCCGT
501	CGTGCCGAAA	AAACGCGAGG	CGATTTCAAA	TAAATTTGTT	TTCACGATC
551	ATCCCAAGCG	GCAGACGGAG	TTTGCAGTCG	CAGAGGTA	ATGTGCGCGT

601 GCTTATTGA

This corresponds to the amino acid sequence <SEQ ID 2910; ORF 952.ng>:

g952.pep (partial)

```

1  ..LSYRLNAAPM FNDNPVYVGK IKLQSWKARR DFNIVKQDLD FSCGAASVAT
51  LLNIFYGQKL TEEVLEKLG KEQMRASFED MRRIMPD LGF EAKGYALSFE
101 QLAQLKIPVI VYLKVRKDDH FSVLRGVDGN TVLLADPSPG HVSMSRAQFL
151 EAWQTREGNL AGKILAVVPK KAEAISNKL FTHHPKQTE FAVGQVKWWR
201 AY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2911>:

m952.seq

```

1  ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT
51  ATCTTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTGTGTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG CGCGCGCGGA TTTCAATATT
151 GTAAAGCAGG ATTTGGATTT TTCCTGTGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAAT TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGCTGGATAA GGAGCAGATG CGCGCGTCGT TTGAGGATAT CGCGCGCATT
301 ATGCTGTGAT TGGGTTTGA GCGGAAGGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCGCAG TTGAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAAG
401 ACGACCATTT TTCGGTATTG CGCGGTATAG ACGGCAATAC GGTTTTGCTT
451 GCCGACCCGT CGCTGGGGCA TGTTC AATG AGCAGGGCGC AGTTTTTGGA
501 TCGTTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCTGTCA
551 TACCGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTTT CACACAACAC
601 CCAAAACGGC AGACGGAGTT TACAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2912; ORF 952>:

m952.pep

```

1  MMKFKYVFL ACVVVLSYR LNAAPMFNDN PVVYGKIKVQ SWKARRDFNI
51  VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRRI
101 MPDLGF EAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFLDAWQ TREGNLAGKI LAVIPKKAET ISNKLFFTOH
201 PKRQTEFTVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 952 shows 92.5% identity over a 201 aa overlap with a predicted ORF (ORF 952) from *N. gonorrhoeae*

g952/m952: 92.5% identity in 201 aa overlap

```

                                10      20      30      40
g952.pep                      LSYRLNAAPMFNDNPVYVGKIKLQSWKARRDFNIVKQDLD FSCG
                                |||
m952                          MMKFKYVFLACVVVLSYRLNAAPMFNDNPVYVGKIKVQSWKARRDFNIVKQDLD FSCG
                                10      20      30      40      50      60

                                50      60      70      80      90      100
g952.pep                      AASVATLLNNFYGQKL TEEVLEKLGKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ
                                |||
m952                          AASVATLLNNFYGQTL TEEVLEKLDKEQMRASFEDMRRIMPD LGF EAKGYALSFEQLAQ
                                70      80      90      100      110      120

                                110     120     130     140     150     160
g952.pep                      LKIPVIVYLKVRKDDHFSVLRGVDGNTVLLADPSPGHVSMSRAQFLEAWQTREGNLAGKI
                                |||
m952                          LKIPVIVYLKVRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI
                                130     140     150     160     170     180

                                170     180     190     200
g952.pep                      LAVVPKKA E AISNKLFFTHHPKQTEFAVGQVKWWRAYX
                                |||
m952                          LAVIPKKAETISNKLFFTOH PKRQTEFTVGQIRQARAE
                                190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2913>:

a952.seq

```

1  ATGATGAAGT TCAAATATGT TTTCTGTTG GCGTGTGTTG TCGTTTCTTT

```

1364

```

51 ATC TTATCGT TTGAATGCTG CACCGATGTT TAACGATAAT CCTGTTGTTT
101 ACGGAAAAAT CAAAGTGCAG AGTTGGAAAG AAAGGCGGGA TTCAATATT
151 GTAAAGCAGG ATTTGGATT TTTCTGCGGG GCGGCTTCGG TGGCGACGCT
201 TTTGAACAA TTTTACGGGC AAACGCTGAC GGAAGAAGAA GTGTTGAAAA
251 AGC TGGATAA GGAGCAGATG CGCGCTCGT TTGAGGATAT GCGGCGCATT
301 ATGCCAGATT TGGGTTTTGA AGCGAAAGGC TATGCCCTGT CTTTCGAGCA
351 GCTCGCACAG TTGAAAATCC CCGTCATCGT GTATCTGAAA TACCGCAAGG
401 ATGATCATTT CTCGGTATTG CGCGGGATAG ACGGCAATAC GGTTTTGCTT
451 GCCGAGCCCGT CGCTGGGTCA TGTTTCAATG AGCAGGGCGC AGTTTNGGA
501 TGC TTGGCAA ACCCGTGAGG GAAATTTGGC AGGTAAGATT TTGGCGGTCC
551 TGC CGAAAAA AGCCGAGACA ATTTCAAATA AATTGTTTT CACACATCAT
601 CCCAAGCGGC AGACGGAGTT TGCAGTCGGA CAAATCAGGC AAGCACGTGC
651 AGAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2914; ORF 952.a>:

```

a952.pep
1 MMKFKYVPELL ACVVVSLSYR LNAAPMFNDN PVVYGKIKVQ SWKERRDFNI
51 VKQDLDFSCG AASVATLLNN FYGQTLTEEE VLKLDKEQM RASFEDMRR
101 MPDLGFEAKG YALSFEQLAQ LKIPVIVYLK YRKDDHFSVL RGIDGNTVLL
151 ADPSLGHVSM SRAQFXDAWQ TREGNLAGKI LAVVPKKAET ISNKLFFTHH
201 PKRQTEFAVG QIRQARAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 952 shows 97.7% identity over a 218 aa overlap with a predicted ORF (ORF 952) from *N. meningitidis*

```

a952/m952    97.7% identity in 218 aa overlap

a952.pep      10      20      30      40      50      60
MMKFKYVPELLACVVVSLSYRLNAAAPMFNDNPVVYGKIKVQSWKERRDFNIVKQDLDFSCG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952          10      20      30      40      50      60
MMKFKYVPELLACVVVSLSYRLNAAAPMFNDNPVVYGKIKVQSWKARRDFNIVKQDLDFSCG

a952.pep      70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952          70      80      90      100     110     120
AASVATLLNNFYGQTLTEEEVLKLDKEQMRASFEDMRRIMPDLGFEAKGYALSFEQLAQ

a952.pep     130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFXDAWQTREGNLAGKI
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952         130     140     150     160     170     180
LKIPVIVYLKYRKDDHFSVLRGIDGNTVLLADPSLGHVSM SRAQFLDAWQTREGNLAGKI

a952.pep     190     200     210     219
LAVVPKKAETISNKLFFTHHPKRQTEFAVGQIRQARAE
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m952         190     200     210
LAVIPKKAETISNKLFFTHHPKRQTEFTVGQIRQARAE

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2915>:

```

g953.seq
1 ATGAAAAAAA TCATCTTCGC CGCGCTCGCA GCGGCAGCCG TCGGCACTGC
51 CTCCGCCACC TACAAAGTGG ACGAATATCA CGCCAACGTC CGTTTCGCCA
101 TCGACCACTT CAACACCAGC ACCAAGCTCG GCGGTTTTTA CGGTCTGACC
151 GGTTCGGTCG AGTTCGATCA AGCAAAACGC GACGGCAAAA TCGACATCAC
201 CATTCCTGTC GCCAACCTGC AAAGCGGTTT GCAACCCTTC ACCGGCCACC
251 TGAAATCCGC CGACATCTTC GATGCCGCTC AATATCCGGA CATCCGCTTC
301 GTTTCACCA AATTCAACTT CAACGGCAAA AAAGTTGTTT CCGTTGACGG
351 CAACCTGACC ATGCCGCGCA AAACCGCCCC CGTCAAACCT AAAGCCGAAA
401 AATTCAACTG CTACCAAAGC CCGATGGCGG AAACCGAAGT TTGGCGCGGC
451 GACTTCAGCA CCACCATCGA CCGCACCAAA TGGGGCGTGG ACTACCTCGT
501 TAACGCGCGT ATGACCAAAA ACGTCCGCAT CGACATCCAA ATCGAAGCTG
551 CAAAACAATA A

```

This corresponds to the amino acid sequence <SEQ ID 2916; ORF 953.ng>:

g953.pep

```

1  MKKI IFAALA AAVGTASAT YKVDEYHANV RFAIDHFNTS TNVGGFYGLT
51  GSV EFDQAKR DGKIDITIPV ANLQSGSQPF TGHLSADIF DAAQYPDIRF
101 VST KFNFGK KLVSDGNLT MRGKTAPVKL KAEKFNCYQS PMAETEVCQG
151 DFST TIDRTK WGVDYLVNAG MTKNVRIDIQ IEAAKQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2917>:

m953.seq

```

1  ATGA AAAAAA TCATCTTCGC CGCACTCGCA GCCGCCGCCA TCAGTACTGC
51  CTCC GCCGCC ACCTACAAAG TGGACGAATA TCAGGCCAAC GCCCGTTTCG
101 CCAT CGACCA TTTCAACACC AGCACCACG TCGGCGGTTT TTACGGTCTG
151 ACCG GTTCCG TCGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACC ATCCCG ATTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCT GAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTG TTTCCA CCAAAATCAA CTCAACGGC AAAAACTGG TTTCCGTTGA
351 CGG AACCTG ACCATGCACG GCAAACCGC CCCCGTCAA CTCAAAGCCG
401 AAAA ATTCAA CTGCTACCAA AGCCCGATGG AGAAAAACGA AGTTGTGGC
451 GCG ACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGT AACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGC CAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2918; ORF 953>:

m953.pep

```

1  MKKI IFAALA AAAISTASAA TYKVDEYHAN ARFAIDHFNT STNVGGFYGL
51  TGSV EFDQAK RDGKIDITIP IANLQSGSQH FTDHLKSADI FDAQYQPDIR
101 FVST KFNFGK KLVSDGNLT TMHGKTAPVK LKAEKFNCYQ SPMEKTEVCG
151 GDFS TTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 953 shows 93.0% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. gonorrhoeae*

m953/g953 93.0% identity in 187 aa overlap

```

m953.pep      10      20      30      40      50      60
               MKKIIFAALAAAIASTASAAATYKVDEYHANARFAIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||::||| |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
g953           10      20      30      40      50
               MKKIIFAALAAAVGTASA-TYKVDEYHANVRFAIDHFNTSTNVGGFYGLTGSVEFDQAK
               10      20      30      40      50

m953.pep      70      80      90      100     110     120
               RDGKIDITIPIANLQSGSQHFTDHLKSADIFDAQYQPDIRFVSTKFNFGKLVSDGNL
               |||||::||| |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
g953           60      70      80      90      100     110
               RDGKIDITIPVANLQSGSQPFTHLKSADIFDAQYQPDIRFVSTKFNFGKLVSDGNL
               60      70      80      90      100     110

m953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKAKEFNQYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
               |||||::||| |||||::||| |||||::||| |||||::||| |||||::||| |||||::|||
g953           120     130     140     150     160     170
               TMRGKTAPVKLKAKEFNQYQSPMAETEVCAGDFSTTIDRTKWGVDYLVNAGMTKNVRIDI
               120     130     140     150     160     170

m953.pep      QIEAAKQX
               |||||
g953           QIEAAKQX
               180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2919>:

a953.seq

```

1  ATGAAAAAAA TCATCATCGC CGCGCTCGCA GCAGCCGCCA TCGGCACTGC
51  CTCCGCCGCC ACCTACAAAG TGGACGAATA TCAGGCCAAC GCCCGTTTCT
101 CTATCGACCA TTTCAACACC AGCACCACG TCGGCGGTTT TTACGGTCTG
151 ACCG GTTCCG TTGAGTTCGA CCAAGCAAAA CGCGACGGTA AAATCGACAT
201 CACCATCCCG GTTGCCAACC TGCAAAGCGG TTCGCAACAC TTTACCGACC
251 ACCTGAAATC AGCCGACATC TTCGATGCCG CCCAATATCC GGACATCCGC
301 TTTGTTTCCA CCAAAATCAA CTCAACGGC AAAAACTGG TTTCCGTTGA

```

1366

```

351 CCGCAACCTG ACCATGCACG GCAAAACCGC CCCCCTCAA CTCAAAGCCG
401 AAAAATTCAA CTGTACCAA AGCCGATGT TGAAAACCGA AGTTTGCGGC
451 GGC GACTTCA GCACCACCAT CGACCGCACC AAATGGGGCA TGGACTACCT
501 CGT TAACGTT GGTATGACCA AAAGCGTCCG CATCGACATC CAAATCGAGG
551 CAGCCAAACA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 2920; ORF 953.a>:

```

a953.pep
  1 MKKIIIAALA AAAIGTASAA TYKVDEYHAN ARFSIDHFNT STNVGGFYGL
 51 TGSVEFDQAK RDGKIDITIP VANLQSGSQH FTDHLKSADI FDAAQYDIR
101 FVSTKFNENG KKLVSVDGNL TMHGKTAPVK LKAKEFNCYQ SPMLKTEVCG
151 GDFSTTIDRT KWGMDYLVNV GMTKSVRIDI QIEAAKQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 953 shows 97.3% identity over a 187 aa overlap with a predicted ORF (ORF 953) from *N. meningitidis*

```

a953/m953      97.3% identity in 187 aa overlap

a953.pep      10      20      30      40      50      60
               MKKIIIAALAAAIGTASAAATYKVDEYHANAREFSIDHFNTSTNVGGFYGLTGSVEFDQAK
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953           MKKIIIFAALAAAISTASAAATYKVDEYHANAREFAIDHFNTSTNVGGFYGLTGSVEFDQAK
               10      20      30      40      50      60

a953.pep      70      80      90      100     110     120
               RDGKIDITIPVANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNENGKKLVSDGNL
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953           RDGKIDITIPANLQSGSQHFTDHLKSADIFDAAQYDIRFVSTKFNENGKKLVSDGNL
               70      80      90      100     110     120

a953.pep      130     140     150     160     170     180
               TMHGKTAPVKLKAKEFNCYQSPMLKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
               |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
m953           TMHGKTAPVKLKAKEFNCYQSPMEKTEVCGGDFSTTIDRTKWGMDYLVNVGMTKSVRIDI
               130     140     150     160     170     180

a953.pep      QIEAAKQX
               |||||
m953           QIEAAKQX

```

g954.seq not found yet

g954.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2921>:

```

m954.seq
  1 ATGAAAAAGT TTTATTTTGT GCTGCTGGCG TTGGGTTTGG CAGCGTGTGG
 51 GCAAGAACAA TCGCAGAAAG CTGATGCGGA GCAGTATTTT TTTGCCAATA
101 AATATCAATT TGCAGATGAG AACAGGCTT TTTATTTTGA ACGCGCCGCC
151 CGTTTCCGTG TATTGCAACA AGGCCTTGGC GGGGATTTTG AGAGGTTTTT
201 AAAAGGAGAA ATACCTAATC AAGAAAATCT TGCAAAGTAT CGTGAAAATA
251 TTA CTCAAGC AGTCGCTTAT TATGCGGACA CGAATGGAGA TGATGACCCA
301 TACCGCGTCT GCAAACAGGC TCGCAAGAT GCAGAAATCC TGATGAAGAG
351 TATGGTAACA AGCGGTGGAG GCGGTACAAC TGATTTAGAT AAGGAAAGTT
401 ATCAAAATTA CCGAAAATCA ATGCAAGAAT GCCGTAAAC AATAACGGAA
451 GCTGAAGCCA ATTTGCCGAA AAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2922; ORF 954>:

```

m954.pep
  1 MKKFYFVLLA LGLAACGQEQ SQKADAEQYF FANKYQFADE KQAFYFERAA
 51 RFRVLQOGLG GDFERFLKGE IPNQENLAKY RENITQAVAY YADTNGDDDP
101 YRVCKQAAQD AEILMKSMVT SGGGGTTDLN KESYQNYRKS MQECKRTITE
151 AEANLPKK*

```

a954.seq not found yet

a954.pep not found yet

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2923>:

g957.seq (partial)

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACAG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTG AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAAGGAATCG ATGAGGACGG AGGAAAGCCT TGCCGGAGCT GTGGATGACG
251 GTC CGTTGCA GTCGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCCAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GGAAGAGGTT TGGCTGGATT ACTATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTT CGCTTTC GCAACGCTCG CCGGAAGCGT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGCTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGATGAAG GCGAACAGTC TTGTGGTCCG
801 cta t gatgcg gacggtctgc CgcaAAAagt ctattggagt gtcgacaatg
851 gaa aaaaacc ccaaagtgtc gaattatttt tgaaaaacgg aaatcttttt
901 attgcccaat cttcgacggt aaccttgaaa acggatggcg taacggcgga
951 tatgcaaacc tatcatgcgc aacaacggt gtatttggat ggg...
```

This corresponds to the amino acid sequence <SEQ ID 2924; ORF 957.ng>:

g957.pep (partial)

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPENPNAFV
51  AKLARLFRNA DRAVVIVKES MRTEESLAGA VDDGPLEQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGEEV WLDYYIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTAHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FREESNRIAS DSRDYVFYQN
251 MRELMPRGNK ANSLVVG YDA DGLPQKVYWS VDNGKKPQSV EYLLKNGNLF
301 IAQSSTVTILK TDGVTADMQT YHAQQTLYLD G...
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2925>:

m957.seq

```

1  ATGTTTAAAA AATTCAAACC GGTACTGTTG TCATTTTTTG CACTTGTATT
51  TGCCTTTTGG CTGGGAACGG GTATTGCCTA TGAGATTAAT CCGCGTTGGT
101 TTTTGAGCGA TACGGCAACT GAAGTACCTA AAAATCCGAA TGCTTTTGTG
151 GCGAAACTTG CCCGCCTGTT CCGAAATGCC GACAGGGCGG TTGTCATCGT
201 GAAGGAATCG ATAAGGACGG AGGAAATCTT TGCCGGAAGT GTGGATGACG
251 TCCGCTTTCG GTCGAGAAG GATTATCTCG CGCTCGCTAT CCGGCTCAGT
301 CGTTTGAAAG AAAAGGCCAA ATGGTTTCAC GTAACGGAGC AGGAACATGG
351 GAAAGAGGTT TGGCTGGATT ACCATATCGG CGAGGGCGGT TTGGTTGCGG
401 TTT CGCTTTC GCAACGCTCG CCGGAAGCAT TTGTTAATGC CGAATATCTG
451 TATCGGAACG ATCGTCCGTT TTCTGTAAAT GTGTACGGCG GAACGGTTCA
501 CCGGGAAAAAT TATGAAACGA CAGGAGAATA TCGGGTTGTT TGGCAACCGG
551 ACGGTTCCGT ATTGATGCG GCGGGGCGCG GGAATATCGG GGAAGATGTT
601 TATGAGCATT GCCTCGGGTG TTATCAGATG GCCCAGGTAT ATTTGGCGAA
651 ATACCGGGAT GTCGCGAATG ACGAGCAGAA GGTTTGGGAC TTCCGCGAAG
701 AGAGCAACCG AATTGCGTCG GACTCGCGCA ATTCTGTGTT TTATCAGAAT
751 ATGCGGGAAT TGATGCCCCG AGGATGAAG GCGAACAGTC TTGTGGTCCG
801 CTATGATGCG GACGGTCTGC CGCAAAAAGT CTATTGGAGT TTCGACAATG
851 GAAAAAAACG CCAGAGTTTC GAATATTATT TGAAAAACGG AAATCTTTTT
901 ATTGCACAAT CTTGACGGT AGCATTGAAA GCGGATGGCG TAACGGCGGA
951 TATGCAAGAC TATCATGCGC AACAGACGTG GTATTGGAT GCGGGCGGA
1001 TTGTCCGCGA AGAGAAACAG GGAGACAGAC TGCCTGATTT TCCTTTGAAC
1051 TTGGAATAAT TGGAAAAAGA GGTGCGCCGT TATGCAGAGG CTGCGGCGAG
1101 ACGTTCGGGC GGCAGGCGCG ACCTTCTCTA CTGA
```

This corresponds to the amino acid sequence <SEQ ID 2926; ORF 957>:

m957.pep

```

1  MFKKFKPVLL SFFALVFAFW LGTGIAYEIN PRWFLSDTAT EVPKNPNAFV
51  AKLARLFRNA DRAVVIVKES IRTEENLAGT VDDGPLEQSEK DYLAALAIRLS
101 RLKEKAKWFH VTEQEHGKEV WLDYHIGEGG LVAVSLSQRS PEAFFVNAEYL
151 YRNDRPFSVN VYGGTVHGEN YETTGEYRVV WQPDGSVFDA AGRGKIGEDV
201 YEHCLGICYQM AQVYLAKYRD VANDEQKVWD FRKESNRIAS DSRNSVFYQN
```



1368

251 MREIMPRGMK ANSLVVG YDA DGLPQKVYWS FDNGKKRQSF EYILKNGNLF  
 301 IAQSSTVALK ADGVTADMOT YHAQQTWYLD GGRIVREEKQ GDRLPDFPLN  
 351 LENLEKEVRR YAEAAARRSG GRRDLSH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 957 shows 95.2% identity over a 331 aa overlap with a predicted ORF (ORF 957) from *N. gonorrhoeae*

g957/m957 95.2% identity in 331 aa overlap

	10	20	30	40	50	60
g957.pep	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPENPNFAVAKLARLFRNA					
m957	MFKKFKPVLLSFFALVFAFWLGTGIAYEINPRWFLSDTATEVPKNPNFAVAKLARLFRNA					
	10	20	30	40	50	60
g957.pep	DRAVVIVKESMRTEESLAGAVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGEEV					
m957	DRAVVIVKESIRTEENLAGTVDDGPLQSEKDYLALAIRLSRLKEKAKWFHVTEQEHGKEV					
	70	80	90	100	110	120
g957.pep	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLNRDRPFSVNVYGGTAHGENYETTGEYRVV					
m957	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLNRDRPFSVNVYGGTVHGENYETTGEYRVV					
	130	140	150	160	170	180
g957.pep	WQPDGVSFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS					
m957	WQPDGVSFDAAGRKGIGEDVYEHCLGICYQMAQVYLAKYRDVANDEQKVWDFRKESNRIAS					
	190	200	210	220	230	240
g957.pep	DSRDYVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSVDNGKKRQSF EYILKNGNLF					
m957	DSRNSVFYQNMRELMPRGMKANSLVVG YDADGLPQKVYWSFDNGKKRQSF EYILKNGNLF					
	250	260	270	280	290	300
g957.pep	IAQSSTVTLKTDGVTADMOTYHAQQTLYLDG					
m957	IAQSSTVALKADGVTADMOTYHAQQTWYLDGGRIVREEKQGDRLPDFPLNLENLEKEVRR					
	310	320	330	340	350	360
g957.pep	YAEAAARRSGGRRDLSHX					
m957	370					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2927>:

a957.seq

1	ATGTTTAAAA	AATTCAAACC	GGTACTGTTG	TCATTTTTTG	CACTTGTATT
51	TGCCCTTTGG	CTGGGAACGG	GTATTGCCCTA	TGAGATTAAT	CCGCGTTGGT
101	TTTTGAGCGA	TACGGCAACT	GAAAATCCGA	ATGCTTTTGT	GGCGAAACTT
151	GCCC CGCTGT	TCCGAAATGC	CGACAGGGCG	GTTGTCATCG	TGAAGGAATC
201	GATGAGGACG	GAGGAAAGTC	TTGCCGGAGC	TGTGGATGAC	GGTCCGTTGC
251	AGTCGGAGAA	GGATTATCTT	GCACTCGCTG	TCCGGCTCAG	TCGTTTGAAA
301	GAAAAGGCGA	AATGGTTTCA	CGTAACGGAG	CAGGAACATG	GGGAAGAGGT
351	TTGGCTGGAT	TACTATATCG	GCGAGGGCGG	TTTGGTTGCG	GTTTCGCTTT
401	CGCAACGCTC	GCCGGAAGCG	TTTGTTAATG	CCGAATATCT	GTATCGGAAC
451	GATCGTCCGT	TTTCTGTAAA	TGTGTACGGC	GGAACGGTTC	ACGGGGAAAA
501	TTATGAAACG	ACAGGAGAAT	ATCGGGTTGT	TTGGCAACCG	GACGGTTCGG
551	TATTTGATGC	GTCGGGGCGC	GGGAAAATCG	GGGAAGATGT	TTATGAGCAT
601	TGCCTCGGGT	GTTATCAGAT	GGCCAGGTA	TATTTGCGGA	AATATCGGGA
651	TGTCGCGAAT	GATGAGCAGA	AGGTTTGGGA	CTTCCGCGAA	GAGAGTAACC
701	GGATTGCGTC	GGAATCGGCG	GATTCTGTGT	TTTATCAGAA	TATGCGGGAA
751	TTGATGCCCC	GAGGGATGAA	GGCAAACAGT	CTTGTGGTCG	GCTATGATGC
801	GGACGGTCTG	CCGCAGAAAG	TCTATTGGAG	TTTCGACAAT	GGGAAAAAAC
851	GCCAGAGTTT	CGAATATTAT	TTGAAAAACG	GAAATCTTTT	TATTGCACAA
901	TCTTCGACGG	TAGCATTGAA	AGCGGATGGC	GTAACGGCGG	ATATGCAGAC

951 CTA TCATGCG CAACAGACGT GGTATTAGA TGGCGGCGG ATTGTCCGCG  
 1001 AAG AGAAACA GGGGACAGA CTGCCTGATT TTCCTTGAA CTTGGAAGAT  
 1051 TTG GAAAAAG AGGTGAGCCG TTATGCAGAG GCTGCGCGA GACGTTCCGG  
 1101 CGG CAGGCGC GACCTTTCTC ACTGA

This corresponds to the amino acid sequence <SEQ ID 2928; ORF 957.a>:

a957.pep  
 1 MFKKFKPVL SFFALVFAEW LGTGIAYEIN PRWFLSDTAT ENPNAFVAKL  
 51 ARLFRNADRA VVIVKESMRT EESLAGAVDD GPLQSEKDY LALAVRLSRLK  
 101 EKA KWFHVTE QEHGEEVWLD YYIGEGGLVA VLSQRSPEA FVNAEYLRYN  
 151 DRPFSNVYGT VHGNYET TGEYRVVWQP DGSVFDASGR GKIGEDVYEH  
 201 CLG CYQMAQV YLAKYRDVAN DEQKVWDFRE ESNRIASDSR DSVFYQNMRE  
 251 LMP RGMKANS LVVGYDADGL POKVYWSFDN GKKRQSFEYY LKNGNLFIAQ  
 301 SST VALKADG VTADMOTYHA QOTWYLDGGR IVREEKQGRD LPDFPLNLED  
 351 LEKEVSRYAE AAARRSGRR DLSH\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a957/m957 96.3% identity in 377 aa overlap

a957.pep	10 20 30 40 50	MFKKFKPVL SFFALVFAEW LGTGIAYEIN PRWFLSDTATE ---NPNAFVAKL ARLFRNA
m957	10 20 30 40 50 60	MFKKFKPVL SFFALVFAEW LGTGIAYEIN PRWFLSDTATE VPKNPNAFVAKL ARLFRNA
a957.pep	60 70 80 90 100 110	DRVVIVKESMRT EESLAGAVDD GPLQSEKDY LALAVRLSRLKEKAKWFHVTE QEHGEEV
m957	70 80 90 100 110 120	DRVVIVKESIRTEENLAGTVDD GPLQSEKDY LALAIRLSRLKEKAKWFHVTE QEHGKEV
a957.pep	120 130 140 150 160 170	WLDYYIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSNVYGGTVHGENYETTGEYRVV
m957	130 140 150 160 170 180	WLDYHIGEGGLVAVSLSQRSPEAFVNAEYLRYNDRPFSNVYGGTVHGENYETTGEYRVV
a957.pep	180 190 200 210 220 230	WQPDGVSVDASGRGKIGEDVYEHCLG CYQMAQVYLAKYRDVANDEQKVWDFREESNRIAS
m957	190 200 210 220 230 240	WQPDGVSVDASGRGKIGEDVYEHCLG CYQMAQVYLAKYRDVANDEQKVWDFRKNRIAS
a957.pep	240 250 260 270 280 290	DSRDSVFYQNMRELMPRGMKANS LVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF
m957	250 260 270 280 290 300	DSRNSVFYQNMRELMPRGMKANS LVVGYDADGLPQKVYWSFDNGKKRQSFEYYLKNGNLF
a957.pep	300 310 320 330 340 350	IAQSSTVALKADGVTADMOTYHAQOTWYLDGGRIVREEKQGRDLPDFPLNLEDLEKEVSR
m957	310 320 330 340 350 360	IAQSSTVALKADGVTADMOTYHAQOTWYLDGGRIVREEKQGRDLPDFPLNLENLEKEVRR
a957.pep	360 370	YAEAAARRSGRRDL SHX
m957		YAEAAARRSGRRDL SHX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2929>:

g958.seq  
 1 TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG  
 51 TTTCCGCACG CATTGCGCCG CCGATACCGT TCGCGCGGAA GAGGCGGACG

```

101 GCGGTGTCGC AGAAGGCGGT GCGCAGGGCG CGTCCGAATC CGCACAAGCT
151 TCCGATTGTA CCCTCGGTTT GACCTGCCTG TTTTGCACTA ACAGAAAGCGG
201 CAGC CCGGAG AGAACCAGAG CCGCCGTCCA AGGCAGCGGC GAAGCATCCG
251 TCCC CGAAGA CTATACGCGC ATTGTTGCCG ACAGGATGGA AGGACAGTCG
301 AAGGTTAAGG TGCAGCGCGA AGGAAGCGTT ATCATCGAAC GGGACGGCGC
351 AGTCCTCAAT ACCGATTGGG CGGATTACGA CCAGTCGGGC GACACCGTTA
401 CCGT AGGCGA CCGGTTGCGC CTCCAACAGG ACGGTACGCT GATTCGGGGC
451 GAAA CCCTGA CCTACAATCT CGATCAGCAG ACCGGCGAAG CGCACAACGT
501 CCGT ATGGAA ACCGAACAAG GCGGACGGCG GCTGCAAAAG GTCAGCCGCA
551 CCGC CGAAAT GTTGGGCGAA GGGCGTTACA AACTGACGGA AACCCAATTC
601 AACA CCTGTT CCGCCGGAGA TGCCGGCTGG TATGTCAAGG CCGCCTCTGT
651 CGAA CCGGAT CGGGGAAAAG GCATAGGCGT TGCCAAACAC GCCGCCTTCG
701 TGTT CCGCGG CGTTCCCTTT TTCTATACGC CTTGGGCGGA CTTCCCGCTT
751 GACG GCAACG GCAAAAGCGG ACTGCTCGTC CCGTCCGTAT CTGCGCGTTC
801 GGAC GCGGTT TCCCTTTCCG TCCCTTATTA TTTCAACCTT GCCCCCAACT
851 TCGA TGCCAC TTTCGCCCCC GGCATTATCG GCGAACCGCG CGCGACGTTT
901 GACG GACAAA TCCGTTACCT GCGTCCGAT TACAGCGGAC AGACCGACCT
951 GACCTGGTTG CCGCAGGATA AGAAAAGCGG CAGGAACAAC CGCTATCAGG
1001 CAAA ATGGCA GCACCGGCAC GACATTTCCG ACACGCTTCA GGCGGGTGTC
1051 GATT TCAACC AAGTCTCCGA CAGCGGCTAC TACCGCGACT TTTACGGCGG
1101 CGAA GAAATC GCCGGCAACG TCAACCTCAA CCGCCGCGTA TGGCTGGATT
1151 ATGG CCGCAG GCGGCGGGA GGCAGCCTGA ATGCGGCGCT TTCGGTTCAG
1201 AAAT ACCAGA CGCTGGCAAA CCAAGAGCGG TACAAAGACG AACCTTACGC
1251 CATC ATGCCC CGCCTTTCTG CCGATTGGCA TAAAAACGCA GGCAGGGCGC
1301 AAAT CGGCGT GTCCGCACAA TTTACCCGCT TCAGCCACGA CGGCCGCCAA
1351 GACG GAGGCC GACTGGTCTG GTATCCCGGT ATCAAATGGG ATTTACAGCA
1401 CAGC TGGGGC TACGTCCGCC CCAAACCTCG GCTGCACGCC ACTTATTACA
1451 GCCT CGACAG TTTGCGCGGC AAAGCATCCC GCAGCGTCGG GCGCGTTTGT
1501 CCGG TTGTCA ATATCGACGG CCGCACAACC TTCGAACGCA ATACGCGCCT
1551 GTTC GCGCGC GGAGTCGTGC AAACCATCGA GCCGCGCCTG TTCTACAAC
1601 ATAT TCCTCG CAAATCTCAA AACGACCTGC CCAATTTTCA TTCGTCGGAA
1651 AGCA GCTTCG GCTACGGGCA GCTTTTCCGC GAAAACCTCT ATTACGGCAA
1701 CGAC CGCATC AACGCCGCCA ACAGCCTTTC CACCGCCCTG CAGAGCCGTA
1751 TTTT GAGCGG CGCGACGGGG GAGGAGCGTT TCCGCGCCGG TATCGGTGAG
1801 AAAT TCTATT TCAAGGATGA TCGGTTGATG CTTGACGGCA GCGTCGGCAA
1851 AAAT CCGCGC AGCGTTCCG ACTGGGTGGC ATTCCGCTCC GCGGCGATAG
1901 CGGG GCGGTT CACCTTCGAC AGCAGCATCC ACTACAACCA AACGACAAA
1951 CCGC CCGAAG ATTACGCGGT CCGCGCAGCG TACCGCCCGC CCGCCGGA
2001 AGTG TTGAAC GCCCGCTACA AATACGGGCG CAACGAAAAA ATCTACCTGC
2051 AGGC GAGCGG TTCCTATTTT TACGACAAAC TCAGCCAGCT CGACCTGTCC
2101 GCAC AATGGC CGCTGACGCG CAACCTGTCT GCCGTGCTCC GCTACAAC
2151 CCGT TTTGAA GCCAAAAAAC CGATAGAAAT GCTTGCCGCT GCAGAATACA
2201 AAAG CAGTTG CCGCTGCTGG GCGCGGGGCG GTACGCCCA ACCTACGTT
2251 ACCG GCGAAA ACACCTACAA AAACGCGCTC TTTTTCAC TTCAATTGAA
2301 AGAC CTCAGC AGCGTCGGCA GAAACCCCGC AGCGAGGATG GATGTCGCGG
2351 TTCC CGGCTA CATCCCCGCC CACTCTCTTT CCGCCGAGC CAACAAACGG
2401 CCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2930; ORF 958.ng>:

```

g958.pep
1  LARLFSLKPL VLALGFCEFT HCAADTVAAE EADGRVAEGG AOGASESAQA
51  SDLTLGSTCL FCSNESGSPE RTEAAVQSGS EASVPEDYTR IVADRMGQS
101 KVKVRAEGSV IIERDGAFLN TDWADYDQSG DTVTVGDRFA LQDGTLLRG
151 ETLYTNLDQO TGEAHNVME TEQGGRRLOS VSRTEMLGE GRYKLTETQF
201 NTCASAGDAGW YVKAASVEAD RGKGIGVAKH AAFVFGGVPL FYTPWADFPL
251 DGNRKSGLLV PSVSAGSDGV SLSVPYYFNL APNFDATFAP GIIGERGATF
301 DGQIRYLPRD YSGQDITLWL PHDKKSGRNN RYQAKWQHRH DISOTLQAGV
351 DFNQVSDSGY YRDFYGGEEI AGNVNLRNRV WLDYGGRAAG GSNAGLSVQ
401 KYQTLANQSG YKDEPYAIMP RLSADWHKNA GRAQIGVSAQ FTRFSHDGRQ
451 DGSRLVVYPG IKWDFSNSWG YVRPKLGLHA TTYSLDSFGG KASRSVGRVL
501 PVVNIDGGTT FERNTLFGG GVVQTIERPL FYNYPKASQ NDLPNFDSSSE
551 SSFGYQGLFR ENLYYGNDR I NAANSLSTAV QSRILDGATG EERFRAGIGQ
601 KFYFKDDAVM LDGSGVGNPR SRSDWVAFAS GGIGGRFTLD SSIHYNQNDK
651 RAEHYAVGAG YRPAPGKVLN ARYKYGRNEK IYLOADGSYF YDKLSQLDLS
701 AQWPLTRNLS AVVRYNYGFE AKKPIENLAG AEYKSSCGCW GAGVYAQRVY
751 TGENTYKNAV FFSLQLKDLN SVGRNPAGRM DVAVPGYIPA HSLSAGRNKR
801 P*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2931>:

```

m958.aeq
1  TTGGCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCCTCTG
51  CTTCCGCGAC CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGAA AGCGTTCGGA GCGTGTCCGA ACCCATAACG

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151 CCTACCAGCC TGAGCCTCGG TTCGACCTGC CTGTTTGTCA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACCG AAGCCGCCGT CCAAGGCAGC GGCGAAGCAT
251 CCA TCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTGC AACGCAACCG
351 GACGACCCTC AATACCGATT GGGCGGATTA CGACCAGTCG GGCGACACCG
401 TTA CCGCAGG CGACCGGTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGC GAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGT CCGCATG GAAATCGAAC AAGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCA CCGCCGA AATGTTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTC AACACCT GTTCCGCCG CGATGCCGGC TGGTATGTCA AGGCAGCCTC
651 TGT CGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCT
701 TCG TGTTCCG CGGCGTTCCC ATTTTCTACA CCCCTTGGCG GGAATTCCTG
751 CTT GACGGCA ACCGCAAAAG CGGCCTGCTT GTTCCCTCAC TGTCCGCCGG
801 TTC GGACGGC GTTTCCTTT CCGTTCCTTA TTATTTCAAC CTGCCCCCA
851 ATC TCGATGC CAGTTCGCG CCCAGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTT GACGGGC AGGTACGCTA CCTGCGGCGG GATTATGCCG GCCAGTCCGA
951 CCT GACCTGG CTGCCGCACG ACAAGAAAAG CCGCAGGAAT AACCGCTATC
1001 AGG CGAAATG GCAGCATCGG CACGACATT CCGACACGCT TCAGCGGGGT
1051 GTC GATTTCG ACCAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAA CAAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCCGT GTATGGCTGG
1151 ATT ATGGCGG CAGGCGGGCG GCGGCGAGCC TGAATGCCGG CTTTCGGTT
1201 CTG AATACC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAAACCGTA
1251 TGC CCTCATG CCGCGCCTTT CGGTGAGTG GCGTAAAAAC ACCGCGAGGG
1301 CGC AATCGG CGTGTCCGCA CAATTTACCC GATTACAGCA CGACAGCCGC
1351 CAA GACGGCA GCCGCCTGGT CGTCTATCCC GACATCAAAAT GGGATTTCAG
1401 CAACAGCTGG GGCTATGTCC GTCCCAAAT CGGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCGACGCGT CAGCCGCACT
1501 CTG CCCATTG TCAACATCGA CAGCGCGGCA ACTTTTGAGC GGAATACGCG
1551 GAT GTTCGGC GGAGAAGTCC TGCAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACT ATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGTCG
1651 GAA AGCAGCT TCGGTACGG GCAGCTCTT CGCGAAAACC TCTATTACGG
1701 CAACGACAGG ATTAACACCG CAAACAGCCT TTCCGCCGCC GTGCAAGGCC
1751 GTATTTTGGG CGGCGCGACG GGGGAAGAGC GTTCCGCGC CGGCATCGGT
1801 CAG AATCTT ATTCAAGGA TGATGCGGTG ATGCTTGACG GCAGCGTCGG
1851 CAAAAACCG CGCAACCGTT CCGACTGGGT GGCATTTGCC TCCGCGAGCA
1901 TCGGCGAGCG CTTTCATCCT GACAGCAGCA TCCACTACAA CAAAAACGAC
1951 AAACGCGCGG AGAAGTACGC CGTCGGTGCA AGTACCCTC CCGCACAGGG
2001 CAAAGTCTG AACGCCCCGT ACAATACGG GCGCAACGAA AAAATCTACC
2051 TGAAGTCCGA CGGTTCTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GCGCGCTGAC GCGCAACCTG TCGGCGGTCC TCCGTTACAA
2151 CTACGGTTT GAAGCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACAAAAGCAG TTGCGGCTGC TGGGGCGCGG GCGTGTACGC CCAACGCTAC
2251 GTTACCGGCG AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAAAGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCCCG CTATATCACC GCCACTCTC TTTCCGCCG ACGCAACAA
2401 CGACCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2932; ORF 958>:

m958.pep

```

1 LARLFSLKPL VLALGLCFGT HCAAADAVAA EETDNPTAGE SVRSVSEPIQ
51 PTLSLGSLG LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMERGQ
101 SQVQVRAEGN VVVERNRTTL NTDWADYDQS GDTVTAGDRF ALQODGTLIR
151 GETLTYNLEQ QTGEAHNVRM EIEQGRRRLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFVFGVGP IFYTPWADFP
251 LDGNNRKSGLL VPSSLAGSDG VLSVPYYFN LAPNLDATFA PSVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSINAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSVEWRN TGRAQIGVSA QFTRFSDHRS
451 QDGSRLVVPY DIKWDFNSW GYVRPKLGLH ATYYSNREFG SQEARRVSRT
501 LPIVNIDSGA TFERNTRMFG GEVLQTLPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYQLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKDDAV MLDGSVGKKP RNRSDWVAFV SGISGRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVVRYNYGF EAKKPIEVLA GAELYKSSCG WGAGVYAORY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIT AHSLSAGRNK
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 958 shows 89.3% identity over a 802 aa overlap with a predicted ORF (ORF 958) from *N. gonorrhoeae*

1372

m958/g958 89.3% identity in 802 aa overlap

	10	20	30	40	50	60
m958.pep	LARLFSLKPLVLALGLCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
g958	LARLFSLKPLVLALGLCFGTHCAA-DTVAEEADGRVAEGGAQGASESAQASDLTLGSTC					
	10	20	30	40	50	
	70	80	90	100	110	120
m958.pep	LFCSNESGSPERTEAAVQGSGEASIPEDYTRIVADRMEGSQVQVRAEGNVVVERNRTTL					
g958	LFCSNESGSPERTEAAVQGSGEASVPEDYTRIVADRMEGSQSKVKVRAEGSVIERDGAVL					
	60	70	80	90	100	110
	130	140	150	160	170	180
m958.pep	NTDWADYDQSGDVTVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ					
g958	NTDWADYDQSGDVTVTGDRFALQQDGTLRGETLTYNLDQQTGEAHNVRMETEQGGRRRLQ					
	120	130	140	150	160	170
	190	200	210	220	230	240
m958.pep	SVSRTAEMLGEGHYKLTETQFNTCSAGDAGWYVKAASVEADREKGIGVAKHAAFFVGGVVP					
g958	SVSRTAEMLGEGRYKLTETQFNTCSAGDAGWYVKAASVEADRGKIGVAKHAAFFVGGVVP					
	180	190	200	210	220	230
	250	260	270	280	290	300
m958.pep	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLVPYYFNLPNLDATFAPSVIGERGAV					
g958	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLVPYYFNLPNLDATFAPGIIGERGAT					
	240	250	260	270	280	290
	310	320	330	340	350	360
m958.pep	FDGQVRYLRPDYAGQSDLTWLPDHDKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
g958	FDGQIRYLRPDYSGQTDLTWLPDHDKSGRNNRYQAKWQHRHDSITLQAGVDFNQVSDSG					
	300	310	320	330	340	350
	370	380	390	400	410	420
m958.pep	YYRDFYGNKEIAGNVNLRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
g958	YYRDFYGGEEIAGNVNLRVWLDYGGRAAGGSLNAGLSVQKYQTLANQSGYKDEPYAIM					
	360	370	380	390	400	410
	430	440	450	460	470	480
m958.pep	PRLSVEWRKNTGRAQIGVSAQFTRFSHDSRQDGSRLVVYPDIKWDFSNSWGYVRPKLGLH					
g958	PRLSADWHKNAGRAQIGVSAQFTRFSHDSRQDGSRLVVYPGIKWDFSNSWGYVRPKLGLH					
	420	430	440	450	460	470
	490	500	510	520	530	540
m958.pep	ATYYSLNRFSGQEARRVSRTPIVNIDSGATFERNTRMFGEVLQTLERLFFNYIPAKS					
g958	ATYYSLDSFGGKASRSVGRVLPVVNIDGGTTFERNTRLFGGGVVQTIEPRLFFNYIPAKS					
	480	490	500	510	520	530
	550	560	570	580	590	600
m958.pep	QNDLPNFDSESSFGYGQLFRENLYYGNDRINTANSLAAVQSRILDGATGEERFRAGIG					
g958	QNDLPNFDSESSFGYGQLFRENLYYGNDRINAANSLSTAVQSRILDGATGEERFRAGIG					
	540	550	560	570	580	590
	610	620	630	640	650	660
m958.pep	QKFYFKDDAVMLDGSVGKKPRNSDWVAFASGSIGSRFILDSSIHYNQNDKRAENYAVGA					
g958	QKFYFKDDAVMLDGSVGKNPRNSDWVAFASGGIGGRFTLDSSIHYNQNDKRAEHYAVGA					
	600	610	620	630	640	650
	670	680	690	700	710	720
m958.pep	SYRPAQGVNLRARYKYGRNEKIYLSKSDGSYFYDKLSQLDLAQWPLTRNLSAVVRYNYGF					
g958	GYRPAQGVNLRARYKYGRNEKIYLAQDGSYFYDKLSQLDLAQWPLTRNLSAVVRYNYGF					
	660	670	680	690	700	710

1373

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          730      740      750      760      770      780
m958.pep  EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR
          |||||
g958      EAKKPIEMLAGAAYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPAGR
          72 O      730      740      750      760      770

          790      800
m958.pep  MDVAVPGYITAHSLSAGRNRKP
          |||||
g958      MDVAVPGYIPAHSLSAGRNRKPX
          78 O      790      800

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2933>:

```

a958.seq
1  TTG GCTCGTT TATTTTCACT CAAACCACTG GTGCTGGCAT TGGGCTTCTG
51  TTT CGGCACG CATTGCGCCG CCGCCGATGC CGTTGCGGCG GAGGAAACGG
101 ACAATCCGAC CGCCGGAGGA AGCGTTCGGA GCGTGTCCGA ACCCATACAG
151 CCTACCAAGC TGAGCCTCGG TTCGACCTGC CTGTTTTCGA GTAACGAAAG
201 CGGCAGCCCC GAGAGAACC GAGCCGCGGT CCAAGGCAGC GGCGAAGCAT
251 CCA TCCCCGA AGACTATACG CGCATTGTTG CCGACAGGAT GGAAGGACAG
301 TCGCAGGTGC AGGTGCGTGC CGAAGGCAAC GTCGTCGTCG AACGCAATCG
351 GACGACCCCTC AATGCCGATT GGGCGGATTA CGACCAGTCG GCGGACACCG
401 TTA CCGCAGG CGACCGGTTC GCCCTCCAAC AGGACGGTAC GCTGATTCCG
451 GGC GAAACCC TGACCTACAA TCTCGAGCAG CAGACCGGGG AAGCGCACAA
501 CGT CCGTATG GAAACCGAAC ACGGCGGACG GCGGCTGCAA AGCGTCAGCC
551 GCA CCGCCGA AATGTGGGC GAAGGGCATT ACAAACTGAC GGAAACCCAA
601 TTC AACACCT GTTCCGCCG CGATGCCGCG TGGTATGTCA AGGCCGCTTC
651 CGT CGAAGCC GATCGGGAAA AAGGCATAGG CGTTGCCAAA CACGCCGCCCT
701 TCG TGTTCGG CGGCGTTCCC ATTTTCTACA CCCCTTGGGC GGACTTCCCG
751 CTT GACGGCA ACCGCAAAAG CGGCCTGCTC GTTCCCTCAC TGTCCGCCGG
801 TTC GGACGGC GTTTCCTTT CCGTTCCTTA TTATTTCAAC CTTGCCCCCA
851 ATC TCGATGC CACGTTCCGC CCCGGCGTGA TCGGCGAAGC CGGCGCGGTC
901 TTT GACGGGC AGGTACGCTA CTTGCCGCCG GATTATGCCG GCCAGTCCGA
951 CCT GACCTGG CTGCGGCACG ACAAGAAAAG CGGCAGGAAT AACCCTATC
1001 AGG CGAATG GCAGCACCAG CACGACATTT CCGACACGCT TCAGGCGGGT
1051 GTC GATTTC AACAAGTCTC CGACAGCGGC TACTACCGCG ACTTTTACGG
1101 CAA CAAGAA ATCGCCGGCA ACGTCAACCT CAACCGCGCT GTATGGCTGG
1151 ATT ATGGCGG CAGGGCGGCG GCGGCGAGCC TGAATGCCGG CCTTTCGGTT
1201 CTG AATATAC AGACGCTGGC AAACCAAGC GGCTACAAAG ACAACCCGTA
1251 TGC CCTGATG CCGCGCCTT CCGCCGATTG GCGCAAAAC ACCGGCAGGG
1301 CGC AATCGG CGTGTCCGCC CAATTTACCC GCTTCAGCCA CGACAGCCGC
1351 CAA GACGGCA GCGGCTCGT CGTCTATCCC GACATCAAT GGGATTTACG
1401 CAACAGCTGG GGTACGTCC GTCCCAAAC CCGACTGCAC GCCACCTATT
1451 ACAGCCTCAA CCGCTTCGGC AGCCAAGAAG CCCGACGCGT CAGCGCACT
1501 CTGCCCATCG TCAACATCGA CAGCGGCATG ACCTTCGAAC GCAATACCGC
1551 GAT GTTCGGC GCGGAGTCC TGCAAAACCT CGAGCCGCGC CTGTTCTACA
1601 ACT ATATTCC TGCCAAATCC CAAAACGACC TGCCCAATTT CGATTCTGCG
1651 GAA AGCAGCT TCGGCTACGG GCAGCTTTT CGTGAAACCT TCTATTACGG
1701 CAA CGACAGG ATTAACACCG CAAACAGCCT TTCCGCGCGC GTGCAAAGCC
1751 GTATTTTGGG CCGCGCGACG GGGGAAGAGC GTTTCGCGC CGGCATCGGG
1801 CAG AATTTCT ACTTCAAAAA CGACGCGATC ATGCTTGACG GCAGTGTCCG
1851 CAAAAAACCG CGCAGCCGTT CCGACTGGGT GGCATTGCGC TCCAGCGGCA
1901 TCGGCAGCCG CTTTATCCTC GACAGCAGCA TCCACTACAA CCAAACGAC
1951 AAACGCGCCG AGAACTACGC CGTCCGTGCA AGCTACCGTC CCGCACAGGG
2001 CAA AGTGCTG AACGCCCGCT ACAAAATACG GCGCAACGAA AAAATCTACC
2051 TGA AGTCCGA CGGTTCTTAT TTTTACGACA AACTCAGCCA GCTCGACCTG
2101 TCCGCACAAT GCGCGCTGAC GCGCAACCTG TCGGCGCTCG TCCGTTACAA
2151 CTACGGTTTT GAAGCCAAAA AACCGATAGA GGTGCTGGCG GGTGCGGAAT
2201 ACA AAGCAG TTGCGGCTGC TGGGGCGCGG CGGTGTACGC CCAACGCTAC
2251 GTTACCGGGC AAAACACCTA CAAAACGCT GTCTTTTCT CACTTCAGTT
2301 GAA AGACCTC AGCAGTGTG GCAGAAACCC CGCAGACAGG ATGGATGTG
2351 CCGTTCCCGG CTATATCCCC GCCCACTCTC TTTCCGCGG ACGCAACAAA
2401 CGGCCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 2934; ORF 958.a>:

```

a958.pep
1  LARLFSLKPL VLALGFCEFGT HCAAADAVAA EETDNPTAGG SVRSVSEPIQ
51  PLSLSLGSST LFCSNESGSP ERTEAAVQGS GEASIPEDYT RIVADRMEOGQ
101 SQVQVRAEGN VVVERNRTTL NADWADYDQS GDTVTAGDRF ALQQDGLTIR
151 GETLTYNLEQ QTGEAHNVRM ETEHGGRRLLQ SVSRTAEMLG EGHYKLTETQ
201 FNTCSAGDAG WYVKAASVEA DREKGIGVAK HAAFFVGGVP IFYTPWADFP

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1374

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251 LDGNNRSGLL VPSLSAGSDG VSLSPYYFN LAPNLDATFA PGVIGERGAV
301 FDGQVRYLRP DYAGQSDLTW LPHDKKSGRN NRYQAKWQHR HDISDTLQAG
351 VDFNQVSDSG YYRDFYGNKE IAGNVNLNRR VWLDYGGRAA GGSNLAGLSV
401 LKYQTLANQS GYKDKPYALM PRLSADWRKN TGRAQIGVSA QFTRFSHDSR
451 QDGSRVLVYP DIKWDFSNSW GYVRPKLGLH ATYYSLNRFQ SQEARRVSRT
501 LPIVNIDSGM TFERNTRMFG GGVLTQLEPR LFYNYIPAKS QNDLPNFDSS
551 ESSFGYGOLF RENLYYGNDR INTANSLSAA VQSRILDGAT GEERFRAGIG
601 QKFYFKNDV MLDGSVGGKP RSRSDWVFA SSGIGSRFIL DSSIHYNQND
651 KRAENYAVGA SYRPAQGVK NARYKYGRNE KIYKSDGSY FYDKLSQLDL
701 SAQWPLTRNL SAVRYNYGF EAKKPIEVL GAEEKSSCGC WGAGVYAQRY
751 VTGENTYKNA VFFSLQLKDL SSVGRNPADR MDVAVPGYIP AHSLSAGRKN
801 RP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 957 shows 96.3% identity over a 377 aa overlap with a predicted ORF (ORF 957) from *N. meningitidis*

a958/m958 98.1% identity in 802 aa overlap

	10	20	30	40	50	60
a958.pep	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGGSVRSVSEPIQPTSLSLGSTC					
m958	LARLFSLKPLVLALGFCFGTHCAAADAVAAEETDNPTAGESVRSVSEPIQPTSLSLGSTC					
	10	20	30	40	50	60
	70	80	90	100	110	120
a958.pep	LFCSNESGSPERTEAAVQSGEASIPEDYTRIVADRMEGQSQQVRAEGNVVVERNRTL					
m958	LFCSNESGSPERTEAAVQSGEASIPEDYTRIVADRMEGQSQQVRAEGNVVVERNRTL					
	70	80	90	100	110	120
	130	140	150	160	170	180
a958.pep	NADWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVRMETEHGGRRLQ					
m958	NTDWADYDQSGDVTAGDRFALQQDGTLRGETLTYNLEQQTGEAHNVMEIEQGGRRRLQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
a958.pep	SVSRTAEMLGEGHYKLTETQFNCTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVP					
m958	SVSRTAEMLGEGHYKLTETQFNCTCSAGDAGWYVKAASVEADREKIGVAKHAAFFVGGVP					
	190	200	210	220	230	240
	250	260	270	280	290	300
a958.pep	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSPYYFNLAAPNLDATFAPGVIGERGAV					
m958	IFYTPWADFPLDGNRKSGLLVPSLSAGSDGVSLSPYYFNLAAPNLDATFAPSVIGERGAV					
	250	260	270	280	290	300
	310	320	330	340	350	360
a958.pep	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
m958	FDGQVRYLRPDYAGQSDLTWLPDCKKSGRNNRYQAKWQHRHDISDTLQAGVDFNQVSDSG					
	310	320	330	340	350	360
	370	380	390	400	410	420
a958.pep	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
m958	YYRDFYGNKEIAGNVNLNRRVWLDYGGRAAGGSLNAGLSVLKYQTLANQSGYKDKPYALM					
	370	380	390	400	410	420
	430	440	450	460	470	480
a958.pep	PRLSADWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
m958	PRLSADWRKNTGTRAQIGVSAQFTRFSHDSRQDGSRLVVPDIKWDFSNSWGYVRPKLGLH					
	430	440	450	460	470	480
	490	500	510	520	530	540
a958.pep	ATYYSLNRFQSGEARRVSRTLPVNIIDSGMTFERNTRMFGGGVLTQLEPRLFYNYIPAKS					
m958	ATYYSLNRFQSGEARRVSRTLPVNIIDSGMTFERNTRMFGGGVLTQLEPRLFYNYIPAKS					

1375

	490	500	510	520	530	540
a958.pep	550	560	570	580	590	600
	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLAAVQSRILDGATGEERFRAGIG					
m958	QNDLPNFDSSSESSFGYGQLFRENLYYGNDRIANTANSLAAVQSRILDGATGEERFRAGIG					
	550	560	570	580	590	600
a958.pep	610	620	630	640	650	660
	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
m958	QKFYFKNDVAVMLDGSVGGKPRSRSDWVAFASSGIGSRFILDSSIHYNQNDKRAENYAVGA					
	610	620	630	640	650	660
a958.pep	670	680	690	700	710	720
	SYRPAQGVNLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRYNYGF					
m958	SYRPAQGVNLNARYKYGRNEKIYKSDGSYFYDKLSQDLDSAQWPLTRNLSAVVRYNYGF					
	670	680	690	700	710	720
a958.pep	730	740	750	760	770	780
	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
m958	EAKKPIEVLAGAEYKSSCGCWGAGVYAQRYVTGENTYKNAVFFSLQLKDLSSVGRNPADR					
	730	740	750	760	770	780
a958.pep	790	800				
	MDVAVPGYIPAHSLSAGRNRKPX					
m958	MDVAVPGYIPAHSLSAGRNRKP					
	790	800				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2935>:

g959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCGCC GCCGCAACCG CACTGTGCG
51  CATTTCCGCC CCCGCACTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACGGCAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCGGC TTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACG ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2936; ORF 959.ng>:

g959.pep

```

1  MNIKHLLLTA AATALLGISA PALAHHDGHG DDDHGHAHQ HGKQDKIISR
51  AQAEEKAANAR VGGKITDIDL EHDGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2937>:

m959.seq

```

1  ATGAACATCA AACACCTTCT CTTGACCTCC GCCGCAACCG CACTGCTGAG
51  CATTTCCGCC CCCGCGCTCG CCCACCACGA CGGACACGGC GATGACGACC
101 ACGGACACGC CGCACACCAA CACAACAAAC AAGACAAAT CATCAGCCGC
151 GCCCAAGCCG AAAAAGCAGC GTTGGCGCGT GTCGGCGGCA AAATCACCAG
201 CATCGATCTC GAACACGACA ACGGCCGTCC GCACTATGAT GTCGAAATCG
251 TCAAAAACGG ACAGGAATAC AAAGTCGTTG TCGATGCCCG TACCGGCCCG
301 GTGATTTCTT CCCGCCGCGA CGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 2938; ORF 959>:

m959.pep

```

1  MNIKHLLLTS AATALLSISA PALAHHDGHG DDDHGHAHQ HNKQDKIISR
51  AQAEEKAALAR VGGKITDIDL EHDNGRPHYD VEIVKNGQEQ KVVVDARTGR
101 VISSRRDD*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 959 shows 95.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. gonorrhoeae*



m959/g959 95.4% identity in 108 aa overlap

	10	20	30	40	50	60
m959.pep	MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	:     :     :     :     :     :					
g959	MNIKHLLLTAAATALLGISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	10	20	30	40	50	60
	70	80	90	100	109	
m959.pep	VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	:     :     :     :     :     :					
g959	VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2939>:

a959.seq

1	ATGAACTTCA	AACGCCTTCT	CTTGACCGCC	GCCGCAACCG	CACTGATGGG
51	CATTTCCTCG	CCCGCACTCG	CCCACCACGA	CGGACACGGC	GATGACGACC
101	ACGGACACGC	CGCACACCAA	CACAGCAAAC	AAGACAAAAT	CATCAGCCGC
151	GCCCAAGCCG	AAAAAGCAGC	GTTGGCGCGT	GTCGGCGGCA	AAATCACCAG
201	CATCGATCTC	GAACACGACA	ACGGCCGTCC	GCACTATGAT	GTCGAAATCG
251	TCAAAAACGG	ACAGGAATAC	AAAGTCGTTG	TCGATGCCCG	TACCGGCCGC
301	GTGATTTCCT	CCCGCCGCGA	CGACTGA		

This corresponds to the amino acid sequence <SEQ ID 2940; ORF 959.a>:

a959.pep

1	MNFKRLLTLTA	AATALMGISA	PALAHHDGHG	DDDHGHAHQ	HSKQDKIISR
51	AQAEEKAALAR	VGGKITDIDL	EHNDNGRPHYD	VEIVKNGQEY	KVVVDARTGR
101	VISSRRDD*				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 959 shows 94.4% identity over a 108 aa overlap with a predicted ORF (ORF 959) from *N. meningitidis*

a959/m959 94.4% identity in 108 aa overlap

	10	20	30	40	50	60
a959.pep	MNFKRLLLTAAATALMGISAPALAHHDGHGDDDHGHAHQHNSKQDKIISRAQAEKAALAR					
	:     :     :     :     :     :     :					
m959	MNIKHLLLTSAATALLSISAPALAHHDGHGDDDHGHAHQHNKQDKIISRAQAEKAALAR					
	10	20	30	40	50	60
	70	80	90	100	109	
a959.pep	VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	:     :     :     :     :     :					
m959	VGGKITDIDLEHDNGRPHYDVEIVKNGQEYKVVVDARTGRVISSRRDDX					
	70	80	90	100		

g960.seq not found yet

g960.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2941>:

m960.seq

1	ATGCAAGTAA	ATATTCAGAT	TCCCTGTATG	CTGTACAGAC	GCGGGAGTGT
51	TAAGCCCCC	TTGTTGAAG	CTCCGCGGCT	CCTGCCGAGC	TTCACCGACC
101	CCGTGTGTC	CAAGCTCTCT	GCTCCCGGCG	GCTACATTGT	CGACATCCCC
151	AAAGGCAATC	TGAAAACCGA	AATCGAAAAG	CTGGCCAAAC	AGCCCCAGTA
201	TGCCCTATCTG	AAACAGCTCC	AAGTAGCGAA	AAACGTCAAC	TGGAACCAGG
251	TGCAACTGGC	TTACGATAAA	TGGGACTATA	AGCAGGAAGG	CTTAACCAGA
301	GCCGGTGCG	CGATTATCGC	GCTGGCTGTT	ACCGTGGTTA	CTGCGGGCGC
351	GGGAGTCGGA	GCCGCACTAG	GCTTAAACGG	CGCAGCCGCA	GCAGCGGCCG
401	ATGCCGCCTT	TGCCTCACTC	GCTTCTCAGG	CTTCCGTATC	GCTCATCAAC
451	AATAAAGGGC	ATGTCGGCAA	AACCTGAAG	GAACCTGGCA	GAAGCCGCAC
501	GGTAAAAAAT	CTGGTTGTAG	CGGCGGCAAC	GGCAGGCGTA	TCCAACAAAC

```

551 TCGGTGCCCTC TTCCCTTGCC ACTTGGAGCG AAACCCCTTG GGTAAACAAC
601 CTC AACGTTA ACCTGGCCAA TCGGGGCGAGT GCCGCGCTGA TCAACACCGC
651 TGT TAACGGC GGCAGCCTGA AAGACAATCT GGAGGCAAT ATCCTGGCGG
701 CAT TGGTGAA TACCGCGCAT GGGGAGGCGG CGAGTAAGAT CAAAGGACTG
751 GAT CAGCACT ATGTGCCCCA CAAAATCGCT CATGCCGTAG CGGGCTGTGC
801 GGC TGCAGCG GCGAATAAGG GCAAAATGTCA GGACGGCGCG ATCGGTGCGG
851 CTGTGGGTGA GATTGTGCGG GAGGCTTGG TTAATAATAC CGATTTTAGC
901 GAT ATGACCC CGGAACAATT AGATCTGGAA GTTAAGAAAA TTACCGCCTA
951 TGC CAAACTT CGCGCAGGTA CAGTTGCAGG CGTAACGGGA GGAGATGTCA
1001 ATA CTGCTGC ACAACCGCA CAAAACGCGG TAGAAAAATA TCGGTTAAAA
1051 GCT GTTGTAA CTGCTGCAAA AGTGTTTAT AAGGTAGCCA GAAAGGATT
1101 AAA AAACGGG AAAATCAACG TTAGAGATTT AAAACAGACG TTGAAAGACG
1151 AAG GTTATAA TTTAGCCGAC AACCTGACCA CCTTATTCTA CGAAACATTG
1201 GAT TGAACG ATGCCAAAGC CGTTATTGAT ATTGTCGTGC GAACAGAGCT
1251 GAA TCGCGCT AATAAAGGGG AAGCGGCACA AAAGGTCAAG GAAGTTTATG
1301 AAA AAAATCG TCCTTATATC CCTAATAAAG GTGCTGTACC GAATATGAGT
1351 ACA TACATGA AAAATAATCC TTTTGAAAA CAGCTGGCTC AAATTTCAGA
1401 AAA GACAACG CTTCCGACGC AGCAAGGGCA GTCTGTCTTC TTGGTAAAAA
1451 GAA ACCAAGG GTTATTAATA ACCGGTGATA GGTTTTATTT AGATGGCCAA
1501 CAT AAAAATC ATTTAGAGGT TTTTGATAAA AATGGGAAT TTAAGTTTGT
1551 TCT AAATATG GATGGTTCGC TTAACCAAAT GAAACTGGG GCAGCAAAAG
1601 GTC GTAAATT AAACCTAAAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 2942; ORF 960>:

```

m960.pep
1  MQVNIQIPCM LYRRGSVKPP LFEAPRLPLS FTDVVPKLS APGGYIVDIP
51  KGNLKTIEIK LAKQPEYAYL KQLQVAKNVN WNQVQLAYDK WDYKQEBLTR
101 AGAAIALAV TVVTAGAVG AALGLNGAAA AAADAAFA SL ASQASVSLIN
151 NKGDVGKTLK ELGRSRTVKV LVVAAATAGV SNKLGASSLA TWSETPWVNN
201 LNVNLANAGS AALINTAVNG GSLKDNLEAN ILAALVNTAH GERASKIKGL
251 DQHYVAHKIA HAVAGCAAAA ANKGRCDQGA IGAAVGEIVG EALVKNTDFS
301 DMTPEQLDLE VKKITAYAKL AAGTVAGVTG GDVNTAAQTA QNAVENNAVK
351 AVVTAAKVY KVARGLKNG KINVRDLKQT LKDEGVNLAD NLTLFDETL
401 DWNDAKAVID IVVGTELNRA NKGEAAQKVK EVLEKNRPYI PNKGAVPNMS
451 TYMKNNPFKG QLAQISEKTT LPTQQGQSVF LVKRNQGLLK TGDRFYLDGO
501 HKNHLEVFDPK NGNFKFVLNM DGSINQMR TG AAKGRKLNK *

```

a960.seq not found yet

a960.pep not found yet

g961.seq not found yet

g961.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2943>:

```

m961.seq
1  ATGAGCATGA AACACTTTCC AGCCAAAGTA CTGACCACAG CCATCCTTGC
51  CACTTTCTGT AGCGGCGCAC TGGCAGCCAC AAGCGACGAC GATGTTAAAA
101 AAGCTGCCAC TGTGGCCATT GTTGCTGCCT ACAACAATGG CCAAGAAATC
151 AACGGTTTCA AAGCTGGAGA GACCATCTAC GACATTGGTG AAGACGGCAC
201 AATTACCCAA AAAGACGCAA CTGCAGCCGA TGTGAAGCC GACGACTTTA
251 AAGGTCTGGG TCTGAAAAA GTCGTGACTA ACCTGACCAA AACCCTCAAT
301 GAAAACAAAC AAAACGTCGA TGCCAAAGTA AAAGCTGCAG AATCTGAAAT
351 AGAAAAAGTTA ACAACCAAGT TAGCAGACAC TGATGCCGCT TTAGCAGATA
401 CTGATGCCGC TCTGGATGAA ACCACCAACG CCTTGAATAA ATTGGGAGAA
451 AATATAACGA CATTGCTGA AGAGACTAAG ACAATATCG TAAAAATTGA
501 TGAAAAATTA GAAGCCGTGG CTGATACCGT CGACAAGCAT GCCGAAGCAT
551 TCAACGATAT CGCCGATTCA TTGGATGAAA CCAACACTAA GGCAGACGAA
601 GCCGTCAAAA CCGCCAATGA AGCCAAACAG ACGGCCGAAG AAACCAAAACA
651 AAA CGTCGAT GCCAAAGTAA AAGCTGCAGA AACTGCAGCA GGCAAGCCG
701 AAGCTGCCGC TGGCACAGCT AATACTGCAG CCGACAAGGC CGAAGCTGTC
751 GCTGCAAAAG TTACCGACAT CAAAGCTGAT ATCGCTACGA ACAAGCTGA
801 TATTGCTAAA AACTCAGCAC GCATCAGACG CTTGGACAAA AACGTAGCTA
851 ATCTGCCGAA AGAAACCCGC CAAGGCCTTG CAGAACAAGC CGCGCTCTCC
901 GGCCTGTTCC AACCTTACAA CGTGGGTCGG TTCAATGTAA CGGCTGCAGT
951 CGGCGGTAC AAATCCGAAT CGGCAGTCGC CATCGGTACC GGCTTCCGCT
1001 TTACCGAAAA CTTGCCGCC AAAGCAGGCG TGGCAGTCGG CACTTCGTCC
1051 GGTTCCTCCG CAGCCTACCA TGTCGGCGTC AATTACGAGT GGTA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 2944>:

```

m961.pep
1  MSMKHFFPAKV LTTAILATFC SGALAATSDD DVKKAATVAI VAAYNNGQEI

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1378

```

51  NGFKAGETIY DIGEDGTITQ KDATAADVEA DDFKGLGLKK VVTNLTKTVN
101 ENKQNVDAKV KAAESEIEKL TTKLADTDAA LADTDAALDE TTNALNKLGE
151 NITTFAEETK TNIVKIDEKL EAVADTVDKH AEA FNDIADS LDETNTKADE
201 AVKTFANEAKQ TAEETKQNV D AKVKAETAA GKAEAAAGTA NTAADKAEAV
251 AAKVTDIKAD IATNKADIAK NSARIDSLDK NVANLRKETR QGLAEQAALS
301 GLFQPYNVGR FNVTAAGGY KSESAVAIGT GFRFTENFAA KAGVAVGTSS
351 GSSAAHYHVG V NYEW*

```

a961.seq not found yet  
a961.pep not found yet

g972.seq not found yet  
g972.pep not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2945>:

```

m972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA
251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTTCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTTC GATGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCAGGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGCGG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGTTCGC AAGAAAAAAT CTCGTTTGTG TCGTGTATAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAAGAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGAT ATTTAATAA ATCAGGGTTC
801 GTTATTTCTG GAGCTTTTTC CAATTTGTAG AAAATTTAAA AATATGCCGG
851 TTCCCAGAAAG GTTTGATCAG AGAAAGAAAA AGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGG TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAAATT GAACCTGATG AATTGGGGGT TATTGCTTTT AAAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2946; ORF 972>:

```

m972.pep
1  LTNRGGAKLK TXSKSSERMS EVEYFSHFIS DGKGLLEIP QRRGKQDGVF
51  VDWFISFTFHE DTLLKVSGCP LPSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQXQNTV LVELKGTGCS VASPGWELRL
151 KQFLDDSI RTITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KKNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFICKRKF NMPVPERFDQ RKKKLNLTFF
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPKG LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPPDYDVE
401 KERKYQEYLS KVVHQNVDYD YF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2947>:

```

a972.seq
1  TTGACTAACA GGGGGGGAGC GAAATTAAAA ACCAATTCCA AGAGTAGTGA
51  ACGAATGAGT GAAGTTGAAT ATTTCTCACA CTTTATATCG GACGGAAAAG
101 GGAAGCTTTT AGAAATTCCG CAGCGAAGAG GTAAGCAAGA CggGGTTTTT
151 GTTGATTGGA TTTCATTCAC ATTCCATGAA GATACTTTAC TGAAAGTTTC
201 CGGTTGCCCT TTATTTTCTG ATGCTGAATA CATGTATGTA TTAAGCAGAA

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1379

```

251 AGCTGGAAGA AATTCTAGGT TTTGGCATAA CGCGCAAATG CAAATCAAGG
301 GGCAACAAAT TCTATGAATC CATGTATAGG TTAGGTTCCG ATGATGTTGA
351 TTATGGAGAG GTGCATTTCG GAGGTCAGCG CAATACTGTT TTAGTTGAGT
401 TGAAAGGTAC TGGTTGCAGC GTTGCAAGTC CGGGTTGGGA GTTGAGGCTA
451 AAGCAGTTTC TCGATGATTC GATAAGGACA AGAATAACGC GAATTGACCT
501 AGCACTTGAT TTTTGTGATG GAGAGTACAC GCCGGATCAG GCGTTGTTAG
551 ATCACGATAA TGGTTTTTTT GATAACAGCA ATCAAAGGCC GAAATCTGAA
601 ACGATCGGTA CGGCTTGGCG GAATGAGGAC GGGAGCGGCA AGACATTTTA
651 TGTAGGTCGC AAGAAAAATT CTCGTTTTGT TCGTGTATTAT GAGAAAGGCA
701 GGCAGCTTGG AGATAAGAAA AGCAAATGGG TAAGGTTCTGA GATCCAGTTT
751 AATTATGGAG ATATAGAAAT ACCCTTGGAT ATTTTAATAA ATCAGGGTTC
801 GTATTTCTGT GGAGCTTTTC CAATTGTAGT AAAATTAAAT AATATGCCGG
851 TTCCCGAAAG GTTTGATCAG AGAAAGAAAA CGCTTAATTT AACTTTCGAG
901 CATAAATTGC ATTACGCGAA AAACGCGGTT GGAAACTGGT TCAATTTTCAT
951 GATTGAAATG GGTTTTGATA ATAGCGAAAT TGTGGAATCT TTAAGGCAG
1001 ATTCGGGATT TCCCAAAGGA TTAGAACCTG AAAAATATGC TCTGGAAATG
1051 TTAAGGGACG GTTTGAAACA CGGTTTTATT CATGAACAGC CGGATATTGA
1101 TTTGGAATTT GAACTTGATG AATTGGGGGT TATTGCTTTT AAAAATCTG
1151 ACAAATTCGA TAGGGAAAAA AGGCTTTTTA GTCCTGATTA TGATGTCGAG
1201 AAAGAAAGGA AATATCAGGA ATATTTAAGT AAAGTTTATC ATCAAATGT
1251 AGATTATGAT TATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 2948; ORF 972.a>:

a972.pep

```

1  LTNRGGAKLK TNSKSSERMS EVEYFSHFIS DGKKGKLEIP QRRGKQDGVF
51  VDWSITFHE DTLLKVS GCP LFSDAEYMYV LSRKLEEILG FGITRKCKSR
101 GNKFYESMYR LGSDDVDYGE VHFQGRNTV LVELKGTGCS VASPGWELRL
151 KQFLDSDSIRT RITRIDLALD FFDGEYTPDQ ALLDHDNGFF DNSNQRPKSE
201 TIGTAWRNED GSGKTFYVGR KNSRFVRVY EKGRQLGDKE SKWVRFEIQF
251 NYGDIEIPLD ILINQGSYFC GAFFPICRKF NMPVPERFDQ RKKTLLNLTFE
301 HKLHYAKNAV GKLNVFMIEM GFDNSEIVES LKADSGFPGK LEPEKYALEM
351 LRDGLKHGFI HEQPDIDLEI ELDELGVIAF KNSDKFDREK RLFSPDYDVE
401 KERKYQEYLS KVIHQNVDDYD YF*

```

m972/a972 99.3% identity in 422 aa overlap

	10	20	30	40	50	60
m972.pep	LTNRGGAKLKTXSKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSITFHE					
a972	LTNRGGAKLKTNKSSERMSEVEYFSHFISDGKKGKLEIPQRRGKQDGVFVDWSITFHE					
	10	20	30	40	50	60
m972.pep	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
a972	DTLLKVS GCP LFSDAEYMYVLSRKLEEILGFGITRKCKSRGNKFYESMYRLGSDDVDYGE					
	70	80	90	100	110	120
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDSDSIRTRITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDSDSIRTRITRIDLALDFFDGEYTPDQ					
	130	140	150	160	170	180
m972.pep	VHFGXQRNTVLVELKGTGCSVASPGWELRLKQFLDSDSIRTRITRIDLALDFFDGEYTPDQ					
a972	VHFGGQRNTVLVELKGTGCSVASPGWELRLKQFLDSDSIRTRITRIDLALDFFDGEYTPDQ					
	190	200	210	220	230	240
m972.pep	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKNSRFVRVYKGRQLGDKE					
a972	ALLDHDNGFFDNSNQRPKSETIGTAWRNEDGSGKTFYVGRKNSRFVRVYKGRQLGDKE					
	250	260	270	280	290	300
m972.pep	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKLLNLTFE					
a972	SKWVRFEIQFNYGDIEIPLDILINQGSYFCGAFFPICRKFKNMPVPERFDQRKKLLNLTFE					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m972.pep	HKLHYAKNAVGLVNFMIEMGFDNSEIVESLKADSGFPGGLEPEKYALEMLRDGLKHGFI					
a972	HKLHYAKNAVGLVNFMIEMGFDNSEIVESLKADSGFPGGLEPEKYALEMLRDGLKHGFI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m972.pep	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
a972	HEQPDIDLEIELDELGVIAFKNSDKFDREKRLFSPDYDVEKERKYQEYLSKVYHQNVVDYD					
	370	380	390	400	410	420
m972.pep	YFX					
a972	YFX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2949>:

g973.seq

```

1  ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCCG
51  actCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA ACAGGAAGTT TTTGATGCCG ACACACTGAC CCGGCTGGAA
151 AAAGTATTGG ACTTTGCCGA GCTGGAAGTG CGCGATCGGA TGATTACGCG
201 CAGCCGCATG AACGTATTGA AAGAAAACGA CAGCATCGAA CGCATCACCG
251 CCTACGTCAT CGATACCGCC CATTTCGCGT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTCAACCCC GAGCAGTTCC ACCTGAAATC CGTCTGCGC CTGCGCGTTT
401 TCGTGCCCGA AGGCAAATCT TTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG
501 TTTGGTCAAC TTTGAAGACA TCATCGAGCa aatcgtcggt gacaTCGAAG
551 ACGAGTTTGA CGAAGACGAA AGCGcgcgacg acatCCAATC cgTTTccgCC
601 GAACGCTGGC GCATCCacgc ggctaCCGAA ATCGAAGaca TCAACGCCTT
651 TTTTCGGTACG GAatacggca gcgaagaagc cgacaccatc ggcggctTGG
701 TCATTACAGG ATTGGGACAC CTGCCCCGTG GCGGCGAAAA AGTCCTTatc
751 ggcgGTTTGC agttcacggt CGCCCCGCC GACAACCGCC GCCTGCACAC
801 GCTGATGGCG ACCCGCGTGA AGTAAGCAGA GCCTGCCcgc accgcggttT
851 CTGCacAGTT TAG

```

This corresponds to the amino acid sequence <SEQ ID 2950; ORF 973.ng>:

g973.pep

```

1  MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLLE
51  KVLDFAELEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFPN EQFHLKSVLR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADDIHSVSA
201 ERWRIHAATE IEDINAFPGT EYGSEEADTI GGLVIQELGH LPVRGEKVLII
251 GGLQFTVARA DNRRLHTLMA TRVK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2951>:

m973.seq

```

1  ATGGACGGCG CACAACCGAA AACGAATTTT TTTGAACGCC TGATTGCCCCG
51  ACTCGCCCGC GAACCCGATT CCGCCGAAGA CGTATTAAAC CTGCTTCGGC
101 AGGCGCACGA GCAGGAAGTT TTTGATGCCG ATACGCTTTT AAGATTGGAA
151 AAAGTCCTCG ATTTTTCGGA TTTGGAAGTG CGCGACGCGA TGATTACGCG
201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAG CGCATCACCG
251 CCTACGTTAT CGATACCGCC CATTTCGCGT TCCCCGTCAT CGGCGAAGAC
301 AAAGACGAAG TTTTGGGCAT TTTGCACGCC AAAGACCTGC TCAAATATAT
351 GTTTAACCCC GAGCAGTTCC ACCTCAAATC CATTCTCCGC CCCGCCGTCT
401 TTTTACCCGA AGGCAAATCG CTGACCGCCC TTTTAAAAGA GTTCCGCGAA
451 CAGCGCAACC ATATGGCGAT TGTCATCGAC GAATACGGCG GCACATCCGG
501 CTTGGTCAAC TTTGAAGACA TCATCGAGCA AATCGTCGGC GAAATCGAAG
551 ACGAGTTTGA CGAAGACGAT AGCGCCGACA ATATCCATGC CGTTTCTTCm
601 GaACGcTGGC GCATCCATGC AGCTACCGAA ATCGAAGACA TCAACACCTT

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1381

651 CTTCGGCACG GAATACAGCA KCGAAGAAGC CGACACCATT GGCGGCCTGG  
 701 TCATTCAAGA GTTGGGACAT CTGCCCCGTGC GCGGCGAAAA AGTCCTTATC  
 751 GCGGGTTTGC AGTTCACCGT CGCACGCGCC GACAACCGCC GCCTGCATAC  
 801 GCTGATGGCG ACCCGCGTGA AGTAA

This corresponds to the amino acid sequence <SEQ ID 2952; ORF 973>:

m973 . pep

1 MDGAQPKTNF FERLIARLAR EPDSAEDVLN LLRQAHEQEV FDADTLRLRLE  
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED  
 101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE  
 151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG EIEDEFDEDD SADNIHAVSS  
 201 ERWRIHAATE IEDINTFFGT EYSXEEADTI GGLVIOELGH LPVRGEKVL  
 251 GGLQFTVARA DNRRLHTLMA TRVK\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 973 shows 95.6% identity over a 274 aa overlap with a predicted ORF (ORF 973.ng) from *N. gonorrhoeae*:

m973/g973

m973 . pep	10	20	30	40	50	60
	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFSDLEV					
g973	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLRLEKVLDFAELEV					
	10	20	30	40	50	60
m973 . pep	70	80	90	100	110	120
	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
g973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
m973 . pep	130	140	150	160	170	180
	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFFEDIIEQIVG					
g973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFFEDIIEQIVG					
	130	140	150	160	170	180
m973 . pep	190	200	210	220	230	240
	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIOELGH					
g973	DIEDEFDEDESADDIHSVSAERWRIHAATEIEDINAFPGTEYGSEADTIGGLVIOELGH					
	190	200	210	220	230	240
m973 . pep	250	260	270			
	LPVRGEKVLIGGLQFTVARADNRRLHTLMA TRVKX					
g973	LPVRGEKVLIGGLQFTVARADNRRLHTLMA TRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2953>:

a973 . seq

1 ATGGACGGCG CACAACCGAA AACAAATTTT TTTGAACGCC TGATTGCCCG  
 51 ACTGCCCGC GAACCCGATT CCGCCGAAGA CGTATTGACC CTGTTGCGCC  
 101 AAGCGCACGA ACAGGAAGTA TTTGATGCGG ATACGCTTTT AAGATTGGAA  
 151 AAAGTCCTCG ATTTTCTGA TTTGGAAGTG CGCGACGCGA TGATTACGCG  
 201 CAGCCGTATG AACGTTTAA AAGAAAACGA CAGCATCGAA CGCATCACCG  
 251 CCTACGTTAT CGATACCGCC CATTCCGCT TCCCCGTCAT CGGTGAAGAC  
 301 AAAGACGAAG TTTTGGGTAT TTTGCACGCC AAAGACCTGC TCAATATAT  
 351 GTTCAACCCC GAGCAGTTCC ACCTCAAATC GATATTGCGC CCTGCCGTCT  
 401 TCGTCCCGCA AGGCAATCG CTGACCGCCC TTTTAAAGA GTTCCGCGAA  
 451 CAGCGCAACC ATATGGCAAT CGTCATCGAC GAATACGGCG GCACGTCGGG  
 501 TTTGGTAACT TTTGAAGACA TCATCGAGCA AATCGTCGCG GACATCGAAG  
 551 ATGAGTTTGA CGAAGACGAA AGCGCGGACA ACATCCACGC CGTTCCGCC

1382

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601 GAACGCTGGC GCATCCACGC GGCTACCGAA ATCGAAGACA TCAACGCCTT
651 TTTCGGCAGC GAATACAGCA GCGAAGAAGC CGACACCATC GGCGGCCTGG
701 TCATTCAGGA ATTGGGACAC CTGCCCCTGC GCGGCGAAAA AGTCCTTATC
751 GCGGCTTTGC AGTTCACCGT CGCCCGCGCC GACAACCGCC GCCTGCATAC
801 GCTGATGGCG ACCCGCGTGA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 2954; ORF 973.a>:

```

a973.pep
  1 MDGAQPKTNF FERLIARLAR EPDSAEDVLT LLRQAHEQEV FDADTLRLLE
 51 KVLDFSDLEV RDAMITRSRM NVLKENDSIE RITAYVIDTA HSRFPVIGED
101 KDEVLGILHA KDLLKYMFP EQFHLKSILR PAVFVPEGKS LTALLKEFRE
151 QRNHMAIVID EYGGTSGLVT FEDIIEQIVG DIEDEFDEDE SADNIHAVSA
201 ERWRIHAATE IEDINAFPGT EYSSEEADTI GGLVIQELGH LPVRGEKVL
251 GGLQFTVARA DNRRLHTLMA TRVK*

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m973/a973 97.8% identity in 274 aa overlap

	10	20	30	40	50	60
m973.pep	MDGAQPKTNFFERLIARLAREPDSAEDVLNLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
a973	MDGAQPKTNFFERLIARLAREPDSAEDVLTLLRQAHEQEVFDADTLRLLEKVLDFSDLEV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m973.pep	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
a973	RDAMITRSRMNVLKENDSIERITAYVIDTAHSRFPVIGEDKDEVLGILHAKDLLKYMFP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m973.pep	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
a973	EQFHLKSILRPAVFVPEGKSLTALLKEFREQRNHMAIVIDEYGGTSGLVTFEDIIEQIVG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m973.pep	EIEDEFDEDDSDADNIHAVSSERWRIHAATEIEDINTFFGTEYSXEEADTIGGLVIQELGH					
a973	DIEDEFDEDESADNIHAVSAERWRIHAATEIEDINAFPGTEYSSEEADTIGGLVIQELGH					
	190	200	210	220	230	240
	250	260	270			
m973.pep	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
a973	LPVRGEKVLIGGLQFTVARADNRRLHTLMATRVKX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2955>:

```

g981.seq
  1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCAC TCGCGCTGTC
 51 TGCCTGCGGC GGTGAGGGCA AAGATGCCGC CGCGCCTGCC GCCAACCCCG
101 GCAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GACGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGCAATT TAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCGCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGATT TCAGCGACCC
351 GTATTTTGAA ATCACCCAAG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT
401 CTCTCTCCGA AGATTGAAA AAGATGAACA AAGTCGGCGT GGTACCGGC
451 CACACGGGCG ATTTCTCCGT TTCCAAACTC TTGGGCAACG ACAATCCGAA
501 AATCGCGCGC TTCGAAAACG TCCCCCTGAT TATCAAAGAA CTGGAACGAC
551 GCGGCTTGGA TTCCGTGGTC AGCGACAGCG CGGTACATCG CAATTATGTG
601 AAAACAACAC CGGCCAAGG AATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAGATCTACG CCAATATTT TGCCAAAGAG GCGGACAGG CTGCGAAATA
801 A

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1383

This corresponds to the amino acid sequence <SEQ ID 2956; ORF 981.ng>:

g981.pep  
1 MKKKWIAAALA CSALALSACG GQKDAAPA ANPGKVYRVA SNAEFAPPES  
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS  
101 GVTTITDDRQ SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK MNKVGVTG  
151 HTGDFS SVKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SD SAVIAN YV  
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD  
251 KIYAKYFAKE GQAAK\*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2957>:

m981.seq  
1 ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCGCGC TCGCGCTGTC  
51 TGCCCTGCGGC GGT CAGGGCA AAGATACGCG CGCGCTGCC GCCAACCCCG  
101 ACAAGTGTA CCGCGTGGCT TCCAACGCGC AGTTTGCCCC CTTTGAATCT  
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC  
201 GATGGCGAAG GCGGGCAATT TTAAATCGA ATTCAAACAC CAGCCGTGGG  
251 ACAGCCTTTT CCGCGCTTA AACACGCGC ATGCGGACGT TGTGATGTCG  
301 GCGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC  
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAAGTAT  
401 CTCTCTCCGA AGATTTGAAA AACATGAACA AAGTCGCGCT GGTAACCGGC  
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAATCCGAA  
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG  
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CGGTCATCGC CAATTATGTG  
601 AAAAACAATC CGGCCAAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC  
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA  
701 AATGCTGAA CGATGCGTTG GAAAAAGTAC GCGAAAGCG CGAATACGAC  
751 AAGATTTACG CCAATATTT TGCAAAGAA GACGACAGG CCGCAAATA  
801 A

This corresponds to the amino acid sequence <SEQ ID 2958; ORF 981>:

m981.pep  
1 MKKKWIAAALA CSALALSACG GQKDTAAPA ANPKVYRVA SNAEFAPPES  
51 LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS  
101 GVTTITDDRQ SMDFSDPYFE ITQVVLVPGK KKVSSSEDLK MNKVGVTG  
151 YTGDFS SVKL LGNDNPKIAR FENVPLIIKE LENGGLDSVV SD SAVIAN YV  
201 KNNPAKGMDF VTLPDFTTEH YGIAVRKGDE ATVKMLNDAL EKVRESGEYD  
251 KIYAKYFAKE DGQAAK\*

m981/g981 98.1% identity in 266 aa overlap

	10	20	30	40	50	60
981.pep	MKKKWIAAALACSALALSACGGQKDTAAPAANPKVYRVASNAEFAPPESLDSKGNVEGF					
g981	MKKKWIAAALACSALALSACGGQKDAAPAANPGKVYRVASNAEFAPPESLDSKGNVEGF					
	10	20	30	40	50	60
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQSMDFSDPYFE					
g981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQSMDFSDPYFE					
	70	80	90	100	110	120
981.pep	ITQVVLVPGKGVSSSEDLKMNKVGVTGTYGDFS SVSKLLGNDNPKIARFENVPLIIKE					
g981	ITQVVLVPGKGVSSSEDLKMNKVGVTGHTGDFS SVSKLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	ITQVVLVPGKGVSSSEDLKMNKVGVTGHTGDFS SVSKLLGNDNPKIARFENVPLIIKE					
g981	ITQVVLVPGKGVSSSEDLKMNKVGVTGHTGDFS SVSKLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
981.pep	LENGGLDSVVSDSAVIAN YVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVVSDSAVIAN YVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	LENGGLDSVVSDSAVIAN YVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
g981	LENGGLDSVVSDSAVIAN YVKNNPAKGMDFVTLPDFTTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				
981.pep	EKVRESGEYDKIYAKYFAKEDGQAAKX					
g981	EKVRESGEYDKIYAKYFAKEGGQAAKX					
	250	260				



The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2959>:

```
a981.seq
1  ATGAAAAAAT GGATTGCCGC CGCCCTTGCC TGTTCCGCGC TCGCGCTGTC
51  TGCCTGCGGC GGTCAAGGTA AAGATGCCGC CGCGCCCGCC GCAAATCCCG
101 ACAAAGTGTA CCGCGTGGCT TCCAACGCCG AGTTTGCCCC CTTTGAATCT
151 TTAGACTCGA AAGGCAATGT CGAAGGTTTC GATGTGGATT TGATGAACGC
201 GATGGCGAAG GCGGGCAATT TTAAAATCGA ATTCAAACAC CAGCCGTGGG
251 ACAGCCTTTT CCCCCTTG AACAACGGCG ATGCGGACGT TGTGATGTCG
301 GCGGTAACCA TTACCGACGA CCGCAAACAG TCTATGGACT TCAGCGACCC
351 GTATTTTGAA ATCACCAGG TCGTCCTCGT TCCGAAAGGC AAAAAATAT
401 CTTCTTCCGA AGATTGAAA AACATGAACA AAGTCGGCGT GGTAACCGGC
451 TACACGGGCG ATTTCTCCGT ATCCAACTC TTGGGCAACG ACAACCCGAA
501 AATCGCGCGC TTTGAAAACG TTCCCTGAT TATCAAAGAA CTGGAAAACG
551 GCGGCTTGA TTCCGTGGTC AGCGACAGCG CAGTCATCGC CAATTATGTG
601 AAAACAATC CGACCAAGG GATGGACTTC GTTACCCTGC CCGACTTCAC
651 CACCGAACAC TACGGCATCG CGGTACGCAA AGGCGACGAA GCAACCGTCA
701 AAATGCTGAA CGATGCGTTG AAAAAAGTAC GCGAAAGCGG CGAATACGAC
751 AAAATCTACG CCAAATATTT TGCAAAGAA GACGACAGG CCGCAAATA
801  A
```

This corresponds to the amino acid sequence <SEQ ID 2960; ORF 981.a>:

```
a981.pep
1  MKKWIAAALA CSALALSACG GQKDAAPA ANPKVYRVA SNAEFAPFES
51  LDSKGNVEGF DVDLMNAMAK AGNFKIEFKH QPWDSLFPAL NNGDADVMS
101 GVTITDDRQK SMDFSDPYFE ITQVVLVPGK KISSSEDLK NMNKVGVTG
151 YTGDFSVSKL LGNDNPKIAR FENVPLIIKE LENGGLDSV SDSAVIANVY
201 KNNPTKGMDF VTLPDFTEH YGIAVRKGDE ATVKMLNDAL KKVRESGEYD
251 KIIYAKYFAKE DGQAAK*
```

m981/a981 98.5% identity in 266 aa overlap

	10	20	30	40	50	60
m981.pep	MKKWIAAALAC SALALSACGGQKDTAAPANPKVYRVASNAEFAPFESLDSKGNVEGF					
a981	MKKWIAAALAC SALALSACGGQKDAAPANPKVYRVASNAEFAPFESLDSKGNVEGF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m981.pep	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
a981	DVDLMNAMAKAGNFKIEFKHQPWDSLFPALNNGDADVMSGVTITDDRQKSMDFSDPYFE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m981.pep	ITQVVLVPGKGVSSSEDLKNMNKVGVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE					
a981	ITQVVLVPGKGVSSSEDLKNMNKVGVTGYTGDFSVSKLLGNDNPKIARFENVPLIIKE					
	130	140	150	160	170	180
	190	200	210	220	230	240
m981.pep	LENGGLDSVVSDSAVIANVYKNNPAKGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
a981	LENGGLDSVVSDSAVIANVYKNNPTKGMDFVTLPDFTEHYGIAVRKGDEATVKMLNDAL					
	190	200	210	220	230	240
	250	260				
m981.pep	EKVRESGEYDKIIYAKYFAKEDGQAAKX					
a981	:					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2961>:

```

g982. seq
1   atcgcatcgc aaaaccttcg attcgacaat cgattcctcc aaaaaatggt
51  caacggcgTg aatattttgc cggccgcGga ttgggtagcC ttgGGcgCA
101 AAGGCCGCAA CGTGGTGGTT GACCGCGCTT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TAAAAGAAGT CCGTCCAAA ACCAacgaCg
251 tagCCGgcga cggtagcact accgCCACCG TATTGGCACA ATCCATCGTT
301 GCCGAaggcA TGAAATACGT TACCGCCGGC ATGAACCCGA CCGATCTGAA
351 ACGCGGCATC GACAAAGccg ttgCCGCTTt ggTTgAAGAg cTGAAAAACA
401 TCGCCAAACC TTGCGATACT TCAAAGAAA TCGCCCAAGT CGGCTCGATT
451 TCCGCCAACT CCGACGAACA AGtcgGCGCG ATTATCGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGgcg tgattacCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCCCTTACT TTATCAACGA CGCGGAAAAA CAAATCGCCG GTCTGGACAA
651 TCCGTTTGTT TTGCTGTTCTG AAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCCGTGTT GGAACAAGTG GCGAAAGCCA GCCGCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGCGC ACTTTGGTCG TGAACAACAT
801 CCGCGGCATC CTGAAAACCG TTGCCGTCAA AGCccccggc tTCGGcGACC
851 CCGCGCAAAGC GATgctgcaa gaCATCGCCA TCCTGACcgg cggcgTagtG
901 ATTTccGAAG Aagtccgcct GTCTTTGGAA AAAGcgactT TGgacgaCTT
951 Gggtcaaac aaACGcatCG AAATCGGtga agaaaacact ACCGTCATcg
1 001 acgGCTTCGG CGACGcagcC CAAAtcgaag cgCGTGTGTC CGAAATCCGC
1 051 CAACAAATCG AAACCGCGAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1 101 CGCGCTTGCC AAACCTGGCAG GAGGCGTGGC AGTGATCAAA GTCGCGCGCG
1 151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGA AGACGCGCTG
1 201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1 251 AGCCCTGTTG CGCGCCCGTG CCGCTTTGGA AAACCTGCAC ACCGGCAATG
1 301 CCGACCAAGA CGCAGGCGTA CAAATCGTAT TGCGCGCCGT TGAGTCTCCG
1 351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGA GAACCCAGCG TGGTGGTGAA
1 401 CAAAGTGTG GAAGGCAAAG GCAactacgG TTACAACGCa ggctcCGGCG
1 451 AATACGgcga CATGATCGGA ATGGGCGTAC TCGACCTGC CAAAGTAACC
1 501 CGTTCCGCGC TGCAACACGC CGCGTCTAtC GCCGGTCTGA TGCTGACGAC
1 551 CGACTGCATG ATTGCCGAAA TCCCTGAAGA AAAACCGGCT GTGCCCGATA
1 601 TGGGGGAAT GGGCGGTATG GCGGCATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2962; ORF 982.ng>:

```

g982. pep
1   IASQNLRFDN RFLQKMVNGV NILPAADWVA LGAKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSIV
101 AEGMKYVTAG MNPTDLKRG I DKAAALVEE LKNIAPCDT SKEIAQVSI
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KSLNELDVV EGMQFDRGYL
201 SPYFINDAEK QIAGLDNPFV LLFDKKISNI RDLLPVLEQV AKASRPLLI
251 AEDVEGEALA TLVVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGVV
301 ISEEVGLSLE KATLDDLQGT KRIEIGEENT TVIDGFGDAA QIEARVAEIR
351 QIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVESP
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYGMIG MGVLDPKVT
501 RSALQHAASI AGLMLTTDCM IAEIPEEKPA VPDMGGMGGM GGM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2963>:

```

m982. seq
1   ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51  AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTGCGAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCG GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAACTGAAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TGCGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCGG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGAAAAA CAAATCGCTG CTTTGGACAA

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1386

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651 TCCGTTTGTGTA TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGGC TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTGTC CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGC GCGCGCTG TGA GTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2964; ORF 982>:

```

m982.seq
1 ATGGCAGCAA AAGACGTACA GTTCGGCAAT GAAGTCCGTC AAAAAATGGT
51 AAACGGCGTG AACATTCTGG CAAACGCCGT CCGCGTAACC TTGGGCCCCA
101 AAGGTCGCAA CGTAGTCGTT GACCGCGCAT TCGGCGGCCC GCACATCACC
151 AAAGACGGCG TAACCGTCGC CAAAGAAATC GAAGTGAAG ACAAGTTTGA
201 AAATATGGGC GCGCAAATGG TGAAGAAGT TGGTCCAAA ACCAACGACG
251 TGGCAGGCGA CGGTACGACT ACCGCCACCG TACTGGCGCA ATCCATCGTT
301 GCCGAAGGTA TGAAATATGT TACCGCAGGT ATGAATCCGA CCGACCTGAA
351 ACGCGGTATC GATAAAGCCG TCGCCGCTTT GGTGACGAA CTGAAAAACA
401 TCGCCAAACC TTGCGCACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CCGACGAACA AGTCGGCGCG ATTATCGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAGTCTTTGG
551 AAAACGAGCT GGACGTAGTT GAAGGTATGC AGTTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TGCGGAAAAA CAAATCGCTG CTTTGGACAA
651 TCCGTTTGTG TTGTTGTTTCG ACAAAAAAAT CAGCAACATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCAAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGAGGCATC CTGAAAACCG TTGCCGTCAA AGCCCCTGGC TTCGGCGACC
851 GCCGCAAAGC GATGTTGCAA GACATCGCCA TCCTGACCGG CGGCGTGGTG
901 ATTTCCGAAG AAGTCGGTCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAAGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1001 ACGGCTTTGG CGACGCAGCC CAAATCGAAG CGCGTGTGTC CGAAATCCGC
1051 CAACAAATCG AAACCGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1101 GCGCGTGGCT AAATTGGCAG GCGGCGTGGC AGTCATCAAA GTCGGTGCCG
1151 CGACCGAAGT CGAAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGGTTGCAG GCGGCGGCGT
1251 AGCCCTGTTG CGTGCCCGTG CTGCTTTGGA AAACCTGCAC ACCGGCAATG
1301 CCGACCAAGA CGCAGGCGTA CAAATCGTCT TGC GCGCGCTG TGA GTCTCCG
1351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1401 CAAAGTATTG GAAGGCAAAG GCAACTACGG TTACAACGCT GGCAGCGGCG
1451 AATACGGCGA TATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1501 CGTTCTGCGC TGCAACACGC CGCATCTATC GCCGCTTGA TGCTGACCAC
1551 TGATTGCATG ATCGCTGAAA TCCCCGAAGA CAAACCGGCT GTGCTGATA
1601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m982/g982 95.8% identity in 544 aa overlap

```

m982.pep      10      20      30      40      50      60
MAAKDVQFGNEVRQKMNNGVNI LANAVRVTLGPKGRNVVVDRAFGGPHITKDGVTVAKEI
: : : : : : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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1387

g982	IASQNLRFDNRFLOKQMVNGVNILPAADWVALGAKGRNVVVDRAFGGPHITKDGVTVAKEI
	10 20 30 40 50 60
m982.pep	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRGI
	70 80 90 100 110 120
g982	ELKDKFENMGAQMVKEVASKTNDVAGDGTATVLAQSIVAEGMKYVTAGMNPDLKRGI
	70 80 90 100 110 120
m982.pep	DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
g982	DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAIIEAMEKVGKEGVITVEDG
	130 140 150 160 170 180
m982.pep	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAALDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
g982	KSLLENLDVVEGMQFDRGYLSPYFINDAEKQIAGLDNPFVLLFDKKISNIRDLLPVLEQV
	190 200 210 220 230 240
m982.pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
g982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV
	250 260 270 280 290 300
m982.pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
g982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTVIDGFGDAAQIEARVAEIRQQIETATSDY
	310 320 330 340 350 360
m982.pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
g982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL
	370 380 390 400 410 420
m982.pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA
	430 440 450 460 470 480
g982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA
	430 440 450 460 470 480
m982.pep	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGMLTTDCMIAEIPEDKPAVPDMGGMGM
	490 500 510 520 530 540
g982	GSGEYGDMIEMGVLDPAKVTRSAHQHAASIAGMLTTDCMIAEIPEEKPAVPDMGGMGM
	490 500 510 520 530 540
m982.pep	GMMX
g982	GMMX

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2965>:

a982.seq

1	ATGGCAGCAA	AAGACGTACA	ATTCGGCAAT	GAAGTCCGCC	AAAAATGGT
51	AAACGGCGTG	AACATTTTGG	CAAACGCCGT	GCGCGTAACC	TTGGGTCCCA
101	AAGGCCGCAA	CGTGGTGGTT	GACCGCGCTT	TCGGCGGCCC	GCACATCACC
151	AAAGACGGCG	TAACCGTCGC	CAAAGAAATC	GAAGTCAAAG	ACAAGTTTGA
201	AAATATGGGC	GCGCAAATGG	TGAAAGAAGT	CGCGTCCAAA	ACCAACGACG
251	TGGCGGGCGA	CGGTACGACT	ACCGCCACCG	TATTGGCGCA	ATCCATCGTT
301	GCCGAAGGTA	TGAAATACGT	TACCGCCGGT	ATGAACCCGA	CCGACCTGAA
351	ACGCGGTATC	GACAAAGCCG	TCGCGGCTTT	GGTTGAAGAG	CTGAAAAACA

1388

```

401 TCGCCAAACC TTGCGACACT TCTAAAGAAA TCGCCCAAGT CGGCTCTATT
451 TCCGCCAACT CTGACGAACA AGTCGGCGCG ATTATTGCCG AAGCGATGGA
501 AAAAGTCGGC AAAGAAGGCG TGATTACCGT TGAAGACGGC AAATCTTTGG
551 AAAACGAGCT GGACGTGGTT GAAGGTATGC AATTCGACCG CGGCTACCTG
601 TCTCCTTACT TCATCAACGA TCGGGAAGAA CAAATCGCCG GCTTGGACAA
651 TCCGTTTGTA TTGCTGTTTCG ACAAAAAAAT CAGCAATATC CGCGACCTGC
701 TGCCTGTTTT GGAACAAGTG GCCAAAGCCA GCCGTCCGCT GTTGATTATC
751 GCTGAAGACG TAGAAGGCGA AGCCTTGGCG ACTTTGGTCG TGAACAACAT
801 CCGCGGCATT CTGAAAACCG TTGCCGTTAA AGCTCCGGGC TTCGGCGACC
851 GCCGCAAAGC GATGCTGCAA GACATCGCTA TCCTGACCGG CGGCACAGTG
901 ATTTCCGAAG AAGTCGGCCT GTCTTTGGAA AAAGCGACTT TGGACGACTT
951 GGGTCAGGCC AAACGCATCG AAATCGGTAA AGAAAACACC ACCATCATCG
1 001 ACGGCTTCGG CGACGCAGCC CAAATCGAAG CGCGTGTTGC CGAAATCCGC
1 051 CAACAAATCG AAACGCAAC CAGCGATTAC GACAAAGAAA AACTGCAAGA
1 101 GCGCGTTGCC AAAGTGGCAG GCGGCGTGGC AGTAATCAAA GTCGGTGCCG
1 151 CGACCGAAGT GGAATGAAA GAGAAAAAAG ACCGCGTGGG AGACGCGCTG
1 201 CACGCTACCC GCGCAGCCGT TGAAGAAGGC GTGTTGTCAG GCGGCGCGCT
1 251 AGCCCTGTTG CGCGCCCGTG CCGCTCTGGA AAACCTGCAC ACCGGCAATG
1 301 CAGACCAAGA CGCAGCGCTA CAAATCGTCT TGCGCGCCGT TGAGTCTCCG
1 351 CTGCGCCAAA TCGTTGCCAA CGCAGGCGGC GAACCCAGCG TGGTTGTGAA
1 401 CAAAGTGTG GAAGGCAAAG GCAACTATGG TTACAACGCT GGCAGCGCGC
1 451 AATACGGCGA CATGATCGAA ATGGGCGTAC TCGACCCCGC CAAAGTAACC
1 501 CGTTCGCGC TGCAACACGC CGCGTCTATC GCCGGCCTGA TGCTGACCAC
1 551 AGACTGCATG ATTGCTGAAA TCCCTGAAGA CAAACCGGCT ATGCCTGATA
1 601 TGGGCGGCAT GGGTGGTATG GCGGCGATGA TGTA

```

This corresponds to the amino acid sequence <SEQ ID 2966; ORF 982.a>:

```

a982.pep
1  MAAKDVQFGN EVRQKMVNGV NILANAVRVT LGPKGRNVVV DRAFGGPHIT
51  KDGVTVAKEI ELKDKFENMG AQMVKEVASK TNDVAGDGTT TATVLAQSI
101 AEGMKYVTAG MNPTDLKRG I DKAVAALVEE LKNIAPCDT SKEIAQVGS
151 SANSDEQVGA IIAEAMEKVG KEGVITVEDG KLENELDVV EGMQFDRGY
201 SPYFINDAEK QIAGLDNPFV LLDKKISNI RDLLPVLEQV AKASRPILLI
251 AEDVEGEALA TLVNNIRGI LKTVAVKAPG FGDRRKAMLQ DIAILTGGTV
301 ISEEGLSLE KATLDDLQQA KRIEIGKENT TIIDGFGDAA QIEARVAEIR
351 QQIETATSDY DKEKLQERVA KLAGGVAVIK VGAATEVEMK EKKDRVEDAL
401 HATRAAVEEG VVAGGGVALL RARAALLENH TGNADQDAGV QIVLRAVES
451 LRQIVANAGG EPSVVVNKVL EGKGNYGYN A GSGEYDMIE MGVLDPARV
501 RSALQHAASI AGLMLTTDCM IAEIPEDKPA MPDMGGMGGM GGMM*

```

m982/a982 99.3% identity in 544 aa overlap

```

          10      20      30      40      50      60
m982.pep  MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          |||
a982      MAAKDVQFGNEVRQKMVNGVNILANAVRVT LGPKGRNVVV DRAFGGPHITKDGVTVAKEI
          10      20      30      40      50      60

          70      80      90      100     110     120
m982.pep  ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          |||
a982      ELKDKFENMGAQMVKEVASKTNDVAGDGTTTATVLAQSIVAEGMKYVTAGMNPTDLKRG I
          70      80      90      100     110     120

          130     140     150     160     170     180
m982.pep  DKAVAALVDELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          |||
a982      DKAVAALVEELKNIAPCDTSKEIAQVGSISANSDEQVGAI IAEAMEKVGKEGVITVEDG
          130     140     150     160     170     180

          190     200     210     220     230     240
m982.pep  KLENELDVVEGMQFDRGYLSPYFINDAEKQI AALDNPFVLLFDKKISNIRDLLPVLEQV
          |||
a982      KLENELDVVEGMQFDRGYLSPYFINDAEKQI AALDNPFVLLFDKKISNIRDLLPVLEQV
          190     200     210     220     230     240

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1389

	250	260	270	280	290	300
m982 . pep	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGVV					
a982	AKASRPLIIAEDVEGEALATLVVNNIRGILKTVAVKAPGFGDRRKAMLQDIAILTGGTV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m982 . pep	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQOIETATSDY					
a982	ISEEVGLSLEKATLDDLQAKRIEIGKENTTIIDGFGDAAQIEARVAEIRQOIETATSDY					
	310	320	330	340	350	360
	370	380	390	400	410	420
m982 . pep	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
a982	DKEKLQERVAKLAGGVAVIKVGAATEVEMKEKKDRVEDALHATRAAVEEGVVAGGGVALL					
	370	380	390	400	410	420
	430	440	450	460	470	480
m982 . pep	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA					
a982	RARAALNLHTGNADQDAGVQIVLRAVESPLRQIVANAGGEPVSVVNVKVLGKNGYGYNA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m982 . pep	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
a982	GSGEYGDMIEMGVLDPAKVTRSALQHAASIAGLMLTTDCMIAEIPEDKPAVPDMGGMGGM					
	490	500	510	520	530	540
m982 . pep	GGMXX					
a982	GGMXX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2967>:

g986 . seq

1	GTGTTCAAAA	AATACCAATA	CTTCGCTTTG	GCGGCACTGT	GTGCCGCCTT
51	GCTGGCAGGC	TGCGAAAAGG	CAGGCAGCTT	TTTCGGTGCG	GACAAAAAAG
101	AAGCATCCTT	CGTAGAACGC	ATCGAACACA	CCAAAGACGA	CGGCAGTGTC
151	AGTATGCTGC	TGCCCCGACTT	TGCCCAACTG	GTTCAAAGCG	AAGGCCCGGC
201	AGTCGTCAAT	ATTCAGGCAG	CCCCCGCCCC	GCGCACCCAA	AACGGCAGCG
251	GCAATGCCGA	AACCGATTCC	GACCCGCTTG	CCGACAGCGA	CCCCTTCTAC
301	GAATTTTTC	AACGCCTCGT	CCCGAACATG	CCCGAAATCC	CCCAAGAAGA
351	AGCAGATGAC	GGCGGATTGA	ACTTCGGTTC	GGGCTTCATC	ATCAGCAAAA
401	ACGGCTACAT	CCTGACCAAT	ACCCACGTCG	TTGCCGGTAT	GGGCAGTATC
451	AAAGTCCTGC	TCAACGACAA	GCGCGAATAT	ACCGCCAAAC	TCATCGGTTC
501	GGATGTCCAA	TCCGATGTCG	CCCTTCTGAA	AATCGACGCA	ACGGAAGAGC
551	TACCCGTCGT	CAAAATCGGC	AATCCCAAAA	ATTGAAACC	GGGCGAATGG
601	GTCGCTGCCA	TCGGCGCGCC	CTTCGGCTTT	GACAACAGCG	TGACCGCCGG
651	CATCGTGTCC	GCCAAAGGCA	GAAGCCTGCC	CAACGAAAgc	tACACACCCT
701	TCATCCAAAC	CGACGTTGCC	ATCAATCCGG	GCAATTCCGG	CGGCCCGCTG
751	TTCAACTTAA	AAGGACAGGt	cgTCGGCATC	AATTCGCAAA	TATACAGCCG
801	CAGCGgcgga	ttCATGGGCA	TCTCCTTTGC	CATCCCGATT	GACGTTGCCA
851	TGAATGTCGC	CGAACAGCTG	AAAAACACCG	GCAAAGTCCA	ACGCGGACAA
901	CTGGGCGTGA	TTATTTCAGGA	AGTATCCTAC	GGTTTGGCAC	AGTCGTTCCG
951	TCTGGATAAA	GCCAGCGGCG	CATTGATTGC	CAAAATCCTT	CCCGGCAGCC
1001	CCGCAGAACG	TGCCGGCCTG	CAGGCGGGCG	ACATCGTCTT	CAGCCTCGAC
1051	GGCGGAGAAA	TACGTTCTTC	CGGCGACCTT	CCCGTCATGG	TCGGCGCCAT
1101	TACGCCGGGA	AAAGAAGTCA	GCCTCGGCGT	ATGGCGCAAA	GGCGAAGAAA
1151	TCACAAACAA	AGCCAAGCTG	GGCAACGCCg	ccgagcATAC	CGGCgcatCA
1201	TCCAAAACAG	ATGAAGcccc	ctacaccgAA	CAGCAATCCG	GTACGTTCTC
1251	GGTCGAATCC	GCAGGCATTA	CCCTTCAGAC	ACATACCGAC	AGCAGCGGca
1301	aacacctcgt	cgtcgtacgg	gtttccgacg	cggcagaacg	cGCAGGCTTA

1390

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1351 AGgcgcggcg acgaaatcct cgcggtcggg caagtccccc tcaatgacga
1401 agccgGTTTC cgcaaaGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
1451 TGGTCAtgcg ccgTGGCAAC ACGTGTTCa TCGCATTAAa CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2968; ORF 986.ng>:

```

g986. pep
  1 VFKKYQYFAL AALCAALLAG CEKAGSFFGA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAETDS DPLADSDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKNYILTN THVVAGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKNLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK ASGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKAKL GNAAEHTGAS
401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGKHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLVMRRGN TLFIALNLQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2969>:

```

m986. seq
  1 GTGTTCAAAA AATACCAATA CCTCGCTTTG GCAGCACTGT GTGCAGCCTC
 51 GCTGGCAGGC TGCACAAAGG CAGGCAGCTT CTTCGTGGCG GACAAAAAAG
101 AAGCATCCTT CGTAGAACGC ATCGAACACA CCAAAGACGA CGGCAGCGTC
151 AGTATGCTGC TGCCCGACTT TGCCCAACTG GTTCAAAGTG AAGGTCCGCG
201 AGTCGTCAAT ATTCAGGCAG CCCCAGCCCC GCGCACCCAA AACGGCAGCG
251 GCAATGCCGA AACGATTCC GACCCGATTG CCGACAACGA CCCGTTCTAC
301 GAATTTTTCa AACGCCTCGT CCCGAATATG CCCGAAATCC CCCAAGAAGA
351 AGCAGATGAC GGCAGATTGA ACTTCGTTTC GGGCTTCATC ATCAGCAAAG
401 ACGGCTACAT CCTGACCAAT ACCCACGTCG TTACCGGCAT GGGCAGTATC
451 AAAGTCCTGC TCAACGACAA GCGCGAATAT ACCGCCAAAC TCATCGGTTT
501 GGATGTCCAA TCCGATGTCG CCCTTCTGAA AATCGACGCA ACGGAAGAGC
551 TGCCCGTCGT CAAATCGGCG AATCCCAAAG ATTTGAAACC GGGCGAATGG
601 GTCGCCGCCA TCGGCGCGCC CTTCGGCTTC GACAACAGCG TGACCGCCCG
651 CATCGTGTCC GCCAAAGGCA GAAGCCTGCC CAACGAAAGC TACACACCCG
701 TCATCCAAAC CGACGTTGCC ATCAATCCGG GCAACTCCGG CGGCCCGCTG
751 TTCAACTTAA AAGGACAGGT CGTCGGCATC AACTCGCAA TATACAGCCG
801 CAGCGGCGGA TTCATGGGCA TTTCCTTCGC CATCCCGATT GACGTTGCCA
851 TGAATGTCGC CGAACAGCTG AAAACACCG GCAAAGTCCA ACGCGGACAA
901 CTGGGCGTGA TTATTCAAGA AGTATCCTAC GGTTTGACAC AATCGTTCCG
951 TTTGGACAAA GCCGGCGGCG CACTGATTGC CAAAATCCTG CCCGGCAGCC
1001 CCGCAGAACG TGCCGGCCTG CAGGCGGGCG ACATCGTCCT CAGCCTCGAC
1051 GGCGGAGAAA TACGTTCTTC CGGCGACCTT CCCGTTATGG TCGGCGCCAT
1101 TACGCCGGGA AAAGAAGTCA GCCTCGGCGT ATGGCGCAA GCGGAAGAAA
1151 TCACAATCAA AGTCAAGCTG GGCAACGCCG CCGAGCATAT CGGCGCATCA
1201 TCCAAAACAG ATGAAGCCCC CTACACCGAA CAGCAATCCG GTACGTTCTC
1251 GGTGCAATCC GCAGGCATTA CCCTTCAGAC ACATACCGAC AGCAGCGGCG
1301 GACACCTCGT CGTCGTACGG GTTTCGACG CGGCAGAACG CGCAGGCTTG
1351 AGGCGCGGCG ACGAAATTCT TGCCGTCGGG CAAGTCCCCG TCAATGACGA
1401 AGCCGGTTTC CGCAAAGCTA TGGACAAGGC AGGCAAAAC GTCCCCCTGC
1451 TGATCATGCG CCGTGGCAAC ACGCTGTTTA TCGCATTAAa CCTGCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 2970; ORF 986>:

```

m986. pep..
  1 VFKKYQYLAL AALCAASLAG CDKAGSFFVA DKKEASFVER IEHTKDDGSV
 51 SMLLPDFAQL VQSEGPVAVN IQAAPAPRTQ NGSGNAENDS DPIADNDPFY
101 EFFKRLVPMN PEIPQEEADD GGLNFGSGFI ISKDGILTN THVVTGMGSI
151 KVLNDKREY TAKLIGSDVQ SDVALLKIDA TEELPVVKIG NPKDLKPGEW
201 VAAIGAPFGF DNSVTAGIVS AKGRSLPNES YTPFIQTDVA INPGNSGGPL
251 FNLKGQVVGI NSQIYSRSGG FMGISFAIPI DVAMNVAEQL KNTGKVQRGQ
301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL QAGDIVLSLD
351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS
401 SKTDEAPYTE QSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAAERAGL
451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ*

```

Computer analysis of this amino acid sequence gave the following results:





	310	320	330	340	350	360
m986. pep	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	:					
g986	LGVIIQEVSYGLAQSFGLDKASGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m986. pep	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	:					
g986	PVMVGAITPGKEVSLGVWRKGEEITIKAKLGNAAEHTGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
	430	440	450	460	470	480
m986. pep	AGITLQTHTDSSGGHLVVVRVSDAAERAGLRGDEILAVGQVPVND EAGFRKAMD KAGKN					
g986	AGITLQTHTDSSGGKHLVVVRVSDAAERAGLRGDEILAVGQVPVND EAGFRKAMD KAGKN					
	430	440	450	460	470	480
	490	500				
m986. pep	VPLLIMRRGNTLFIALNLQX					
g986	VPLLVMRRGNTLFIALNLQX					
	490	500				

```

a986.seq
1      GTGTTCAAAG  AATACCAATA  CCTCGCTTGT  GCAGCACTGT  GTGCCGCCCTC
51     AGCTGGCAGG  TGCACAAAG  CCGGCAGCTT  TTTCAAGTGC  GACAAAAAAG
101    AAGCATCCTT  TGTAGAACGC  ATCAAAACACA  CCAAGAGACA  CGGCAGCGTC
151    AGTATGCTGC  TGCCCGACTT  TGTCCAACTG  GTTCAAAGCG  AAGGCCCGGC
201    AGTCGTCAAT  ATTCAAGGCA  CCCC CGCCCC  GCGCACCCAA  AACGGCAGCA
251    GCAATGCCGA  AACC GATTCC  GACCCGCTTG  CCGCAGCGCA  CCCGTTCTAC
301    GAATTTTTCA  AACGCCTCGT  CCGGAACATG  CCGGAATCCG  CCGAAGAAGA
351    AGCAGATGAC  GNGG GATTGA  ACTTCGGTTC  GGGCTTCATC  ATCAGCAAAG
401    ACGGCTATAT  TCTGACCAAT  ACGCACGTGC  TTACCGGCAT  GGGCAGTATC
451    AAAGTCCTGC  TCAACGACAA  GCGCGAATAT  ACCGCAAAAT  TCATCGGTTG
501    GGATGTCCTA  TCCGATGTCG  CCCTTCTGAA  AATCGACGCA  ACGGAAGAGC
551    TGCCCGTCGT  CAAAATCGGC  AATCCCAAAG  ATTTGAAACC  GGGCGAATGG
601    GTCGCCGCCA  TCGGCGCGCC  CTTCGGCTTC  GACAACAGCG  TGACCGCCGG
651    CNTCGTGTC  GCCAAAGGCA  GAAGCCTGCC  CAACGAAAGC  TACACACCTT
701    TCATCCAAAC  CGACGTTGCC  ATCAATCCGG  GCAACTCCGG  CGGCCCGCTG
751    TTCAACTTAA  AAGGACAGGT  CTGCGGCATC  AACTCGCAAA  TATACAGCCG
801    CAGCGGCGGA  TTCATGGGCA  TTTCTTTCGC  CATCCCGATT  GACGTTGCCA
851    TGAATGTCGC  CGAACAGCTG  AAAAACACCG  GCAAAGTCCA  ACGCGGACAA
901    CTGGGCGTGA  TTATTCAAGA  AGTATCCTAC  GGTTTGGCAC  AATCGTTCGG
951    TTTGGACAAA  GCGCGCGGCG  CACTGATTGC  CAAATCTGTG  CCGGCAGCCG
1001   CCGCAGAAAG  TGC CGGCGCTG  CGGGCGGGCG  ACATCGTCCT  CAGCCTCGAC
1051   GCGCGAGAAA  TACGTTCTTC  CGGCGACCTT  CCCGTTATGG  TCGGCGCCAT
1101   TACGCGGGGA  AAAGAAGTCA  GCCTCGGCGT  ATGGCGCAAA  GGGCAGAATA
1151   TCACAATCAA  AGTCAAGCTG  GGCAACGCGG  CCGAGCATAT  CGGCGCATCA
1201   TCCAAAACAG  ATGAAGCCCC  CTCACCGGAA  CAGCAATCCG  GTACGTTCTC
1251   GGTGGAATCC  GCAGGCATTA  CCCTTCAGAC  ACATACCGAC  AGCAGCGGCG
1301   GACACCTCGT  CGTCGTACGG  GTTTCGACG  CGGCAAGAAG  CGCAGGCTTG
1351   AGGCGCGGCG  ACGAAATTCT  TGCGTCAGGG  CAAGTCCCCG  TCAATGACAT
1401   AGCCGGTTTC  CGGAAGACTA  TGGACAAGGG  AGGCAAAAAC  GTCCCCCTGC
1451   TGATCATGCG  CGCTGGCAAC  ACGCTGTTTA  TCGCATATAA  CTTGCAATAA

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a986.pap

1	VFKKYQYLAL	AALCAASLAG	CDKAGSFFGA	DKKEASFVER	IKHTKDDGSV
51	SMLLPDFVQL	VQSEGPVVN	IQAPAPRTQ	NGSSNAETDS	DPLADSDFFY
101	EFFKRLVPM	PEIQEEADD	GGINFGSGFI	ISKDGYLTN	THVVTMGSI
151	KVLLNDKREY	TAKLIGSDVQ	SDVALLKIDA	TEELPVVTK	NPKDKLPGEW
201	VAAIGAPFGF	DNSVTAGDVQ	AKGRSLPNES	YTPFIQTDVA	INFGNSGGPL
251	FNILKGQVVG	NSQIYSRSGG	FMGISFAIPI	DVAMNVAEQL	KNTGKVGQGO

1393

301 LGVIIQEVSY GLAQSFGLDK AGGALIAKIL PGSPAERAGL RAGDIVLSLD  
 351 GGEIRSSGDL PVMVGAITPG KEVSLGVWRK GEEITIKVKL GNAAEHIGAS  
 401 SKTDEAPYTE QQSGTFSVES AGITLQTHTD SSGGHLVVVR VSDAERAGL  
 451 RRGDEILAVG QVPVNDEAGF RKAMDKAGKN VPLLIMRRGN TLFIALNLQ\*

m986/a986 98.2% identity in 499 aa overlap

m986 . pep	10	20	30	40	50	60
	VFKKYQYLALAALCAASLAGCDKAGSFFVADKKEASFVERIEHTKDDGSVSMMLLPDFAQL					
a986	VFKKYQYLALAALCAASLAGCDKAGSFFGADKKEASFVERIKHTKDDGSVSMMLLPDFVQL					
	10	20	30	40	50	60
m986 . pep	70	80	90	100	110	120
	VQSEGPVAVNIQAAPAPRTQNGSGNAENDSDPIADNDPFYEFFKRLVPMPEIPQEEADD					
a986	VQSEGPVAVNIQAAPAPRTQNGSSNAETDSPLADSDPFYEFFKRLVPMPEIPQEEADD					
	70	80	90	100	110	120
m986 . pep	130	140	150	160	170	180
	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
a986	GGLNFGSGFIISKDGYILTNTHVVTGMGSIKVLNDKREYTAKLIGSDVQSDVALLKIDA					
	130	140	150	160	170	180
m986 . pep	190	200	210	220	230	240
	TEELPVVKIGNPKDLKPGEWAAIGAPFGFNSVTAGIVSAKGRSLPNESYTPFIQTDA					
a986	TEELPVVKIGNPKDLKPGEWAAIGAPFGFNSVTAGXVSAKGRSLPNESYTPFIQTDA					
	190	200	210	220	230	240
m986 . pep	250	260	270	280	290	300
	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
a986	INPGNSGGPLFNLKGQVVGINSQIYSRSGGFMGISFAIPIDVAMNVAEQLKNTGKVQRGQ					
	250	260	270	280	290	300
m986 . pep	310	320	330	340	350	360
	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLQAGDIVLSLDGGEIRSSGDL					
a986	LGVIIQEVSYGLAQSFGLDKAGGALIAKILPGSPAERAGLRAGDIVLSLDGGEIRSSGDL					
	310	320	330	340	350	360
m986 . pep	370	380	390	400	410	420
	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
a986	PVMVGAITPGKEVSLGVWRKGEEITIKVKLGNAAEHIGASSKTDEAPYTEQQSGTFSVES					
	370	380	390	400	410	420
m986 . pep	430	440	450	460	470	480
	AGITLQTHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
a986	AGITLQTHTDSSGGHLVVVRVSDAERAGLRRGDEILAVGQVPVNDEAGFRKAMDKAGKN					
	430	440	450	460	470	480
m986 . pep	490	500				
	VPLLIMRRGNTLFIALNLQX					
a986	VPLLIMRRGNTLFIALNLQX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2973>:

g987. seq

1 ATGAAAACAC GCAGCCTCAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG

1394

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51  TTCTTCATGG TTGCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTTA
101 ATACTTCCAA ACCTGTCTC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATAACA ACGGGCTATC CGACATCTAC CTGCTCGACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATTGG CGCAACGaCA TTTCCGGCAG GCTGCTGTTC
301 AACCTCATGT ACCTTGCCGC agaacgcGGC GTGCGCGTAC GCCTGCTGTt
351 ggacgacaAC AACAcgcgcg gcttgacga tctcctGCTC GCCCTCGACA
401 GCCATCCCAA TAtctaagtG CGCTGTTCa ACCCCTtctg CTACGCAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACATCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACGGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT GATCAGCGAC AGCCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GAGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCTACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTACGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCGTCCCGC GCCACAAAAG ACAAGGCCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGacg gCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCAATACCG
1301 AAATGGGCGT CGTCATCGAA AGCCCCAAAA TCGCAGAACA GATGGAGCGC
1351 AccctCGCCG AtacCACACC CGAATACGCC TACCGCGTTA CCCTCGACAA
1401 ACACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACC CGAAGAACTT TGGAACGCA TCGCCGCAAA AATCCTATCC
1501 CTGCTGCCCA TCGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2974; ORF 987.ng>:

```

g987.pep
1  MKTRSLISLL CLLLSCSSW LPPLEERTES RHFNTSKPVL LDNILQIRHT
51  PHNNGLSDIY LLDDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLMYLAERG VVRVLLDDN NTRGLDOLL ALDSHPNI*V RLENPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD SPAKGLDRDR
301 RKPPIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPRESAR LNTEMGVIE SPKIAEQMER
451 TLADTTPEYA YRVTLDKHNR LQWHPATRK TYPNEPEAKL WKRIAAILK
501 LLPIEGLL*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2975>:

```

m987.seq
1  ATGAAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAACG GACGGAAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTGTAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTTCCGGCAG GCTGCTGTTC
301 AACCTCGTGT ACCTTGCCGC AGAACCGCGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCCTGCTT GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCTGTTCa ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCCCCTCA ACCGCCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTTCGCC
601 GATTGAGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CGACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAAATAC AGACAGGATG CATCGACTGG CAGAGCGTCC
851 GAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC

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1395

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901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCCG
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTTCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTTCTG
1051 ACCAACTCGC TGCAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCCAACCA TGCCGTCCCC GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCACGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGT TCGTTCAACC TCGACCCCG TTCCGCGCGT CTAACACCG
1301 AAATGGGCGT TGTTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCACACC CGCCTACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCCTATCC
1501 CTGCTGCCCA TAGAAGGTTT ATTATAG

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This corresponds to the amino acid sequence <SEQ ID 2976; ORF 987>:

```

m987.pep
1 MKTRSLISLL CLLLCSCSSW LPFLEERTES RHFNTSKPVR LDNILQIRHT
51 PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRLLLDDN NTRGLDDLLL ALDSHPNIEV RLFNPFVLRK
151 WRALGYLTDF PRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGDIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGCIDW QSVRTRLISD DPAKGLDRDR
301 RKPIIAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL
351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS
401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER
451 TLADTTPAYA YRVTLDRHNR LQWHDPATRK TYPNEPEAKL WKRIAAILSL
501 LLPIEGLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m987/g987 97.8% identity in 508 aa overlap

m987.pep	10	20	30	40	50	60
	MKTRSLISLLCLLLCSCSSWLPFLEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
g987	MKTRSLISLLCLLLCSCSSWLPFLEERTESRHFNTSKPVLLDNILQIRHTPHNGLSDIY					
	10	20	30	40	50	60
m987.pep	70	80	90	100	110	120
	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
g987	LLDDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLMYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
m987.pep	130	140	150	160	170	180
	NTRGLDDLLLALDSHPNIEVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
g987	NTRGLDDLLLALDSHPNIXVRLFNPFVLRKWRALGYLTDFPRLNRRMHNKSFTADNRATI					
	130	140	150	160	170	180
m987.pep	190	200	210	220	230	240
	LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
g987	LGGRNIGDEYFKVGEDTVFADLDILATGSVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
m987.pep	250	260	270	280	290	300
	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGCIDWQSVRTRLISDDPAKGLDRDR					
g987	KGLQALGYNDETSRHALLRYRETVEQSPLYQKIQTGRIDWQSVQTRLISDSPAKGLDRDR					
	250	260	270	280	290	300
m987.pep	310	320	330	340	350	360
	RKPIIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA					

1396

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|||||
g987      RKPP|IAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVT|VL|TNSLQATDVA
           310      320      330      340      350      360

           370      380      390      400      410      420
m987. pep AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
           |||||
g987      AVHSGYVVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTS|LHAKTFIVDGKRIFIG
           370      380      390      400      410      420

           430      440      450      460      470      480
m987. pep SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PAYAYRVTLDRHNRLQWHPATRK
           |||||
g987      SFNLDPRSARLNT|EMGVVIESPKIAEQMERTLADTT|PEYAYRVTLDKHNRLQWHPATRK
           430      440      450      460      470      480

           490      500      509
m987. pep TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
           |||||
g987      TYPNEPEAKLWKRIA|AAKILSLLPIEGLLX
           490      500

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2977>:

```

a987. seq
1  ATGAAACAC GCAGCCTAAT TTCCCTTTTA TGCTCCTTC TCTGTTTCATG
51  TTCTTCATGG TTGCCCCAC TGGAAGAAGC GACGGAAGC CGTCATTTCA
101 ATACTTCCAA ACCCGTCCGC CTGGACAACA TCCTGCAAT CCGGCACACC
151 CCTCATACCA ACGGGCTATC CGATATCTAT CTGTTGAACG ACCCCACGA
201 AGCCTTTGCC GCCCGCGCCG CCCTTATCGA ATCTGCCGAA CACAGCCTCG
251 ATTTGCAATA CTACATCTGG CGCAACGACA TTCCCGGCGG ACTGCTGTTT
301 AACCTCGTGT ACCTTGCCGC AGAACGCGGT GTGCGCGTAC GCCTGCTGTT
351 GGACGACAAC AACACGCGCG GATTGGACGA CCTCTGCTC GCCCTCGACA
401 GCCATCCCAA TATCGAAGTG CGCCTGTTCA ACCCCTTCGT CTTACGAAAA
451 TGGCGCGCAC TCGGCTACCT GACCGACTTC CCGCGCTCA ACCGCGCAT
501 GCACAACAAA TCCTTTACCG CCGACAACCG CGCCACCATA CTCGGCGGAC
551 GCAATATCGG CGACGAATAC TTCAAAGTCG GTGAGGACAC CGTTTTCGCC
601 GACCTGGACA TCCTCGCCAC CGGCAGCGTC GTCGGCGAAG TATCGCACGA
651 CTTGACCGC TACTGGGCAA GCCATTCCGC CCACAACGCC ACGCGCATCA
701 TCCGCAGCGG CAACATCGGC AAGGGTCTTC AAGCACTCGG ATACAACGAC
751 GAAACGTCCA GACACGCGCT CCTGCGCTAC CGCGAAACCG TCGAACAGTC
801 GCCCCTCTAC CAAAAATAC AGACAGGACG CATCGACTGG CAGAGCGTCC
851 AAACCCGCCT CATCAGCGAC GACCCTGCAA AAGGACTCGA CCGCGACCGC
901 CGCAAACCGC CGATTGCCGG GCGGCTGCAA GACGCGCTCA AACAGCCCGA
951 AAAAAGCGTC TATCTGGTTT CACCCTATTT CGTCCCCACA AAATCCGGCA
1001 CAGACGCACT GGCAAACTG GTGCAGGACG GCATAGACGT TACCGTCCTG
1051 ACCAACTCGC TACAGGCGAC CGACGTTGCC GCCGTCCATT CCGGCTATGT
1101 CAAATACCGA AAACCGCTGC TCAAAGCCGG CATCAAATC TACGAGCTGC
1151 AACCAACCA TGCCGTCCCT GCCACAAAAG ACAAAGGCCT GACCGGCAGC
1201 TCCGTAACCA GCCTGCATGC CAAAACCTTC ATTGTGGACG GCAAACGCAT
1251 CTTTCATCGG TCATTCAACC TCGACCCCGG TTCCGCACGG CTCATACTG
1301 AAATGGGCGT TGTATCGAA AGCCCCAAA TCGCAGAACA GATGGAGCGC
1351 ACCCTTGCCG ATACCTCACC CGAATACGCC TACCGCGTTA CCCTCGACAG
1401 GCACAACCGC CTGCAATGGC ACGATCCCGC CACCCGAAAA ACCTACCCGA
1451 ACGAACCCGA AGCCAACTT TGGAAACGCA TCGCCGCAA AATCTATCC
1501 CTGCTGCCCA TAGAAAGTTT ATTATAG

```

This corresponds to the amino acid sequence <SEQ ID 550; ORF 2978.a>:

```

a987. pep
1  MKTRSLISLL CLLLCSCSSW LPPLEERTES RHFN|TSKPVR LDNILQIRHT
51  PHTNGLSDIY LLNDPHEAFA ARAALIESAE HSLDLQYYIW RNDISGRLLF
101 NLVYLAERG VRVRL|LLDN NTRGLD|LLL ALD|SHPNIEV RLFNPFVLRK
151 WRALGYLTD FRLNRRMHNK SFTADNRATI LGGRNIGDEY FKVGEDTVFA
201 DLDILATGSV VGEVSHDFDR YWASHSAHNA TRIIRSGNIG KGLQALGYND
251 ETSRHALLRY RETVEQSPLY QKIQTGRIDW QSVQTRLISD DPAKGLDRDR
301 RKPP|IAGRLQ DALKQPEKSV YLVSPYFVPT KSGTDALAKL VQDGIDVTVL

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1397

351 TNSLQATDVA AVHSGYVKYR KPLLKAGIKL YELQPNHAVP ATKDKGLTGS  
 401 SVTSLHAKTF IVDGKRIFIG SFNLDPARSAR LNTEMGVVIE SPKIAEQMER  
 451 TLADTSPEYA YRVTLDRHNR LQWHDPAIRK TYPNEPEAKL WKRIAAILLS  
 501 LLPIESLL\*

m987/a987 98.8% identity in 508 aa overlap

	10	20	30	40	50	60
m987. pep	MKTRSLISLLCLLLSCSSWLPPEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
a987	MKTRSLISLLCLLLSCSSWLPPEERTESRHFNTSKPVRLDNILQIRHTPHTNGLSDIY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m987. pep	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
a987	LLNDPHEAFAARAALIESAEHSLDLQYYIWRNDISGRLLFNLVYLAERGVRVRLLLDDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m987. pep	NTRGLDDLLALDSHPNIEVRLNPFVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI					
a987	NTRGLDDLLALDSHPNIEVRLNPFVLRKWRALGYLTDFPRLNRRMHNKSFADNRATI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m987. pep	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGDIG					
a987	LGGRNIGDEYFKVGEDTVFADLDILATGSVVGEVSHDFDRYWASHSAHNATRIIRSGNIG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m987. pep	KGLQALGYNDTSRHALRYRETVEQSPLYQKIQTGCIDWQSVTRTLISDDPAKGLDRDR					
a987	KGLQALGYNDTSRHALRYRETVEQSPLYQKIQTGRIDWQSVQTRTLISDDPAKGLDRDR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m987. pep	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA					
a987	RKPPPIAGRLQDALKQPEKSVYLVSPYFVPTKSGTDALAKLVQDGIDVTVLNLSLQATDVA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m987. pep	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLSHAKTFIVDGKRIFIG					
a987	AVHSGYVKYRKPLLKAGIKLYELQPNHAVPATKDKGLTGSSVTSLSHAKTFIVDGKRIFIG					
	370	380	390	400	410	420
	430	440	450	460	470	480
m987. pep	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTTPAYAYRVTLDRHNRLLQWHDPAIRK					
a987	SFNLDPARSARLNTEMGVVIESPKIAEQMERTLADTSPEYAYRVTLDRHNRLLQWHDPAIRK					
	430	440	450	460	470	480
	490	500	509			
m987. pep	TYPNEPEAKLWKRIAAILLSLLPIESLLX					
a987	TYPNEPEAKLWKRIAAILLSLLPIESLLX					
	490	500				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2979>:

g988.seq

1 ATGAATAAAA ATATTAAATC TTAAATTTA CGGGAAAAAG ACCCGTTTTT

1398

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51  AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCCAGT CGGgaATGGA
101 TAATCGAATT GTTGGAGCGC AAAGGTGTGC CTTCAAAAAT CGAATCGCTT
151 GCACGCGAGC TGTCGATTAC GGAAGacgag tATGTCTTTT TTGAACGCCG
201 TCTGAaggCG atgGCGCGGG AcggtCAGGT TTTAATCAAC CGCCgaggcg
251 CagttTGCGc gGCGgacaag ctgGATTtGG TCAAATGccg .Cgtcgaggcg
301 catAAGGAcg gtttcggctt cgcCGTGCCG CTCATGCCGA TGGACGAAGG
351 GGATTTCTGT TTATACGAAC GCCAgatgcg tggTGtcatG CAcggcgaca
401 ccggttACCGT CCGTCCTGcG ggtatggaCC GCAGGGGccg ccgcGAAGgg
451 acgtttcttGG ATATTGTCTGA ACGCGCGCAA AGCAAAGTTG TCGGCCGTTT
501 CTATATGGAT AGGGGCGTGG CGATTTTGGG GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTGTtGGAA CCGGACGGCG TGGCGCGTTT CAAACCCGAA
601 TCCGGTCAGG TTATCGTCGG CAAAATTGAG GTTTATCCCG AGCAAAACCG
651 GCCTGCAGTG GCAAAAATCA TTGAAGTTTT GGGCGATTAT GCCGACAGCG
701 GGATGGAAAt cgAAATTGCC GTGCGCAAGC ATCATTtGCC GCaccgaATC
751 AGTGAagcgt gtGcCAAAATC CGcgaAAAAA Attcccgacc ATGTACGCAA
801 AAGCGATTtG AAAGGCCGCG TCGATTtGTG CGACCTtCCT TTGGTAACGA
851 TAGACGCGCA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
901 GTCGGACGCA ATTACCGCCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
951 TGTCCGCCCT GACGATGCGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
1001 CGGTGTATTT CCCGCGCCGT ATGATTCCGA TGCTGCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
1101 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTATC
1151 CCGCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGGAAA
1201 TGGCTTTTcAG ACGGCATCGG GAATCCGCAC AAAGCCCAAA TCGACACGCT
1251 TTAACAAGCTG TTTAAATTTT TGCAGAAAAA ACGTCTGGCG CGCGGGGCGG
1301 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGACGA CAACGGCAAA
1351 ATCGAAAAAA TTGTCCCGCT CGTCCGCAAC gatGCCACA AGCTGATTGA
1401 AGAATGTATG CTGGCGGCGA ATGTTTGCGC GCGGATTTT CTGTTGAAAA
1451 ACAACATAC GGCTTTGTTC CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1501 CTCGCCACCC TCGCGAGCA GCTCGGTCTG TTGGGGCTTc AACTTGGCGG
1551 CGGCGACAAC CCGTCGCGGA AAGACTATGC CGCGCTTGCC GAACAATTCA
1601 AAGGCAGGCC GGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1651 CAGCAGGCGG TTTACGAACC GCATTGCGAA GGGCATTTCG GTTTGGCTTA
1701 TGAAGCATAC GCCCACTTTA CCTCGCCCAT CCGCGCTAT CCGACCTGA
1751 CCGTCCACCG TGCCATCAAA GCCGTATTGA ACCGGAACAC CTACACGCCA
1801 AACAAAAGCT GGCAGGCTTT GGGCGTGCAT ACTTCGTTTT GCGAACGCCG
1851 TGCCGACGAT GCTGGCCGCG ATGTGGAATA CTGGCTGAAA ACTTATTATA
1901 TGCGCGATAA GGTCCGGTGA ATATTtGAAG GcaaaatCtc ccgggggtgtg
1951 gcaaaTtttg gaATATTtGT CACTTtGGAC GATATccata tcgacggtct
2001 ggtacaTATC AGCGatttgg gcgaAGATTA TTTCaacttc cgccccgAAA
2051 TCATGGCAAT CGAAGGCGAA CGCAGCGGCA TCCGTTTCAA TATGGGGGAC
2101 AGGGTTGCCG TCCGGGTCGC GCGTGCCGAT TTGGATGATG GAAAAATCGA
2151 CTTTGTCTTA ATTGCCGGAG AAAGCGGCAG GCGGCGGAAG GTCAAATTAT
2201 CCGCATCTGC CAAACCGGCA GGGGCGGCGG GGAAAGGGA ATCGAAAAAC
2251 ACCGCCGAGA AAAAAACAGC CCGATGCGGC AAAGTAAGGG GAAGGGGCGT
2301 GCCTGCCGTT GCCGAATCGG GAAAAAGGC AAAGAAACCG GTTCCGATTA
2351 AGGTCAAAAA ACGGAAAGGC AAATCATAA

```

This corresponds to the amino acid sequence <SEQ ID 2980; ORF 988.ng>:

g988.pep

```

1  MNKNIKSLNL REKDPFLSRE KQRYEHPLPS REWIIELLER KGVPSKIESL
51  ARELSITEDE YVFFERRLKA MARDGQVLIN RRGAVCAADK LDLVKCRVEA
101 HKDGFGFVAV LMPMDEGDFV LYERQMRGVM HGDTVTVRPA GMDRRGRREG
151 TFLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSVILE PDGVARFKPE
201 SQQVIVGKIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHRF
251 SEACAKSAKK IPDHVRKSDL KGRVDLCDLP LVTIDGETAR DFDDAVFAEK
301 VGRNRYRLVA IADVSHYVRP DDAIDADAQE RSTSVYFPRR MIPMLPENLS
351 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK
401 WLSDGIGNPH KAQIDTLTKL FKILQKKRLA RGAVEFESVE TQMIFDDNGK
451 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK
501 LATLREQLGL LGQLQGGGDN PSPKDYAALA EQFKGRPDAE LLQVMMLRSM
551 QQAVYEPHCE GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNRKTYTP
601 NKSWQALGVH TSFCERRADD AGRDVENWLK TYMRDKVGE IFEGKISRGV
651 ANFGIFVTLD DIHIDGLVHI SDLGEDYFNF RPEIMAIEGE RSGIRFNMGD
701 RVAVRVARAD LDDGKIDFVL IAGESGRRRK VKLSASAKPA GAAGKGKSKT
751 TAEKKTARCG KVRGRGVPVAV AESGKKAKKP VPIKVKRKG KS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2981>:

```

m988. seq (partial)
1  ..ACAGTTCTGG ATATTGTCGA ACGCGCGCAA AGCAAAGTGG TCGGCCGTTT
51  CTATATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
101 ACCAAAGCAT CGTATTGGAA CCGGACGGCG TGGCGCGTTT CAAACCTGAA
151 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
201 GCCGGCAGTG GCAAAAATCA TCGAAGTTTT GGGCGATTAT GCCGACAGCG
251 GCATGGAGAT TGAATTGCC GTGCGCAAGC ATCATTTGCC GCACCAATTC
301 AGTGAAGCGT GTGCCAAAGC TGCGAAAAAA ATTCCCGTCC ATGTACGCAA
351 AAGCGATTG AAAGGCCGCG TCGATTGCG CGACCTGCCT TTGGTAACGA
401 TAGACGGCGA AACGGCGCGC GATTTCGACG ACGCGGTGTT TGCCGAAAAA
451 GTCGGACGCA ATTACCGTCT GGTCTGGCG ATTGCGGATG TCAGCCATTA
501 TGTCCGCCCT GACGATGTGA TTGATGCAGA TGCTCAAGAA CGCAGTACCA
551 GCGTATATTT CCCGCGCCGT GTGATTCCGA TGCTGCCGGA AAACCTGTCT
601 AACGGCATT TCTCGCTCAA TCCCGATGTC GAGCGTTTGT GTATGGTGTG
651 CGATATGGTC GTTACCTATG CGGGCAATAT CAAAGAATAC CGCTTCTACC
701 CCGCCGTAAT GCGCTCTCAT GCCGCGCTGA CCTACAACCA AGTTTGGAAA
751 TGGATTTTCA ACGCATCGA CCATCGTAC AAAGCCCAA TCGACACCTT
801 TTACAACTC TTCAAATCC TTCAGAAAAA GCGTTTCGAA CGCGGCGCGG
851 TGGAGTTTGA AAGCGTCGAA ACCCAGATGA TTTTCGATGA CAACGGCAAA
901 ATCGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
951 AGAATGTATG CTGGCGGCGA ATGTTTGCGC AGCGGATTC CTGTTGAAAA
1 001 ACAAGCATAC GGCTTTGTTT CGCAACCATT TGGGCCCCAC GCCCGAAAAA
1 051 CTCGCCACCC TGGCGAGCA GCTCGGTCTG TTGGGGCTTC AACTTGGCGG
1 101 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGTC GAACAATTCA
1 151 AAGGCAGACC TGATGCCGAA TTGCTGCAAG TCATGATGTT GCGCTCCATG
1 201 CAGCAGGCGG TTACGAACC GCATTGCGAC GGACACTTTG GTCTTGCTTA
1 251 CGAAGCATAC GCCCACTTCA CCTCGCCCAT CCGCCGCTAT CCCGACCTGA
1 301 CCGTACACCG CGCCATCAA GCCGTGTTGA ATCAGCAAAC CTACACGCCA
1 351 AAAAAAGCT GGCAGGCTTT GGGCGTGCAT ACCTCGTTCT GTGAGCGCCG
1 401 TGCCGACGAC GCCAGCCGCG ACGTGAAAAA CTGGCTGAAA ACCTATTATA
1 451 TGCGCGATAA GGTGGCGGAA GTATTGCAAG GTAAAATCTC CGGCATGACC
1 501 AGTTTTGGTA TCTTTGTAAC ACTGGACGGC ATCCACATTG ACGGCTTGGT
1 551 GCATATCAGC GATTTGGGCG AAGACTATTT CAACTTCCGC CCCGAAATCA
1 601 TGGCAATCGA AGGCGAACGC AGCGGCATCC GTTTCACAT GGGGGACAGG
1 651 GTTGCCGTCC GGGTCGCCC TGCCGATTG GATGACGGAA AAATCGATTT
1 701 TGTCTGATT GCCGGGGGGA GCGGCAGGG GCGGAAAGTT AAATCATCCG
1 751 CGTCTGCCAA ACCGGCAGGG ACGGCGGGGA AAGGGAAGCC GAAAAACGCC

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1400

1801 GCCGAGAAAA AAACAGCCCG AGGCGGCAAA GTAAGGGGAA GGGGCGCGTC  
 1851 TGCCGCCGCA GAATCGAGGA AAAAGGCAAA GAAACCGTT CCGATTAAGG  
 1901 TAAAAAACG GAAAGGCAAA TCATAA

This corresponds to the amino acid sequence <SEQ ID 2982; ORF 988>:

m988.pep (partial)

1 ..TVLDIVERAQ SKVVGRFYMD RGVAILEPED KRLNQSIVLE PDGVARFKPE  
 51 SGQVIVGEIE VYPEQNRPAV AKIIEVLGDY ADSGMEIEIA VRKHHLPHQF  
 101 SEACAKAAK IPVHVRKSDL KGRVDLRDL LVTIDGETAR DFDDAVFAEK  
 151 VGRNYRLVVA IADVSHYVRP DDVIDADAQE RSTSVYFPRR VIPMLPENLS  
 201 NGICSLNPDV ERLCMVCDMV VTYAGNIKEY RFYPAVMRSH ARLTYNQVWK  
 251 WISDGIDHPY KAQIDTLYKL FKILQKKRFE RGAVEFESVE TQMIFDDNGK  
 301 IEKIVPVVRN DAHKLIEECM LAANVCAADF LLKNKHTALF RNHLGPTPEK  
 351 LATLREQLGL LGLQLGGGDN PSPKDYAALV EQFKGRPDAE LLQVMMLRSM  
 401 QQAVYEPHCD GHFGLAYEAY AHFTSPIRRY PDLTVHRAIK AVLNQOQTYTP  
 451 KKSQWALGVH TSFCERRADD ASRDVENWLK TYMRDKVGE VFEGKISGMT  
 501 SFGIFVTLDG IHIDGLVHIS DLGEDYFNFR PEIMAIEGER SGIRENMGDR  
 551 VAVRVARADL DDGKIDFVLI AGGSGRGRKV KSSASAKPAG TAGKGKPKTA  
 601 AEKKTARGGK VRGRGASAAA ESRKKAKKPV PIKVKRKGK S\*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m988/g988 94.2% identity in 642 aa overlap

m988.pep				10	20	30
				TVLDIVERAQSKVVGRFYMDRGVAILEPED		
g988	LYERQMRGVMHGDTVTVRPAGMDRRGRREGTF	LDIVERAQSKVVGRFYMDRGVAILEPED				
	130	140	150	160	170	180
m988.pep		40	50	60	70	80
		KRLNQSIVLEPDGVARFKPESGQVIVGEIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA				
g988		KRLNQSIVLEPDGVARFKPESGQVIVGKIEVYPEQNRPAVAKIIEVLGDYADSGMEIEIA				
	190	200	210	220	230	240
m988.pep		100	110	120	130	140
		VRKHHLPHQFSEACAKAAKIPVHVRKSDLKGRVDLRDLPLVTIDGETARDFDDAVFAEK				
g988		VRKHHLPHRFSEACAKSAKIPDHVRKSDLKGRVDLCDLPLVTIDGETARDFDDAVFAEK				
	250	260	270	280	290	300
m988.pep		160	170	180	190	200
		VGRNYRLVVAIADVSHYVRPDDVIDADAQERSTSVYFPRRVIPMLPENLSNGICSLNPDV				
g988		VGRNYRLVVAIADVSHYVRPDDAIDADAQERSTSVYFPRRMIPMLPENLSNGICSLNPDV				
	310	320	330	340	350	360
m988.pep		220	230	240	250	260
		ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWISDGIDHPYKAQIDTLYKL				
g988		ERLCMVCDMVVTYAGNIKEYRFYPAVMRSHARLTYNQVWKWLSDGIGNPHKAQIDTLYKL				
	370	380	390	400	410	420
m988.pep		280	290	300	310	320
		FKILQKKRFERGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
g988		FKILQKKRLARGAVEFESVETQMIFDDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988.pep		340	350	360	370	380
		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALVEQFKGRPDAE				
g988		LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSPKDYAALAEQFKGRPDAE				

	490	500	510	520	530	540
m988. pep	400	410	420	430	440	450
	LLQVMMLRSMQQAVYEPHCDGHFGLAYEAYAHFTSP	IRRYPD	LT	VHRAIKAVLN	QQTYTP	
g988	LLQVMMLRSMQQAVYEPHCEGHFGLAYEAYAHFTSP	IRRYPD	LT	VHRAIKAVLN	NRRTYTP	
	550	560	570	580	590	600
m988. pep	460	470	480	490	500	509
	KKSWQALGVHTSFCERRADDASRDVENWLKTY	YMRDKVGEVF	EKGIS-GMTS	FGIFVTLD		
g988	NKSWQALGVHTSFCERRADDAGR	DVENWLKTY	YMRDKVGEIF	EKGISRGVAN	FGIFVTLD	
	610	620	630	640	650	660
m988. pep	510	520	530	540	550	569
	GIHIDGLVHISDLGEDYFNFRPEIMAIEGERSG	IRFNMGDRVAVR	VARADLDDG	KIDFVL		
g988	DIHIDGLVHISDLGEDYFNFRPEIMAIEGERSG	IRFNMGDRVAVR	VARADLDDG	KIDFVL		
	670	680	690	700	710	720
m988. pep	570	580	590	600	610	629
	IAGGSGRGRKVKSSASAKPAGTAGKGPKTAAE	KKTARGGKVRGR	GSAAAESR	KKAKKP		
g988	IAGESGRRRKVKLSASAKPAGAAGKGKSKTTAE	KKTARCGKVRGR	GVPAVAES	GKKAKKP		
	730	740	750	760	770	780
m988. pep	630	640				
	VPIKVKKRKGK	KSX				
g988	VPIKVKKRKGK	KSX				
	790					

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a988.seq
1 ATGAATAAAA ATATTAATC TTTAAATTTA CGGGAAAAAG ACCCGTTTTT
51 AAGTCGTGAA AAACAGCGTT ATGAACATCC TTTGCCAGT CCGGAATGGA
101 TAATCGAGCT GCTTGAACGT AAAGGCCTAC CATCCAAGAT TGAAGCTTTG
151 GTACGCGAAT TGTCGATTAA GGAAGAAGAG TACGAATTTT TCGAACGTCG
201 TCTGAAGGCG ATGGCGCGGG ACAGTCAGGT TTTFATCAAC CGTCGGGGCG
251 CGGTTTGCGC GCGGACAAA TTGGATTGCG TCAAATGCCG TGTCAGGCGC
301 CACAAAGACC GCTTCGGTTT CGCGTGCCG CTCACGCCCG CCAAAGACGG
351 TGATTTTGTC TTGTACGAAC GCCAGATGCG CGGCATTATG CACGGCGATA
401 TTGTCACTGT TCGTCCTGCC GGCATGGACG GTAGGGGCGG CCGCGAAGGG
451 ACGGTTCTGG ATATTGTGCA AGCGCGCAA AGCAAAGTGG TCCTCGGTTT
501 CTANATGGAT AGGGGCGTGG CGATTTTGGA GCCGGAAGAC AAGCGTCTGA
551 ACCAAAGCAT CGTATTGGAA CCGACGGCG TGCGCGTTT CAAACCTGAA
601 TCCGGTCAGG TCATCGTCGG CGAAATTGAG GTTTATCCTG AGCAAAACCG
651 GCCGCGAGT GC AAAAATCA TCGAAGTTT GGGCGATTAT GCCGACAGCG
701 GCATGGAGAT TGAATTGCC TGCACAAGC ATCATTTGCC GCACCAATTC
751 AGTGAAGCGT GTGCCAAAGC CGCGAAAAAA ATTCCCGACC ATGTACGCAA
801 AAGCGATTG AAAGGCCGCG TCGATTGCG CGACTGCCT TTGGTAACGA
851 TAGACGGCGA AACGGCTCGA GATTTTGACG ATCGCGTGT TGCCGAGAAA
901 ATCGGACCA ATTACCGTCT GGTCTGGCG ATTGCCGATG TCAGCCATTA
951 TGTCGCCCC GATGACGCTA TCGACAGCA CGCTCAGGAA CGCAGCACCA
1001 GTGTTTACTT CCCGCGCCGC GTGATTCCCA TGTGTCCGGA AAACCTGTCC
1051 AACGGCATCT GCTCGCTCAA TCCTCATGTC GAGCGTTTGT GTGTGGTGTG
1101 CGATATGGTT ATCACTTAGC CGGGCAATAT CAAAGAATAC CGCTTCTACC
1151 CGCCCGTGAT GCGCTCTCAT GCCCGCCTGA CCTACAACCA AGTTTGAAA
1201 TCGCTTTAG CCGCATCGA GCATCCGTTT AAAACCCAAA TCGCACGCT
1251 TTACAAATC TTCAAATCC TTCAGAAAAA GCGTTTCAA CGCGGGGCGG
1301 TGGAGTTTGA CAGCATCGAA ACCCAAATGC TTTTCGACGA CAACGGTAAA
1351 ATTGAAAAAA TCGTCCCCGT TGTCCGCAAC GATGCCACA AGCTGATTGA
1401 AGAATGTAT TTGGCGGCAA ACGTTTGCGC AGCGGATTTT CTGTTGAAAA
1451 ACAAGCATAC CGCATGTTC GCAACCAATT TGGGGCCCAC GCCCGAAAA
1501 CTCGCGCCT TCGCGAGCA GCTCGTCTG TTGGGGCTTC AACTTGGCGG
1551 CGGCGACAAC CCGTCGCCGA AAGACTATGC CGCGCTTGCC GGACAGTTCA
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a988.pcp

Dep	1	MNKNIKSLNL	REKDFFLSRE	KORYEHPLPS	REWIIELLER	KGVPSKIEAL
	51	VRELSIKEEE	YEFFERRLKA	MARDGOVLIN	RRGAVCAADK	LDLVKCRVKA
	101	HKDRFGFAVP	LTPAKDGFV	LYERQMRGIM	HGDIVTVRPA	GMDGRRREG
	151	TVLDIVERAQ	SKVVGRFXMD	RGVAILEPED	KRLNQSVILE	PDGVARFKPE
	201	SGQVIVGEIE	VYPEQNRPAV	AKIIEVLGDY	ADSGMEIEIA	VRKHHLPHQF
	251	SEACAKAAKK	IPDHVRKSDL	KGRVLDRLDL	LVTMDEIETAR	DFDDAVFAEK
	301	IGRNYRLVVA	IADVSHYVRP	DDAIDTDAQE	RSTSVYFPRR	VIPMLPENLS
	351	NGICSLNPHV	ERLCVVCDMV	ITYAGNIKEY	RFYPAVMRSH	ARLTYNQVWK
	401	WLSGGIEHPF	KTQDITLYKL	FKILQKKRFE	RGAVEFDSIS	TQMLFDDNGK
	451	IEKIVPVVRN	DAHKLIEECM	LAANVYAAAL	LLKNKHTALF	RNHLGPTPEK
	501	LAALREQLGL	LGLQGGGDN	PSPKDYAALA	GQFKGRPDAE	LLQVMTLRSM
	551	QQAVYEPHCD	GHFGLAYEAY	AHFTSPIRRY	PDLTVHRAIK	AVLNQQTYP
	601	KKSQWALGVH	TSFCERRADD	ASRDVENWLK	TYYMRDKVGE	VFEGKISGMT
	651	SFGIFVTLDG	IHIDGLVHS	DGEDGYFNFR	PEIMAIEGER	SGIRFNMGDR
	701	VAVRVARADD	DDGKIDFVLI	AGGSGRGRKV	KSSASAKPAG	TAGKGPKPTA
	751	AEEKTARGGK	VRGRGASAAA	ESRKKAAKPV	PIKVKKRKGK	S*

m988/a988 97.0% identity in 641 aa overlap

				10	20	30
m988.pep				TVLDIVERAQS	KVVGRFYMDRG	VAILPED
a988	LYERQMRGIMHGD	IVTVRPAGMDGR	GRREGTVLD	DIVERAQS	KVVGRFXMDRG	VAILPED
	130	140	150	160	170	180
	40	50	60	70	80	90
m988.pep	KRLNQSIVLEPD	GVARFKPESGQ	VIVGEIEVYPE	QNRPAVAKIIE	VLGDYADSGME	IEIA
a988	KRLNQSIVLEPD	GVARFKPESGQ	VIVGEIEVYPE	QNRPAVAKIIE	VLGDYADSGME	IEIA
	190	200	210	220	230	240
	100	110	120	130	140	150
m988.pep	VRKHHLPHQFSE	ACAKAAKKIPV	HVRKSDLKGRV	DLRDLPLVTID	GETARDFDDAV	FAEK
a988	VRKHHLPHQFSE	ACAKAAKKIPD	HVRKSDLKGRV	DLRDLPLVTID	GETARDFDDAV	FAEK
	250	260	270	280	290	300
	160	170	180	190	200	210
m988.pep	VGRNYRLVVAIA	ADVSHYVRPDD	VIDADAQERST	SVYFPRRVIP	MLPENLSNGIC	SLNPDV
	:					
a988	IGRNYRLVVAIA	ADVSHYVRPDD	AIDTDAQERST	SVYFPRRVIP	MLPENLSNGIC	SLNPHV
	310	320	330	340	350	360
	220	230	240	250	260	270
m988.pep	ERLCMVCDMVV	TYAGNIKEYRF	YPAVMRSHARL	TYNQVWKWISD	GIDHPYKAQID	TLTKL
a988	ERLCVCDMVITY	AGNIKEYRFY	PAVMRSHARLT	YNQVWKWLSGG	IEHPFKTOIDT	LYKL

1403

	370	380	390	400	410	420
m988. pep	280	290	300	310	320	330
a988	FKILQKKRFERGAVEFESVETQMIFFDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF	FKILQKKRFERGAVEFDSIETQMLFFDNGKIEKIVPVVRNDAHKLIEECMLAANVCAADF				
	430	440	450	460	470	480
m988. pep	340	350	360	370	380	390
a988	LLKNKHTALFRNHLGPTPEKLATLREQLGLLGLQLGGGDNPSFKDYAALVEQFKGRPDAE	LLKNKHTALFRNHLGPTPEKLAALREQLGLLGLQLGGGDNPSFKDYAALAGQFKGRPDAE				
	490	500	510	520	530	540
m988. pep	400	410	420	430	440	450
a988	LLQVMMLRSMQQAVYEPHCDGHFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP	LLQVMMLRSMQQAVYEPHCDGHFLAYEAYAHFTSPIRRYPDLTVHRAIKAVLNQQTYP				
	550	560	570	580	590	600
m988. pep	460	470	480	490	500	510
a988	KKSWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG	KKSWQALGVHTSFCERRADDASRDVENWLKTYIMRDKVGEVFEGKISGMTSFGIFVTLDG				
	610	620	630	640	650	660
m988. pep	520	530	540	550	560	570
a988	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI	IHIDGLVHISDLGEDYFNFRPEIMAIEGERSGIRFNMGDRVAVRVARADLDDGKIDFVLI				
	670	680	690	700	710	720
m988. pep	580	590	600	610	620	630
a988	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV	AGGSGRGRKVKSSASAKPAGTAGKGPKTAAEKKTARGGKVRGRGASAAAESRKAKKPV				
	730	740	750	760	770	780
m988. pep	640					
a988	PIKVKKRKGKXS					
	790					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2985>:

g989. seq

```

1   ATGACCCCTT TCACACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51  TGCCGCCGCA TCTGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCACGGCA AATGCCGCCG ACGCGTCGAC CATCTTCTAC
151 AATCCC GCCGCTGACAA ACTCGACAGC AGCCAGATT CCGTCAACGC
201 CAACATCGTG CTGCCCAGCA TTCATTATGA AGCAGATTCC GCCACCGACT
251 TTACCGGGCT TCCCGTCCAA GGTTCATAAA ACGGCAAAAT CACCAAAACC
301 ACGGTCGCAC CCCACATTTA CGGCGCATAA AAAGTCAACG ACAATCTGAC
351 CGTGGGCTTG GCGGTGTACG TCCCCTTCGG CTCTGCCACC GAATACGAAA
401 AAGATTCGGT GTTGCGCCAC AACATCAACA AACTCGGTCT GACCAGCATC
451 GCCGTCGAAC CTGTCGCCGC GTGGAAACTC AACGAACGCC ATTCCTTCGG
501 CGCAGGCATC ATCGCCCAAC ATAATTCCGC CGAACTGCCG AAATATGCCG
551 ACTGAGGAAT CCCAAAAAAA GCGCAATGCG TGCAAGCAAC ACCTTCTAAT
601 CCTACTGCCG CTGCTCAAAT CAAGGCCGAC GGACACGCCG ATGTCAAAGG
651 CAGCGATTGG GCGCTCGGCT ACCAATGGC GTGGATGTGG GACATCAACG
701 ACCGCGCGCG CGTGGGCGTG AACTACCGTT CCAAAGTTTC ACACACGCTC
751 AAAGGCGATG CCGAATGGGC GGCAGACGGC GCGGCGGCGA AACACAGTG
801 GAATGACAAT ATGCTCACAC CGCTCGGTTA CACGCGCAAT GAAAAAGCCA
851 GTGTCAAAT CGTAACGCCT GAGTCTTGT CCGTACACGG CATGTACAAA

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1404

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901 GTGTCCGACA AAGCCGACCT GTTCGGCGAC GTAACCTGGA CGCGCCACAG
951 CCGCTTCAAT AAGGCGGAAC TGTTTTTTGA AAAAGAAAAA AATATTGCTA
1001 ATGGCAAAAA ATCCGACCGC ACCACCATCA CCCCCAACTG GCGCAACACC
1051 TACAAAGTCG GCTTGGGCGG TTCTTATCAA ATCAGCGAAC CGCTGCAACT
1101 GCGCGTCGGC ATCGCTTTTG ACAAACCGCC TGTCCGCAAC GCCGACTacc
1151 GCATGAACAG CCTGCCCGAC GGCAACCGCA TCTGGTTCTC CGCCGGCATG
1201 AAATACCATA TCGGCAAAAA CCACGTCGTC GATGCCGCCT ACACCCACAT
1251 CCACATCAAC GACACCAGCT ACCGCACGGC GAAGGCAAGC GGCAACGATG
1301 TGGACAGCAA AGGTGCGTCT TCGGCACGTT TCAAAAACCA CGCCGACATC
1351 ATCGGCCTGC AATACACCTA CAAATTCAAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 2986; ORF 989.ng>:

```

g989. pep
1 MTPFTLKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAADASTIFY
51 NPAGLTKLDS SQISVNANIV LPSIHYEADS ATDFTGLPVQ GSKNGKITKT
101 TVAPHIYGAY KVNDNLTVGL GVVVPFGSAT EYEKDSVLRH NINKLGLTSI
151 AVEPVAAWKL NERHSFGAGI IAQHNSAELR KYAD*GIPKK AQMLQATPSN
201 PTAAAIQKAD GHADVKGSDW GVGYQLAWMW DINDRARVGV NYRSKVSHTL
251 KGDAEWAADG AAQKQWQNDN MLTPLGYTAN EKASVKIVTP ESLSVHGMKY
301 VSDKADLFGD VTWRHSRFN KAELFFEKEK NIANGKKS DR TTITPNWRNT
351 YKVLGGSYQ ISEPLQLRVG IAFDKPPVRN ADYRMNSLPD GNRIWFSAGM
401 KYHIGKNHVV DAAYTHIHIN DTSYRTAKAS GNDVDSKGAS CARFKNHADI
451 IGLQYTYKFK *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2987>:

```

m989. seq
1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTGCTGCTCG GCACTGCCTT
51 TGCCGCGGCA TCCGTCCACG CATCCGGCTA CCACTTCGGC ACACAGTCGG
101 TCAACGCGCA AAGCAGCGCA AATGCCGCGC CCGCAGAAGC CGCCGACGCA
151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAAACTCG ACAGCAGCCA
201 GATTTCGGTC AACGCCAACA TCGTGTGCTC CAGCATTTCAT TATGAGGCGG
251 ATTCGCGCAC CGACTTTACC GGGCTTCCCG TCCAAGGTTT GAAAAGCGGC
301 AAAATCACCA AAACCAACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTGG GCTTGGGCGT GTACGTCCCC TTCGGCTCTG
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGGA AACTCAACGA
501 CCGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCGCAAC
551 TGCGCAAATA TGCCGACTGG GGGATTAAGA GTAAAGCAGA GATATTGACG
601 GCAAAACCGC CCAAACCTAA CGGTGTAGCC GAAGCTGCAA AAATTGAGGC
651 CGACGGACAC GCCGATGTCA AAGGCAGCGA TTGGGGCTTC GGCTACCAAC
701 TGGCGTGGAT GTGGGACATC AACGACCGTG CGCGCGTGGG CGTGAACATC
751 CGTTCCAAAG TCTCGCACAC GCTCAAAGGC GATGCCGAAT GGGCGGCAGA
801 CGGCGCGGCG GCGAAAGCAA TGTGGAGTAC GATGCTTGCA GCAAACGGCT
851 ACACGGCGAA TGAAAAGGCC CGCGTTAAAA TCGTTACGCC TGAGTCTTTG
901 TCCGTACACG GTATGTACAA AGTGTCCGAT AAAGCCGACC TGTTCGGCGA
951 CGTAACTTGG ACGCGCCACA GCCGCTTCGA TAAGGCGGAA CTGGTTTTTG
1001 AAAAAGAAAA AACCGTCGTC AAAGGCAAAT CCGACCGCAC CACCATCACC
1051 CCCAACTGGC GCAACACCTA CAAAGTCGGC TTCGGCGGTT CTTATCAAAT
1101 CAGCGAACCG CTGCAACTGC GCGCCGGCAT CGCTTTTGAC AAATCGCCCG
1151 TCCGCAACGC CGACTACCGC ATGAACAGCC TACCCGACGG CAACCGCATC
1201 TGGTTCTCCG CCGGTATGAA ATACCATATC GGTA AAAACC ACGTCGTGCA
1251 TGCCGCCCTAC ACCCATATCC ACATCAACGA CACCAGCTAC CGCAGGCGA
1301 AGGCAAGCGG CAACGATGTG GACAGCAAAG GCGCGTCTTC CGCACGTTTC
1351 AAAAACCCAG CCGACATCAT CGGTCTGCAA TACACCTACA AATTCAAATA
1401 A

```

This corresponds to the amino acid sequence <SEQ ID 2988; ORF 989>:

```

m989. pep
1 MTPSALKKTV LLLGTAFAAA SVHASGYHFG TQSVNAQSTA NAAAAEADA
51 STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNDRHS FGAGIIAQHT SAELRKYADW GIKSKAEILT
201 AKPPKPNQVA EAAKIQADGH ADVKGS DWGF GYQLAWMWDI NDRARVGVNY
251 RSKVSHTLKG DAEWADGAA AKAMWSTMLA ANGYTANEKA RVKIVTPESL
301 SVHGMKYKSD KADLFGDVTW TRHSRFDKAE LVFEKEKTVV KGKSDRTTIT

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1405

351 PNWRNTYKVG FGGSYQISEP LQIRAGIAFD KSPVRNADYR MNSLPDGNRI  
 401 WFSAGMKYHI GKNHVVDAAI THIHINDTSY RTAKASGNDV DSKGASSARF  
 451 KNHADIIGLQ YTYKFK\*

Computer analysis of this amino acid sequence gave the following results:  
Homology with a predicted ORF from *N. gonorrhoeae*

g989/m989 90.0% identity in 468 aa overlap

	10	20	30	40	50
g989. pep	MTPFTLKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAA-----DASTIFYNPAGL				
m989	MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL				
	10	20	30	40	50
	60	70	80	90	100
g989. pep	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKNKGKITKTTVAPHIYGAYKVNDN				
m989	TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVNDN				
	70	80	90	100	110
	120	130	140	150	160
g989. pep	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSFGAGIIAQHN				
m989	LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSFGAGIIAQHT				
	130	140	150	160	170
	180	190	200	210	220
g989. pep	SAELRKYADXGIPKKAQMLQATPSNPTA---AAQIKADGHADVKGSDWGVGYQLAWMWDI				
m989	SAELRKYADWGIKSKAEILTAKPPKPNGVAEAAKIQADGHADVKGSDWGFYQLAWMWDI				
	190	200	210	220	230
	240	250	260	270	280
g989. pep	NDRARVGVNYSKVSHTLKGDAEWAADGAAKQQWNDNMLTPLGYTANEKASVKIIVTPES				
m989	NDRARVGVNYSKVSHTLKGDAEWAADGAAKAMWS-TMLAANGYTANEKARVKIIVTPES				
	250	260	270	280	290
	300	310	320	330	340
g989. pep	LSVHGMKYVSDKADLFGDVTWTRHSRFNKAELFFEKEKNIANGKKSDDRTTITPNWRNTYK				
m989	LSVHGMKYVSDKADLFGDVTWTRHSRFDKAEVFEKEKTVVKGK-SDRTTITPNWRNTYK				
	300	310	320	330	340
	360	370	380	390	400
g989. pep	VGLGGSYQISEPLQLRVGIAFDKPPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
m989	VGFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVDA				
	360	370	380	390	410
	420	430	440	450	460
g989. pep	AYTHIHINDTSYRTAKASGNDVDSKGASCARFKNHADIIGLQYTYKFKX				
m989	AYTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX				
	420	430	440	450	460

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2989>:

a989. seq

1 ATGACCCCTT CCGCACTGAA AAAAACCGTC CTACTGCTCG GCACTGCCTT  
 51 TGCCGCCGCA TCCGCACAAG CCTCCGGCTA CCACTTCGGC ACACAGTCGG  
 101 TCAACGCGCA AAGCACGGCA AATGCCGCGG CCGCAGAAGC CGCCGACGCA  
 151 TCGACCATCT TCTACAACCC TGCCGGCCTG ACCAACTCG ACAGCAGCCA  
 201 GATTTCGGTC AACGCCAACA TCGTGCTGCC CAGCATTCAT TATGAGGCGG  
 251 ATTCCGCCAC CGACTTTACC GGGCTTCCG TCCAAGGTC GAAAAGCGGC

1406

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301 AAAATCACCA AAACCACGGT CGCGCCCCAC ATCTACGGCG CATACAAAGT
351 CAACGACAAT CTGACCGTAG GCTTGGGCGT GTACGTCCCC TTCGGTTCGT
401 CCACCGAATA CGAAAAAGAT TCCGTGTTGC GCCACAACAT CAACAAACTC
451 GGTCTGACCA GCATCGCCGT CGAACCTGTC GCCGCGTGA AACTCAACGA
501 ACGCCATTCC TTCGGCGCAG GCATCATCGC CCAACATACT TCCGCCGAGC
551 TGCGCAAATA TGCCGACTGG GGGATTATGG AAAAAGCGAA AGCACTAAAA
601 GAAACACCCC CCAATCCAAC TAAAGCCGCC CAAATCAAAG CCGACGGACA
651 CGCCGATGTC AAAGGCAGCG ATTGGGGCTT CGGCTACCAA CTGGCGTGGA
701 TGTGGGACAT CAACGACCGT GCGCGCGTGG GCGTGAACTA CCGTTCCTAA
751 GTCTCACACA CGCTCAAAGG CGATGCCGAA TGGGCGGCAG ACGACGCAAT
801 GCGGAAACAG TTATGGGATG CAAACAAACT CGCACTGCTC GGCTACACGC
851 CAAGCGAAAA AGCCCGCGTT AAAATCGTTA CGCCCGAGTC TTTGTCCGTA
901 CACGGTATGT ACAAAGTGTC CGACAAAGCC GACCTGTTCG GCGACGTAAC
951 TTGGACGCGC CACAGCCGCT TCGATAAGGC GGAAGTGGTT TTTGAAAAAG
1 001 AAAAAACCAT CGTCAACGGC AAATCCGACC GCACCACCAT CACCCCCAAC
1 051 TGGCGCAACA CCTACAAAGT CGGCTTCGGC GGTTCTTATC AAATCAGCGA
1 101 ACCGCTGCAA CTGCGCGCCG GCATCGCTTT TGACAAATCG CCCGTCCGCA
1 151 ACGCCGACTA CCGCATGAAC AGCCTGCCCG ACGGCAACCG CATCTGGTTC
1 201 TCCGCCGCGA TGAATATCCA TATCGGCAAA AACCACGTCG TCGATGCCCG
1 251 CTACACCCAC ATCCACATCA ACGACACCAG CTACCGCAGC GCGAAGGCAA
1 301 GCGGCAACGA TGTGGACAGC AAAGGCGCGT CTCCGCACG TTTCAAAAAC
1 351 CACGCCGACA TCATCGGCCT GCAATACACC TACAAATTCA AATAA

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This corresponds to the amino acid sequence <SEQ ID 2990; ORF 989.a>:

```

a989.pep
1  MTPSALKKTV LLLGTAFAAA SAQASGYHFG TQSVNAQSTA NAAAAEAADA
51  STIFYNPAGL TKLDSSQISV NANIVLPSIH YEADSATDFT GLPVQGSKSG
101 KITKTTVAPH IYGAYKVDN LTVGLGVYVP FGSATEYEKD SVLRHNINKL
151 GLTSIAVEPV AAWKLNERHS FGAGIIAQHT SAELRKYADW GIMEKAKALK
201 ETPPNPTKAA QIKADGHADV KGSWDWFGYQ LAWMWDINDR ARVGVNYRSK
251 VSHTLKGDAE WAADDAMAKQ LWDANKLALL GYTPSEKARV KIVTPESLSV
301 HGMVKVSDKA DLFGDVTWTR HSRFDKAEIV FEKEKTIVNG KSDRTTITPN
351 WRNTYKVGFG GSYQISEPLQ LRAGIAFDKS PVRNADYRMN SLPDGNRIWF
401 SAGMKYHIGK NHVVDAAATH IHINDTSYRT AKASGNDVDS KGASSAREFN
451 HADIIGLQYT YKFK*

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m989/a989 93.1% identity in 467 aa overlap

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              10      20      30      40      50      60
m989.pep      MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
a989           MTPSALKKTVLLLGTAFAAASVHASGYHFGTQSVNAQSTANAAAAEAADASTIFYNPAGL
              10      20      30      40      50      60
m989.pep      TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVDN
a989           TKLDSSQISVNANIVLPSIHYEADSATDFTGLPVQGSKSGKITKTTVAPHIYGAYKVDN
              70      80      90      100     110     120
m989.pep      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
a989           LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGAGIIAQHT
              130     140     150     160     170     180
m989.pep      LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNDRHSGAGIIAQHT
a989           LTVGLGVYVPFGSATEYEKDSVLRHNINKLGLTSIAVEPVAAWKLNERHSGAGIIAQHT
              190     200     210     220     230     240
m989.pep      SAELRKYADWGIKSAEILTAQPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
a989           SAELRKYADWGIKSAEILTAQPPKPNGVAEAAKIQADGHADVKGSDWFGYQLAWMWDI
              250     260     270     280     290     299
m989.pep      NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANAEKARVKIVTPES
a989           NDRARVGVNYRSKVSHTLKGDAEWAADGAAAKAMW-STMLAANGYTANAEKARVKIVTPES

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1407

	240	250	260	270	280	290
m989. pep	300	310	320	330	340	350
	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEIVFEKEKTVVKGKSDRTTITPNWRNTYKV					
a989	LSVHGMVKVSDKADLFGDVTWTRHSRFDKAEIVFEKEKTVVNGKSDRTTITPNWRNTYKV					
	300	310	320	330	340	350
m989. pep	360	370	380	390	400	410
	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
a989	GFGGSYQISEPLQLRAGIAFDKSPVRNADYRMNSLPDGNRIWFSAGMKYHIGKNHVVDAA					
	360	370	380	390	400	410
m989. pep	420	430	440	450	460	
	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
a989	YTHIHINDTSYRTAKASGNDVDSKGASSARFKNHADIIGLQYTYKFKX					
	420	430	440	450	460	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2991>:

m990. seq

1	ATGTTTCAGAG	CTCAGCTTGG	TTCAAATACT	CGTTCTACCA	AAATCGGCGA
51	CGATGCCGAT	TTTTCATTTT	CAGACAAGCC	GAAACCCGGC	ACTTCCCATT
101	ATTTTTCAG	CGGTAAAACC	GATCAAAATT	CATCCGAATA	TGGGTATGAC
151	GAAATCAATA	TCCAAGGTAA	AAATTACAAT	AGCGGCATCC	TCGCCGTCGA
201	TAATATGCCC	GTGTCAAAA	AATATATTAC	AGAGAAGTAT	GGGGCTGATT
251	TAAAGCAGGC	GGTAAAAAGT	CAATTACAGG	ATTTATACAA	AACAAGACCG
301	GAAGCTTGGG	CAGAAAATAA	AAAACGGACT	GAGGAGGCGT	ATATAGCACA
351	GTTTGAACA	AAATTTAGTA	CGCTCAAACA	GACGATGCC	GATTTAATTA
401	ATAAATTGGT	AGAAGATTCC	GTACTCACTC	CTCATAGTAA	TACATCACAG
451	ACTAGTCTCA	ACAACATCTT	CAATAAAAAA	TTACACGTCA	AAATCGAAAA
501	CAAATCCAC	GTCGCCGGAC	AGGTGTTGGA	ACTGACCAAG	ATGACGCTGA
551	AAGATTCCCT	TTGGGAACCG	CGCCGCCATT	CCGACATCCA	TACGCTGGAA
601	ACTTCCGATA	ATGCCCGCAT	CGCCTGAAC	ACGAAAGATG	AAAACTGAC
651	CGTCCATAAG	GATTATGCGG	GCGGCGCGGA	TTTCTGTTC	GGCTACGACG
701	TGCGGGAGTC	GGACGAACCC	GCCCTGACCT	TTGAAGACAA	AGTCAGCGGA
751	CAATCCGGCG	TGGTTTGGGA	ACGCCGCCG	GAAAATCTGA	AAACGCTCGA
801	CGGGCGCAAA	CTGATTGCGG	CAAAAACGGC	GGATTCCGGT	TCGTTTGCCT
851	TTAAACAAAA	TTACCGGCAG	GGACTGTACG	AATTATTGCT	CAAGCAATGC
901	GAAGGCGGAT	TTTGCTTGGG	CGTGACGCGT	TTGGCTATCC	CCGAGGCGGA
951	AGCGGTTTTA	TATGCCCAAC	AGGCTTATGC	GGCAAATACT	TTGTTTGGGC
1001	TGCGTGCCGC	CGACAGGGGC	GACGACGTGT	ATGCCGCCGA	TCCGTCCCGT
1051	CAAAAATTGT	GGCTGCGCTT	CATCGGCGGC	CGGTGCGATC	AAAATATACG
1101	GGGCGGCGCG	GCTGCGGACG	GGTGGCGCAA	AGGCGTGCAA	ATCGGCGGCG
1151	AGGTGTTTGT	ACGGCAAAAT	GAAGGCAGCC	GACTGGCAAT	CGGCGTGATG
1201	GGCGGCAGGG	CCGGCCAGCA	CGCATCAGTC	AACGGCAAAG	GCGGTGCGGC
1251	AGGCAGTGAT	TTGTATGGTT	ATGGCGGGGG	TGTTTATGCT	GCGTGGCATC
1301	AGTTGCGCGA	TAAACAAACG	GGTGCCTATT	TGGACGGCTG	GTTGCAATAC
1351	CAACGTTTCA	AACACCGCAT	CAATGATGAA	AACCGTGCGG	AACGCTACAA
1401	AACCAAAGGT	TGGACGGCTT	CTGTCGAAGG	CGGCTACAAC	GCGCTTGTGG
1451	CGGAAGGCAT	TGTCGGAAAA	GGCAATAATG	TGCGGTTTTA	CCTACAACCG
1501	CAGCGCAGT	TTACCTACTT	GGGCGTAAAC	GGCGGCTTTA	CCGACGCGGA
1551	GGGGACGGCG	GTCGGACTGC	TCGGCAGCGG	TCAGTGGCAA	AGCCGCGCCG
1601	GCATTGCGGC	AAAAACCCGT	TTTGCTTTGC	GTAACGGTGT	CAATCTTCAG
1651	CCTTTTGCCG	CTTTTAATGT	TTTGACAGG	TCAAAATCTT	TCGGCGTGGA
1701	AATGGACGGC	GAAAAACAGA	CGCTGGCAGG	CAGGACGGCA	CTCGAAGGGC
1751	GTTTCGGTAT	TGAAGCCGGT	TGGAAGGCC	ATATGTCCGC	ACGCATCGGA
1801	TATGGCAAAA	GGACGGACGG	CGACAAAGAA	GCCGCATTGT	CGCTCAAATG
1851	GCTGTTTTGA				

This corresponds to the amino acid sequence <SEQ ID 2992; ORF 990>:

m990. pep



1408

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1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITEKY GADLKQAVKS QLQDLYKTRP
101 EAWAENKKRT EEAYIAQFGT KFSTLKQTMP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHTLE
201 TSDNARIRLN TKDEKLTVHK DYAGGADFLF GYDVRESDEP ALTFEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAKTADSG SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGWRKGVQ IGGEVFRQON EGSRLAIGVM
401 GGRAGQHASV NGKGAAGSD LYGYGGGVYA AWHQLRDKQT GAYLDGWLQY
451 QRFKHRINDE NRAERYKTKG WTASVEGGYN ALVAEGIVGK GNNVRFYLQP
501 QAQFTYLGVN GGFTDSEGTA VGLLGSQWQ SRAGIRAKTR FALRNGVNLO
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG
601 YGKRTDGDKE AALSLKWLF*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2993>:

```

a 990 . seq
1 ATGTTTCAGAG CTCAGCTTGG TTCAAATACT CGTTCTACCA AAATCGGCCGA
51 CGATGCCGAT TTTTCATTTT CAGACAAGCC GAAACCCGGC ACTTCCCATT
101 ATTTTTCAG CGGTAAAACC GATCAAAATT CATCCGAATA TGGGTATGAC
151 GAAATCAATA TCCAAGGTAA AAACATAAT AGCGGCATAC TCGCCGTCGA
201 TAATATGCCC GTTGTTAAGA AATATATTAC AGATACTTAC GGGGATAATT
251 TAAAGGATGC GGTAAAGAAG CAATTACAGG ATTTATACAA AACAAGACCC
301 GAAGCTTGGG AAGAAAATAA AAAACGACT GAGGAGGCGT ATATAGAACA
351 GCTTGACCA AAATTTAGTA TACTCAAACA GAAAACCCC GATTTAATTA
401 ATAAATTGGT AGAAGATTCC GTACTCACTC CTCATAGTAA TACATCACAG
451 ACTAGTCTCA ACAACATCTT CAATAAAAAA TTACACGTCA AAATCGAAAA
501 CAAATCCAC GTCGCCGAC AGGTGTTGGA ACTGACCAAG ATGACGCTGA
551 AAGATTCCCT TTGGGAACCG CGCCGCCATT CCGACATCCA TATGCTGGAA
601 ACTTCCGATA ATGCCCGCAT CCGCCTGAAC ACGAAAGATG AAAAAGTAC
651 CGTCCATAAA GCGTATCAGG GCGGTGCGGA TTTCCTGTTC GGCTACGACG
701 TGCGGGAGTC GGACAAACCC GCCCTGACCT TTGAAGAAAA AGTCAGCGGA
751 CAATCCGGCG TGGTTTGGGA ACGCCGGCCG GAAATCTGA AAACGCTCGA
801 CGGGCGCAAA CTGATTGCGG CGGAAAAGGC AGACTCTAAT TCGTTTGCCT
851 TTAACAAAA TTACCGCAGG GGACTGTACG AATTATTGCT CAAGCAATGC
901 GAAGCGGAT TTGCTTGGG CGTGCAGCGT TTGGCTATCC CCGAGGCGGA
951 AGCGGTTTTA TATGCCCAAC AGGCTTATGC GGCAATAACT TTGTTCCGGC
1001 TGCGTGCCGC CGACAGGGG GACGACGTGT ATGCCGCCGA TCCGTCCTCGT
1051 CAAAATTGT GGCTGCGCTT CATCGCGGCG CGGTGCGATC AAAATATACG
1101 GGGCGGCGCG GCTGCGGACG GCGGCGCGCA AGCGGTGCAA ATCGGCGGCG
1151 AGGTGTTGT ACGGCAAAAT GAAGGCAGCC GGCTGGCAAT CGGCGTGATG
1201 GGGCGGAGG CTGGCCAGCA CGCATCAGT AACGGCAAG GCGGTGCGGC
1251 AGGCAGTTAT TTGCATGTT ATGGCGGGG TGTATTGCT GCGTGCGATC
1301 AGTTGCGCGA TAAACAAAC GGTGCGTATT TGGACGGCTG GTTGCAATAC
1351 CAACGTTTCA AACACCGCAT CAATGATGAA AACCGTGCGG AACGCTACAA
1401 AACCAAGGT TGGACGGCTT CTGTGGAAG CGGCTACAAC GCGTTTGTGG
1451 CGGAAGGCGT TGTGCGAAAA GGCAATAATG TGCGGTTTTA CCTGCAACCG
1501 CAGGCGCAGT TTACCTACTT GGGCGTAAAC GCGGCTTTA CCGACAGCGA
1551 GGGGACGGCG GTCGGACTGC TCGGCAGCGG TCAGTGCGAA AGCCGCGCCG
1601 GCATTGCGGC AAAAACCCTT TTTGCTTTC GTAACGGTGT CAATCTTCAG
1651 CCTTTTGCCG CTTTAAATGT TTTGCACAGG TCAAATCTT TCGGCGTGGA
1701 AATGGACGGC GAAAAACAGA CGCTGGCAGG CAGGACGGCG CTCGAAGGGC
1751 GGTTCCGCAT TGAAGCCGT TGAAGAGGCC ATATGTCCGC ACGCATCGGA
1801 TACGGCAAAA GGACGACGG CGACAAAGAA GCCGATTGT CGCTCAAATG
1851 GCTGTTTTGA

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This corresponds to the amino acid sequence <SEQ ID 2994; ORF 990.a>:

```

a 990 . pep
1 MFRAQLGSNT RSTKIGDDAD FSFSDKPKPG TSHYFSSGKT DQNSSEYGYD
51 EINIQGNKYN SGILAVDNMP VVKKYITDY GDNLKDAVKK QLQDLYKTRP
101 EAWAENKKRT EEAYIEQLGP KFSILKQKNP DLINKLVEDS VLTPHSNTSQ
151 TSLNNIFNKK LHVKIENKSH VAGQVLELTK MTLKDSLWEP RRHSDIHMLE
201 TSDNARIRLN TKDEKLTVHK AYQGGADFLF GYDVRESDEP ALTFEEDKVSG
251 QSGVVLERRP ENLKTLDGRK LIAAEKADSN SFAFKQNYRQ GLYELLKQOC
301 EGGFCLGVQR LAIPEAEAVL YAQQAYAANT LFGLRAADRG DDVYAADPSR
351 QKLWLRFIGG RSHQNIRGGA AADGRRKGVQ IGGEVFRQON EGSRLAIGVM

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1409

401 GGRAGQHASV NGKGGAGSY LHGYGGGVYA AWHQLRDKQT GAYLDGWLQY  
451 QRFKHRINDE NRAERYKTG WTASVEGGYN ALVAEGVVGK GNNVRFYLQP  
501 QAQFTYLGVN GGFTDSEGTA VGLLGSGQWQ SRAGIRAKTR FALRNGVNLQ  
551 PFAAFNVLHR SKSFGVEMDG EKQTLAGRTA LEGRFGIEAG WKGHMSARIG  
601 YGKRTDGDKE AALSLKWL<sup>+</sup>

m990/a990 96.0% identity in 619 aa overlap

m990 . pep	10	20	30	40	50	60
a990	10	20	30	40	50	60
m990 . pep	70	80	90	100	110	120
a990	70	80	90	100	110	120
m990 . pep	130	140	150	160	170	180
a990	130	140	150	160	170	180
m990 . pep	190	200	210	220	230	240
a990	190	200	210	220	230	240
m990 . pep	250	260	270	280	290	300
a990	250	260	270	280	290	300
m990 . pep	310	320	330	340	350	360
a990	310	320	330	340	350	360
m990 . pep	370	380	390	400	410	420
a990	370	380	390	400	410	420
m990 . pep	430	440	450	460	470	480
a990	430	440	450	460	470	480
m990 . pep	490	500	510	520	530	540
a990	490	500	510	520	530	540
m990 . pep	550	560	570	580	590	600
a990	550	560	570	580	590	600

1410

	550	560	570	580	590	600
	610	620				
m990 . pep	YGKRTDGDKEAALSLKWLF	X				
a990	YGKRTDGDKEAALSLKWLF	X				
	610	620				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2995>:

```

g992 . seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGGCGCGTTG GGTATACGG
101 GATATGACAG TGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GGCACCTGCAG GGGACGTGGG TTTGACGCGC CCCGTTCCGC GACGGGCATC
201 GCGCAATCC GGCACAGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGATACCTT TCACGTCATC GACGGCGACG GCGCGAAACA TAAAATTCGG
301 ATGGCGTATA TCGACGCACC GGAGATGAAA CAGGCTTACG GTACACGTTT
351 GCGCGACAAC CTGCGCGCGG CGGCGGAGG TAGGAAAGTC AGTGACGTG
401 TGTGTGAAAC CGACCGCTAT CAGCGCGAAG TGGCGCAGGT ATCCGCGGCG
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGG CGTGGCATT
501 TAAAAGTTAT GCTAAGAAG AGCAGGATAA GCGCGATTTT GCCGACTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGGCGAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATCCGTGGG CGAATGGTTG GGCATTGGT
701 AA
  
```

This corresponds to the amino acid sequence <SEQ ID 2996 ORF 992.ng>:

```

g992 . pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTGVDSEAV RTAVAVLDVL
51  GTAGDVGFDA PVRRRASAKS GHSYTGTVSK VYDGDTHLVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQE ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDSVGEWL GIW*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2997>:

```

m992 . seq
1  ATGTTTCAGAC GGCATCGGCA TTTGAAAAAT ATGCAGATTA AAAAAATCAT
51  GAAATGGCTT CCCGTCGCCC TGTCGCTTTT GGTGCGTTG GGTATACGG
101 GGTACGGCAG CGAGGCGGTG CGGACGGCGG TTGCCGTACT CGACGTACTC
151 GCGCGGCGAG GGGACGCGGG TTTGACGCGC CCCGCGCGCC GCCGAGCATC
201 GCGCAATCC GGCACCGCT ACACAGGCAC GGTGTCCAAA GTCTATGACG
251 GCGACACCTT TCACGTTATC GACGGCGACG GCGCGAAACA CAAATCCGG
301 ATGGCGTATA TCGACGCGCC GGAGATGAAA CAGGCTTACG GCACGCGTTC
351 GCGCGACAAC CTGCGCGCGG CGGCGGAAG CAGGAAAGTC AGCGTGCAGG
401 TGTTGATAC CGACCGCTAC CAGCGCGAAG TGGCGCAGGT TTCTGTCGGC
451 AAAACCGATT TGAACCTGAT GCAGGTGCAG GACGGGCGG CGTGGCATT
501 TAAAAGTTAT GCTAAGAAG AGCAGGATAA GCGCGATTTT GCCGATTATG
551 CCGACGCTCA AATTCAGGCG GAAAGGGAAC GCAAAGGATT GTGGAAAGCT
601 AAAAATCCGC AAGCGCCGTG GCGGTACCGC CGAGCAGGCA GGAGCGGCGG
651 GGGCAATAAG GATTGGATGG ATGCCGTGGG CGAATGGTTG GGCATTGGT
701 AA
  
```

This corresponds to the amino acid sequence <SEQ ID 2998; ORF 992>:

```

m992 . pep
1  MFRRHRHLKN MQIKKIMKWL PVALSLLGAL GYTYGSEAV RTAVAVLDVL
51  GAAGDAGSDA PARRRASAKS GHRYTGTVSK VYDGDTHLVI DGDGAKHKIR
101 MAYIDAPEMK QAYGTRSRDN LRAAAEGRKV SVRVFETDRY QREVAQVSAG
151 KTDNLNMQVQ DGAAWHYKSY AKEQQDKADF ADYADAQIQE ERERKGLWKA
201 KNPQAPWAYR RAGRSGGGNK DWMDAVGEWL GIW*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 992 shows 96.1% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. gonorrhoeae*

m992/g992 96.1% identity in 233 aa overlap

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	10	20	30	40	50	60
m992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
g992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYDSEAVRTAVAVLDVLGTAGDVGFDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m992.pep	PARRRASAKSGHRYTGTVSKVYDGDTHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
g992	PVRRRASAKSGHSYTGTVSKVYDGDTHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m992.pep	LRAAAEGRKVSVRVFDTDYQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF					
g992	LRAAAEGRKVSVRVFETDQREVAQVSVGKTDNLNMQVQDGAAWHYKSYAKEQQDKADF					
	130	140	150	160	170	180
	190	200	210	220	230	
m992.pep	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DAVGEWLGIWX					
g992	ADYADAQIQAEERERKGLWKAKNPQAPWAYRRAGRSGGGNKDWM DSVGEWLGIWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2999>:

a992.seq

1	A	T	G	T	T	C	A	G	A	C	G	G	C	A	T	T	G	A	A	A	A	A	A	T	C	A	T	
51	G	A	A	T	G	G	C	T	T	C	C	G	T	C	G	C	T	T	T	G	G	T	G	C	G	T	T	G
101	G	G	T	A	C	G	C	G	A	G	G	C	G	T	G	C	C	G	T	A	C	T	C	G	A	C	T	C
151	G	G	C	G	C	G	C	A	G	G	C	G	G	T	C	C	A	C	G	C	G	C	C	C	C	C	C	C
201	G	G	C	G	A	A	T	C	C	A	C	C	G	C	T	A	C	A	C	A	G	G	C	A	A	G	T	C
251	G	C	G	A	C	C	C	T	C	A	C	G	T	A	T	C	A	C	G	G	C	A	C	A	A	C	C	C
301	A	T	G	G	C	G	T	A	T	C	G	A	C	G	C	C	G	A	G	A	T	C	A	C	A	G	A	T
351	G	C	G	C	A	A	C	T	G	C	G	C	G	C	G	C	G	A	A	G	G	C	A	A	G	T	C	C
401	T	G	T	C	G	A	C	A	C	G	C	T	A	C	A	G	C	G	C	A	A	G	T	T	C	T	G	C
451	A	A	A	C	C	G	A	T	T	G	A	A	C	T	G	A	T	C	A	G	G	T	C	A	G	A	T	A
501	T	A	A	A	G	T	T	A	A	G	A	A	C	A	G	C	A	A	A	G	A	A	C	A	G	A	T	A
551	C	C	G	A	C	G	T	C	A	A	T	C	A	G	G	C	G	A	A	A	G	G	A	A	C	A	A	G
601	A	A	A	A	T	C	C	G	A	A	G	C	C	G	T	G	A	A	A	G	A	A	C	A	A	G	A	T
651	G	G	C	A	A	T	A	A	G	A	A	G	C	C	G	T	G	A	A	A	G	A	A	C	A	A	G	T
701	A	A																										

This corresponds to the amino acid sequence <SEQ ID 3000; ORF 992.a>:

a992.pep

1	M	F	R	R	H	R	L	K	N	M	Q	I	K	K	M	K	W	L	P	V	A	L	S	L	L	G	A	L
51	G	A	A	G	D	A	G	S	D	A	P	A	R	R	R	S	A	K	S	G	H	R	Y	T	G	T	V	S
101	M	A	Y	I	D	A	P	E	M	K	Q	A	Y	G	T	R	S	R	D	N	L	R	A	A	A	E	G	R
151	K	T	D	L	N	L	M	Q	V	Q	D	G	A	A	W	H	Y	K	S	Y	A	K	E	Q	Q	D	K	A
201	K	N	P	Q	A	P	W	A	Y	R	R	A	G	R	S	G	G	G	N	K	D	W	M	D	A	V	G	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 992 shows 100.0% identity over a 233 aa overlap with a predicted ORF (ORF 992) from *N. meningitidis*

a992/m992 100.0% identity in 233 aa overlap

	10	20	30	40	50	60
a992.pep	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
m992	MFRRRHRLKNMQIKKIMKWL PVALSLLGALGYTGYGSEAVRTAVAVLDVLGAAGDAGSDA					
	10	20	30	40	50	60
	70	80	90	100	110	120
a992.pep	PARRRASAKSGHRYTGTVSKVYDGDTHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
m992	PARRRASAKSGHRYTGTVSKVYDGDTHVIDGDGAKHKIRMAYIDAPEMKQAYGTRSRDN					
	70	80	90	100	110	120
	130	140	150	160	170	180

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```

a992.pep      LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
|||||
m992          LRAAAEGRKVSVRVFDTRYQREVAQVSVGKTDNLNMQVDGAAWHYKSYAKEQQDKADF
              130      140      150      160      170      180

              190      200      210      220      230
a992.pep      ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGKNKDWMDAVGEWLGIXW
|||||
m992          ADYADAQIQAERERKGLWKAKNPQAPWAYRRAGRSGGKNKDWMDAVGEWLGIXW
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3001>:

```

g993.seq
1   CTGAAAGTCG TATTGGGCAG TTTTCAAGGC CCTTTGGATC TGCTGCTCTA
51  CCTTATCCGC AAGCAGAACA TCGATGTTCT CGATATTCCG ATGGTGGAAG
101 TTACCGGGCA GTATCTGCAC TATATTGCC AAATGGAAGC CTATCAGTTT
151 GATTGGCGG CGGAATATCT TTTGATGGCG GCAATGCTGA TTGAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAGGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TTGCCTACGA GCAATGAAA
301 CTGCGCGCGC AGGGTTTGA CGCGCTGCCG CGTGCGGGAC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCAGC CGAGACGAAG CTGCCCGAGG
401 TTTACATCGC CGATTGATG CAGGCATGGT TGGGCATTCT TTCTCGGGCA
451 AAACATACGC GCAGCCACGA AGTAATCCAA GAAACCCCTT CCGTGCGCGC
501 GCAATGACG GCAATCCTGC GCCGTTTGA CGAACACGGG ATATGCAGGT
551 TTCACGCCCT GTTCAATCCC GAACAGGGCG CGGCTTACGT GATCGTCAAC
601 TTCATCGCCC TGTGGAGCT TGCCAAAGAA GGATTGGTCG GAATCGTACA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTTCGGC ACACGGGGCG GGCAGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3002 ORF 993.ng>:

```

g993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MVEITGOYLH YIAQMEAYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTAEVD EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAAETK LPEVYIADLM QAWLGILSRA
151 KHTRSHEVIQ ETLVRAQMT AILRLNEHG ICRFHALFNP EQGAAYVIVN
201 FIALLELAKE GLVGIVQEDG FGEIRISLNH EGAHSDGIFG TRGGRDVF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3003>:

```

m993.seq
1   TTGAAAGTCG TATTGGGCAG CTTCCAAGGC CCTTTGGATC TACTGCTGTA
51  TCTGATCCGC AAACAGAATA TCGACGTACT GGATATTCCG ATGGTGGAAG
101 TTACCGAGCA GTATCTGCAC TACATCGCCC AAATAGAAAC CTATCAGTTT
151 GATTGGCGG CGGAATATCT TTTGATGGCA GCAATGCTGA TTGAATCAA
201 ATCGCGCCTG CTGCTGCCGC GTACCGAAGC CGTCGAAGAC GAAGAAGCCG
251 ACCCGCGTGC CGAGTTGGTG CGCCGCTGCG TGGCTTACGA ACAGATGAAG
301 CTGCGCGCGC AGGGTTTGA CGCGCTGCCG CGAGCCGAGC GGGATTTCGC
351 GTGGGCTTAC CTGCCGCTGG AAATTGCCGT CGAAGCCAAG CTGCCCGAAG
401 TCTATATTAC CGACTTGACG CAAGCGTGGC TGGGTATTTT GTCTCGGGCA
451 AAACACACGC GCAGCCACGA AGTAATCAAA GAAACCATCT CCGTGCGCGC
501 GCAATGACG GCAATCCTGC GCCGTTTGA CGGACACGGA ATATGCAGGT
551 TTCACGACCT GTTCAATCCC AAACAGGGCG CGGCTTACGT GGTCTGCAAC
601 TTCATCGCAC TGTGGAGCT TGCCAAAGAA GGATTGGTCA GAATCGTGCA
651 GGAAGACGGT TTCGGAGAAA TCCGAATCAG CCTCAATCAT GAGGGGGCGC
701 ATTCAGACGG CATTTCCGGC ACACGAGGCG GGCAGATGT GTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 3004; ORF 993>:

```

m993.pep
1   LKVVLSFGQ PLDLLLYLIR KQIDVLDIP MKVITEQYLH YIAQIETYQF
51  DLAAEYLLMA AMLIEIKSRL LLPRTETVED EADPRAELV RRLAYEQMK
101 LAAQGLDALP RAGRDFAWAY LPLEIAVEAK LPEVYITDLT QAWLGILSRA
151 KHTRSHEVIK ETISVRAQMT AILRLNGHG ICRFHDLFNP KQGAAYVVVN
201 FIALLELAKE GLVRIVQEDG FGEIRISLNH EGAHSDGISG TRGGRDVF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 993 shows 93.1% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. gonorrhoeae*

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m993/g993 93.1% identity in 248 aa overlap

	10	20	30	40	50	60
m993.pep	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA				
g993	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVEITGQYLHYIAQMEAYQFDLAAEYLLMA				
	10	20	30	40	50	60
	70	80	90	100	110	120
m993.pep	AMLIEIKSRLLLPRTETVEDEEADPRAELVRRL	LAYEQMKLAAQGLDALPRAGRDFAWAY				
g993	AMLIEIKSRLLLPRTAEVEDEEADPRAELVRRL	LAYEQMKLAAQGLDALPRAGRDFAWAY				
	70	80	90	100	110	120
	130	140	150	160	170	180
m993.pep	LPLEIAVEAKLPEVYITDLTQAWLGILSR	AKHTRSHEVIKETISVRAQMTAILRRLNKG				
g993	LPLEIAAETKLPEVYIADLMQAWLGILSR	AKHTRSHEVIQETLSVRAQMTAILRRLNEHG				
	130	140	150	160	170	180
	190	200	210	220	230	240
m993.pep	ICRFHDLFNPQGAAYVVVNFIALLELAKEGLV	RIVQEDGFGEIRISLNHEGAHSDGISG				
g993	ICRFHALFNPQGAAYVIVNFIALLELAKEGLV	GIVQEDGFGEIRISLNHEGAHSDGIFG				
	190	200	210	220	230	240
	249					
m993.pep	TRGGRDVF					
g993	TRGGRDVF					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3005>:

a993.seq

1	CTGAAAGTCG	TATTGAGCAG	TTTCAAGGC	CCTTTGGATC	TGCTGCTCTA
51	CCTTATCCGC	AAGCAGAACA	TCGATGTTCT	CGATATCCG	ATGGTGAAGA
101	TTACCGAACA	GTATCTGCAC	TACATCGCCC	AAATAGAAAC	CTATCAGTTT
151	GATTTGGCGG	CGGAATATCT	TTGATGGCA	GCAATGCTGA	TTGAAATCAA
201	ATCGCGCCTG	CTGCTGCCGC	GTACCGAAAC	CGTCGAAGAC	GAAGAAGCCG
251	ACCCGCGTGC	CGAGTTGGTG	CGCCGCCTGC	TGGCTTACGA	GCAGATGAAG
301	CTGGCGGCAC	AAGGGTTGGA	TGCGCTTCCT	CGTCCGGGCC	GGGATTTCGC
351	ATGGGCATAC	CTGCCACTGG	AAATTGCCGT	CGAAGCCAAG	CTGCCCGAAG
401	TCTATATTAC	CGACTTGACG	CAGGCGTGGC	TGAGTATTTT	GTCTCGGGCA
451	AAACATACGC	GCAGCCACGA	AGTTATCAAA	GAAACCATCT	CCGTGCGCCG
501	GCAAATGACG	GCAATCCTGC	GCCGTTTGAA	CAAACACGGG	ATATGCAGGT
551	TTACAGACCT	GTTCAATCCC	GAACAGGGCG	CGGCTTACGT	GGTCGTCAAC
601	TTCATCGCAC	TGTTGGAGCT	TGCCAAAGAA	GGTTTGGTCG	GAATCGTACA
651	GGAAAGTCGGT	TTCGGAGAAA	TCCGAATCAG	CCTCAATCAT	GAGGGGGCCG
701	ATTACAGACG	CATTCCGGC	ACACGGGGCG	GGCGCGATGT	GTTCTAA

This corresponds to the amino acid sequence &lt;SEQ ID 3006; ORF 993.a&gt;:

a993.pep

1	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQF
51	DLAAEYLLMA	AMLIEIKSRLLLPRTETVED
101	LAAQGLDALP	RAGRDFAWAYLPLEIAVEAK
151	KHTRSHEVIK	ETISVRAQMTAILRRLNKG
201	FIALLELAKE	GLVGIVQEVG

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*ORF 993 shows 97.6% identity over a 248 aa overlap with a predicted ORF (ORF 993) from *N. meningitidis*

a993/m993 97.6% identity in 248 aa overlap

	10	20	30	40	50	60
a993.pep	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA				
m993	LKVVLSFQGPLDLLLYLIRKQ	NIDVLDIPMVKITEQYLHYIAQIETYQFDLAAEYLLMA				

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	10	20	30	40	50	60
a993.pep	70	80	90	100	110	120
m993	70	80	90	100	110	120
a993.pep	130	140	150	160	170	180
m993	130	140	150	160	170	180
a993.pep	190	200	210	220	230	240
m993	190	200	210	220	230	240
a993.pep	249					
m993	249					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3007>:

g996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TTCTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTGCTTGC CTTGGGCGAT TCGCTACCT TCGGCTACGG AGCAAACCCC
151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACGTCCGC GCAAGCCCTA TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCACAAAGT TCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AAAAGGAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACA CTG GCGCGTTGT TCGGGCATT GAGCGACCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGT TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCAATAATA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTC CCGAAATTT GAATCAATTT
601 TTGAGAAAAC ATGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3008 ORF 996.ng>:

g996.pep

```

1  MNRRTFLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPALQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG
101 NDFLRKPVEE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLSDH
151 PLYEDLSEY GIPLEGGAWA EILGNLNLKS DQIHANGKGY RKFAENLNQF
201 LRKHGFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3009>:

m996.seq

```

1  ATGAACAGAA GAACCTTCCT CCTCGGCGCA GCGCGTTGC TGCTACCGC
51  CTGCGGCAGA AAATCCGCCC GAACCCACGC CAAAATTCCC GAAGGAAGCA
101 CCGTACTTGC CTTGGGCGAT TCGCTACCT TCGGCTACGG CGCAAACCCCT
151 GCGGAATCCT ACCCGCGCA ACTGCAAAA CTGACGGGT GGAATATTGT
201 CAACGGCGGC GTATCGGGCG ATACATCTGC CCAAGCCCTG TCGCGCCTGC
251 CCGCGCTGTT GGCACGCAAA CCCAAGCTTG TGATTGTCGG CATAGGCGGC
301 AACGACTTTC TGCACAAAGT TCCGAGGAG CAGACCCGCG CCAATATCGC
351 GAAAATCATC GAAACCGTGC AGAAGGAAA CATCCCGCC GTCTCGTCG
401 GCGTGCCGCA CATCACA CTG GGTGCGTTGT TCGGGCATT GAGCGATCAT
451 CCGCTGTATG AGGATTTGTC CGAGGAATAC GGCATTCCGC TGTTCGGCGG
501 CCGGTGGGCG GAAATTTTGG GCGATAATA TCTGAAATCC GACCAATCC
551 ACGCCAACGG CAAAGGCTAT CGGAAATTC CCGAAGATT GAATCAATTT
601 TTGAGAAAAC AGGGGTTTAG ATAA

```

This corresponds to the amino acid sequence <SEQ ID 3010; ORF 996>:

m996.pep

```

1  MNRRTFLGA GALLLTACGR KSARTHAKIP EGSTVLALGD SLTFGYGANP
51  GESYPALQK LTGWNIVNGG VSGDTSQAAL SRLPALLARK PKLVIVGIGG

```

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101 ND~~FL~~RKVPKE QTRANIAKII ETVQKENIPA VLVGVPHITL GALFGHLS~~SDH~~  
 151 PL~~YED~~LSE~~EY~~ GIP~~LF~~GGAWA EILG~~DN~~NLKS DQIHANGKGY RKFAEDLNQF  
 201 L~~RK~~QGF~~R~~

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 996 shows 98.1% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. gonorrhoeae*

m996/g996 98.1% identity in 207 aa overlap

	10	20	30	40	50	60
m996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
g996	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m996.pep	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANI <del>AKII</del>					
g996	LTGWNIVNGGVSGDTSQAQLSRLPALLARKPKLVIVGIGGNDFLRKVP <del>E</del> EQTRANI <del>AKII</del>					
	70	80	90	100	110	120
	130	140	150	160	170	180
m996.pep	ETVQKENIPAVLVGVPHITL <del>GALFGHLS</del> DHPLYEDLSE <del>EY</del> GIP <del>LF</del> GGAWAEILG <del>DN</del> NLKS					
g996	ETVQKENIPAVLVGVPHITL <del>GALFGHLS</del> DHPLYEDLSE <del>EY</del> GIP <del>LF</del> GGAWAEILG <del>NN</del> NLKS					
	130	140	150	160	170	180
	190	200				
m996.pep	DQIHANGKGYRKFAEDLNQFLRKQGF <del>R</del>					
g996	DQIHANGKGYRKFAENLNQFLRK <del>H</del> GFR <del>X</del>					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3011>:

a996.seq

1	ATGAACAGAA	GAACCTTCCT	CCTCGGCGCA	GGCGGTTGC	TCCTTACCGC
51	CTGCGGCAGA	AAATCCGCC	GAACCCACGC	CAAAATTCCC	GAAGGAAGCA
101	CCGTACTTGC	CTTGGGCGAT	TCGCTTACCT	TCGGCTACGG	CGCAAACCCC
151	GGCGAATCCT	ACCCCGCGCA	ACTGCAAAAA	CTGACGGGTT	GGAATATTGT
201	CAACGGCGGC	GTATCGGGCG	ATACATCCGC	CCAAGCCCTG	TCGCGCCTGC
251	CCGCGCTGTT	GGCAGCAAA	CCCAAGCTTG	TGATTGTCGG	CATAGCGCGC
301	AAACGACTTC	TGCGCAAAGT	TCCCAAGGAG	CAGACCCGCG	CCAATATCGC
351	GAAATCATC	GAAACCGTGC	AGAAGGAAA	CATCCCCGCC	GTCCTCGTCG
401	GCGTGCCGCA	CATTACCTTG	GGCGCGTTGT	TCGGGCATT	GAGCGATCAT
451	CCGCTGTATG	AGGATTGTG	CGAGGAATAC	GGCATTCCGC	TGTTCCGCGG
501	CGCGTGGCG	GAAATTTTGG	GCGATAATA	TCTGAAATCC	GACCAATCC
551	ACGCCAACGG	CAAAGGCTAT	CGGAAATTG	CCGAGATT	GAATCAATT
601	TTGAGAAAC	AGGGTTTAG	ATAA		

This corresponds to the amino acid sequence <SEQ ID 3012; ORF 996.a>:

a996.pep

1	MNRRTFLLGA	GALLLTACGR	KSARTHAKIP	EGSTVLALGD	SLTFGYGANP
51	GESYPALQK	LTGWNIVNGG	VSGDTSQAQ	SRLPALLARK	PKLVIVGIGG
101	ND <del>FL</del> RKVPKE	QTRANIAKII	ETVQKENIPA	VLVGVPHITL	GALFGHLS <del>SDH</del>
151	PLYEDLSE <del>EY</del>	GIP <del>LF</del> GGAWA	EILG <del>DN</del> NLKS	DQIHANGKGY	RKFAEDLNQF
201	L <del>RK</del> QGF <del>R</del> *				

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 996 shows 100.0% identity over a 207 aa overlap with a predicted ORF (ORF 996) from *N. meningitidis*

a996/m996 100.0% identity in 207 aa overlap

	10	20	30	40	50	60
a996.pep	MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK					



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|||||
m996  MNRRTFLLGAGALLLTACGRKSARTHAKIPEGSTVLALGDSLTFGYGANPGESYPALQK
      10      20      30      40      50      60
      70      80      90      100     110     120
a996.pep LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
|||||
m996  LTGWNIVNGGVSGD TSAQALSRLPALLARKPKLVIVGIGGNDFLRKVPKEQTRANIAKII
      70      80      90      100     110     120
      130     140     150     160     170     180
a996.pep ETVQKENIPAVLVGVPHITLGALFGHLSHDPLYEDLSEEYGIPLFGGAWAEILGDNNLKS
|||||
m996  ETVQKENIPAVLVGVPHITLGALFGHLSHDPLYEDLSEEYGIPLFGGAWAEILGDNNLKS
      130     140     150     160     170     180
      190     200
a996.pep DQIHANGKGYRKFAEDLNQFLRKQGF
|||||
m996  DQIHANGKGYRKFAEDLNQFLRKQGF
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 3013>:

```

g997.seq (partial)
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGCGC TTGTCCGCCG CCGTCACCTT GCGCGGCAC GCGACGTTA
101 CCCTGTTTGA AGCCGCCCGG CAGGCGGGCG GAAGGCGCG CACACTGGCC
151 GGAATACCG ACGGTTTCGG TTTTGTGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGTGT TGCCTGAT GAAACCATC GGTTCAGACC
251 CCCGTGCCGC CTTTTCGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCGCGCG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGCGCG TACCGTCCG ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTTGCAC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTAAT
501 GCAGTTTGG CAGCCCTTGG TCTGGGCGC GCTCAACACG CCTTTGGAAA
551 CCGCAAGCCT GCGCGTGTG TGCAACGTT TGTCCGACG CGTGCTGACG
601 AAAAAATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGTCGCCGAA CCGCCTTGG CGGAGCTTCA ACGGCTCGG CCGGACATCC
701 GCCTCGAACC GCGCGTATG CGTCTGAACA CCCTCCCGGA CGGAAAAGTC
751 CTCGTCAACG GCGAAGCCTT CGATGCCGCC ATACTTGCCA CCGCGCCCTA
801 CCACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CATATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GCCGAACCCG TCCGCTGCG CGCCCGCTG ACCGGCATtg CCGAcggcAC
951 ggcaCaatg CTGCTTTgcc cgGGGcAGGc tccggactgc CcccaaAacg
1001 aagTCTCCGc cGTCAAttagc GTTTCGgAcc GCGTcggcgc Gtttgcaaac
1051 cga...

```

This corresponds to the amino acid sequence <SEQ ID 3014 ORF 997.ng>:

```

g997.pep (partial)
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51 GNTDGFGLD NGQHILLGAY RGVLRMLMTI GSDPRAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLQPDIT
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVLV
201 KKSQSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRVC RLNTLPDGKV
251 LVNGEAFDAA ILATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGIADGTAQW LLCPGQAPDC PQNEVSAVIS VSDRVGAFAN
351 R....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3015>:

```

m997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51 CTGGGCGAGGA CTGTCCGCCG CCGTCACCTT GCGCGGCAC GCGACGTTA
101 CCCTGTTTGA AGCCGCCCGG CAGGCGGGCG GCAGGCGCG CACACTGGCC
151 GGAATACCG ACGGTTTCGG TTTTGTGAC AACGGGCAGC ACATTTTGCT
201 CGGCGCATAC CGGGCGTGT TGCCTGAT GAAACCATC GGTTCGGATC
251 CCCGTGCCGC CTTTTCGCG GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTGCAGTTCC GCGCCCTCCC CTGCGCGCG CCGCTGCATA TTTGGGCGG
351 CGTGCTGCTT GCCCGCGTG CACCGACTGC ATTCAAAGCC AAAGTCTTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACAGTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCGTGAT
501 GCAGTTTGG CAGCCCTTGG TTTGGGCGC GCTCAACACG CCTTTGGAAA

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```

551 CC GCAAGCCT GCGCGTGTG TGCAACGTTT TGTCCGACGG CGTGCTGACG
601 AA AAAATCCG GCAGCGACTA TCTCCTACCC AAGCAGGATT TGGGCGCAAT
651 CG TCGCCGAA CCCGCCCTGG CGGATCTTCA ACGGCTCGGC GCGGACATCC
701 GC CTCGAAAC GCGCGTATGC CGTCTGAACA CCTTCCCGGA CGGGAAGTG
751 CT CGTCAACG GCGAAGCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CC ACGCCGCC GCGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CA TATCAAAA CCTTCGCTAC CACGCCATCA CCACCGTCTA TCTGCGCTAC
901 GC CGAACCCG TCCGCCCTGCC CGCCCGCTG ACCGGCCTTG CCGACGGCAC
951 GG TGCAATGG CTGCTTTGCC GGGGCAGGCT CGGACTGCCT GAAAACGAAG
1001 TG TCCGCCGT CATCAGCGTT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GC GTGGGCGG ACAAAGCCCA CGCCGACCTC AAACGCATCC TTCCGCATTT
1101 GG GCGAAGCC GAAGCCGTGC GCGTCATCAC CGAAAACGC GCCACAACCG
1151 CA GCCGATGC CCGCCGCCG GACTTGTCGT GGTTCACCG GCACCGCATC
1201 TT CCCCCTCG GCGACTACCT CCACCCGGAC TACCCCGCCA CGCTCGAAGC
1251 CG CCGTACAA TCAGGTTTCG CGTCGGCGGA AGCCTGCCTG CAAAGCCTGA
1301 GC GATGCCGT CTGA

```

This corresponds to the amino acid sequence <SEQ ID 3016; ORF 997>:

m997.pep

```

1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARTLA
51  GN TDGFGFLD NGQHILGAY RGVRLMKT I GSDPRAAFLR VPLHWHMHGG
101 LQ FRALPLPA PLHILGGVLL ARRAPTAFKA KLLADMSDLQ KSARLGQPD
151 TV AQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KK SGSDYLLP KQDLGAIVAE PALADLQRLG ADIRLETRVC RLNTLPDGKV
251 LV NGEAFDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AE PVRLPAPL TGLADGTQVQW LLCRGLGLP ENEVSAVISV SDRVGAFA
351 AW ADKAHADL KRILPHLGEP EAVRVITEKR ATTAADAPPP DLSWLHRRH
401 FP AGDYLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 997 shows 96.0% identity over a 351 aa overlap with a predicted ORF (ORF 997) from *N. gonorrhoeae*

g997/m997 96.0% identity in 351 aa overlap

	10	20	30	40	50	60
g997.pep	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
m997	MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD					
	10	20	30	40	50	60
	70	80	90	100	110	120
g997.pep	NGQHILGAYRGVRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
m997	NGQHILGAYRGVRLMKTIGSDPRAAFLRVPLHWHMHGGLQFRALPLPAPLHILGGVLL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g997.pep	ARRVPSAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
m997	ARRAPTAFKAKLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT					
	130	140	150	160	170	180
	190	200	210	220	230	240
g997.pep	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
m997	PLETASLRVLCNVLSGVLTKKSGSDYLLPKQDLGAIVAEPAELQRLGADIRLETRVC					
	190	200	210	220	230	240
	250	260	270	280	290	300
g997.pep	RLNTLPDGKVLVNGEAFDAAILATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
m997	RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY					
	250	260	270	280	290	300
	310	320	330	340	350	
g997.pep	AEPVRLPAPLTGIADGTAQWLLCPGQAPDCPQNEVSAVISVSDRVGAFANR					
m997	AEPVRLPAPLTGLADGTQWLLCRGRL-GLPENEVSAVISVSDRVGAFANRAWADKAHAD					
	310	320	330	340	350	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3017>:

```
a997.seq
1  ATGATGAACA CGCCGCATCC GCGCCCGAAA ATCGCCGTCA TCGGCGCAGG
51  CTGGGCGGCG TTGTCCGCGG CCGTTACCTT GCGCGGCGAC GCCGACGTTA
101 CCC TGTTTGA AGCCGCGCCG CAGGCGGGCG GCAGGGCGCG CGCACTGGCC
151 GGA AATACCG ACGGTTTCGG TTTTGTGGAC AACGGGCAGC ATATTTTACT
201 CGGCGCATAC CGGGGCGGTG TCGCCCTGAT GAAAACCATC GGTTCAGACC
251 CCC ATGCGCG CTTTTTGCGC GTACCGCTGC ACTGGCATAT GCACGGCGGT
301 TTG CAGTTC GCGCCCTCCC CCTGCCCGCG CCCCTGCATA TTTTGGGCGG
351 CGT GCTGCTT GCCCGGCGCG TACCGTCCGC ATTCAAAGCC AAACGTGCTG
401 CCGATATGTC CGATTTCAG AAGTCCGCAC GCCTCGGACA GCCCGACACG
451 ACA GTGGCGC AATGGCTGAA ACAGCGGAAC GTGCCGCGTG CCGCCGTAAT
501 GCA GTTTTGG CAGCCCTTGG TTTGGGGCGC GCTCAACACG CCTTTGGAAG
551 CCG CAAGCTT GCGCGTGTG TGCAACGTTT TGTCGACGG CGTGCTGACG
601 AAAA AATCCG GCAGCGACTA TCTCCTACCC AAACAGGATT TGGGCGCAAT
651 CGT CGCCGAA CCCGCTTGG CGGAGCTTCA ACGGCTCGGC GCGGACATCC
701 GCC TCGAAAC GCGCATATGC CGTCTGAACA CCCTCCCGGA CGGGAAGTG
751 CTC GTCAACG GCGAACCTTT CGATGCCGCC GTCCCGGCCA CCGCGCCCTA
801 CCA CGCCGCG CGGCTCCTGC CCGAAGGCAC GCCCGAACAC GTTCAGACGG
851 CAT ATCAAAA CCTTCGCTAT CAGGCCATCA CCACCGTCTA TCTGCGCTAT
901 GCC GAACCCG TCCGCTTGCC TGCCCGCGTG ACCGGACTTG CCGACGGCAC
951 GGT GCAATGG CTGCTTTGCC GGGGCGAGGCT CGGACTGCCT GAAAACGAAG
1001 TGT CCGCCGT CATCAGCGT TCCGACCGCG TCGGCGCGTT TGCAAACCGG
1051 GCG TGGGCGG ACAAAGTTCA CGCCGACCTC AAACGCATCC TTCCGCATT
1101 GGG CGAACCC GAAGCCGTGC GGTTCATCAC CGAAAAACGC GCCACAACCG
1151 CAG CCGATGC CCCGCCGCC GATTGTGCGT GGTTCACCG GCACCGCATC
1201 TTC CCCGCCG GCGACTACCT CCACCCAGAC TACCCCGCCA CGCTCGAAGC
1251 CGC CGTACAA TCAGGTTTCG CGTCGGCGGA AGCTGCCTG CAAAGCCTGA
1301 GCGATGCCGT CTGA
```

This corresponds to the amino acid sequence <SEQ ID 3018; ORF 997.a>:

```
a997.pep
1  MMNTPHPRPK IAVIGAGWAG LSAAVTLARH ADVTLFEAGR QAGGRARALA
51  GNTDGFGLD NGQHILLGAY RGVRLRMKTI GSDPHAAFLR VPLHWHMHGG
101 LQFRALPLPA PLHILGGVLL ARRVPFAFKA KLLADMSDLQ KSARLGQPD
151 TVAQWLKQRN VPRAAVMQFW QPLVWGALNT PLETASLRVL CNVLSGVL
201 KKS GSDYLLP KQDLGAIVAE PALAELQRLG ADIRLETRIC RLNTLPDGKV
251 LVNGEFPDAA VPATAPYHAA ALLPEGTPEH VQTAYQNLRY HAITTVYLRY
301 AEPVRLPAPL TGLADGTVOV LLCRGRGLP ENEVSAVISV SDRVGAFANR
351 AWADKVHADL KRILPHLGEP EAVRVITEKR ATTAADAPP DLWLHHRHRI
401 FPGDYLLHPD YPATLEAAVQ SGFASAEACL QSLSDAV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 997 shows 98.2% identity over a 437 aa overlap with a predicted ORF (ORF 997) from *N. meningitidis*

```
a997/m997 98.2% identity in 437 aa overlap

      10      20      30      40      50      60
a997.pep MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARALAGNTDGFGLD
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m997      MMNTPHPRPKIAVIGAGWAGLSAAVTLARHADVTLEAGRQAGGRARTLAGNTDGFGLD
          10      20      30      40      50      60

      70      80      90      100     110     120
a997.pep NGQHILLGAYRGVRLRMKTIGSDPHAAFLRVPLHWHMHGGLOFRALPLPAPLHILGGVLL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m997      NGQHILLGAYRGVRLRMKTIGSDPRAAFLRVPLHWHMHGGLOFRALPLPAPLHILGGVLL
          70      80      90      100     110     120

      130     140     150     160     170     180
a997.pep ARRVPFAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
m997      ARRAPTAFKA KLLADMSDLQKSARLGQPDTTVAQWLKQRNVPRAAVMQFWQPLVWGALNT
          130     140     150     160     170     180

      190     200     210     220     230     240
a997.pep PLETASLRVLCNVLSGVLTKSGSDYLLPKQDLGAIVAEPALAELQRLGADIRLETRIC
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```

m997      PLETASLRVLCNVLSDGVLTKKSGSDYLLPKQDLGAIVAEPALADLQRLGADIRLETRVC
           190      200      210      220      230      240

a997.pep      250      260      270      280      290      300
RLNTLPDGKVLVNGEPFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
|||||
m997      RLNTLPDGKVLVNGEAFDAAVPATAPYHAAALLPEGTPEHVQTAYQNLRYHAITTVYLRY
           250      260      270      280      290      300

a997.pep      310      320      330      340      350      360
AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKVHADL
|||||
m997      AEPVRLPAPLTGLADGTVQWLLCRGRLGLPENEVSAVISVSDRVGAFANRAWADKAHADL
           310      320      330      340      350      360

a997.pep      370      380      390      400      410      420
KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRRHRIFPAGDYLHPDYPATLEAAVQ
|||||
m997      KRILPHLGEPEAVRVITEKRATTAADAPPPDLSSLHRRHRIFPAGDYLHPDYPATLEAAVQ
           370      380      390      400      410      420

a997.pep      430
SGFASAEACLQSLSDAVX
|||||
m997      SGFASAEACLQSLSDAVX
           430

```

g999.seq Not found yet

g999.pep Not found yet

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 3019>:

```

m999.seq
1  ATGAATATGA AAAAATTGAT TTCCGCAATT TGTGTTTCAA TTGTTTTATC
51  AGCCTGCAAC CAACAATCAA AAACGGCACA AGCCGAAGAA CCTGTCCAAA
101 GTATCCAGGC TGCTGATTGT ACCGCCCCAA TGGACATCAC AGTTGAACAA
151 TATCTCATCA ATTTGGAGCA AGCATTTAAA ACTCAGAACG TCTCAACAAA
201 AATCCATAAT AAAAATATTG TCAAGACCGA TTGTGGTTAT GACCTTACTT
251 TGGTAATGGA TTTTGGGGCG ATTGCGCTCA AACTGGACGA GCAGCAAAAA
301 ATTAGAGCTA TCTCAGTAGG CTACATTTTA AAAACCGACG GAGAGAAAGG
351 ACAAAATCTA GTCAATAATG CCATAAATGG ATTACACAGT ATTCAGGCAG
401 TTCTGTCTTT AACTACCACA GACAAATTGG GCGAATCGGA AGCAGGAAAA
451 CAACCTTTTA CAGCTTTAAC CGAAGTCGTC AAAGAATCCA ATCAGACAGG
501 AGCAACAGCG CAAAAGACG TTCCGGCAGA TGGTATTTTA TATAGCGTTG
551 TTTTGAATAA AGAAACAAAC ACCATTGCAA TAATCGGCAG AAAACAACCC
601 TAA

```

This corresponds to the amino acid sequence &lt;SEQ ID 3020; ORF 999&gt;:

```

m999.pep
1  MNMKKLISAI CVSIVLSACN QOSKTAQAE PVQSIQAADC TAPMDITVEQ
51  YLINLEQAFK TQNVSTKIHN KNIVKDCGY DLTIVMDFGA IALKLDEQOK
101 IRAISVGYIL KTDGEKGQNL VNNAINGLHS IQAVLSLTIT DKLGESEAGK
151 QLFTALTEVV KESNOTGATA QKDVFPADGIL YSVVFEKETN TIAIIGRKQP

```

a999.seq Not found yet

a999.pep Not found yet

The foregoing examples are intended to illustrate but not to limit the invention.

## CLAIMS

1. A protein comprising a fragment of an amino acid sequence from SEQ ID 2790 wherein said fragment comprises at least 7 amino acids from said sequence.
2. A protein comprising an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020.
3. A protein having 50% or greater homology to a protein according to claim 1.
4. A protein comprising a fragment of an amino acid sequence selected from the group consisting of even numbered SEQ IDs from SEQ ID number 2 through SEQ ID number 3020, wherein said fragment comprises 7 or more consecutive amino acids from said sequence.
5. An antibody which binds to a protein according to any one of claims 1 to 3.
6. A nucleic acid molecule which encodes a protein according to any one of claims 1 to 3.
7. A nucleic acid molecule according to claim 5, comprising a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019.
8. A nucleic acid molecule comprising a fragment of a nucleotide sequence selected from the group consisting of odd numbered SEQ IDs from SEQ ID number 1 through SEQ ID number 3019, wherein said fragment comprises 10 or more consecutive nucleotides from said sequence.
9. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 5.
10. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 6.
11. A nucleic acid molecule comprising a nucleotide sequence complementary to a nucleic acid molecule according to claim 7.
12. A composition comprising a protein, a nucleic acid molecule, or an antibody according to any preceding claim.
13. A composition according to claim 11 being a vaccine composition or a diagnostic composition.
14. A composition according to claim 11 for use as a pharmaceutical.
15. The use of a composition according to claim 11 in the manufacture of a medicament for the treatment or prevention of infection due to Neisserial bacteria.

16. A composition comprising a protein of claim 1 wherein said composition is immunogenic.

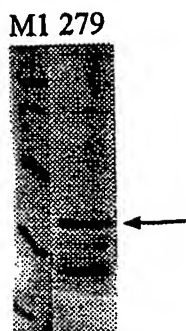
17. A composition comprising a protein of claim 2 wherein said composition is immunogenic.

18. A composition comprising a protein of claim 3 wherein said composition is immunogenic.

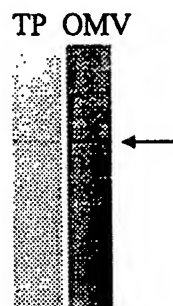
Fig. 2

279 (10.5 kDa)

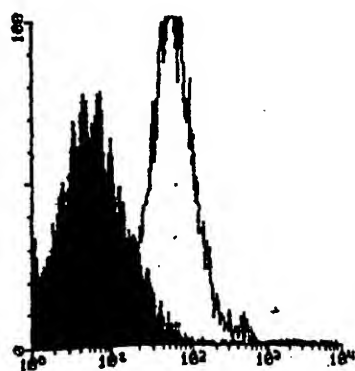
## A) PURIFICATION



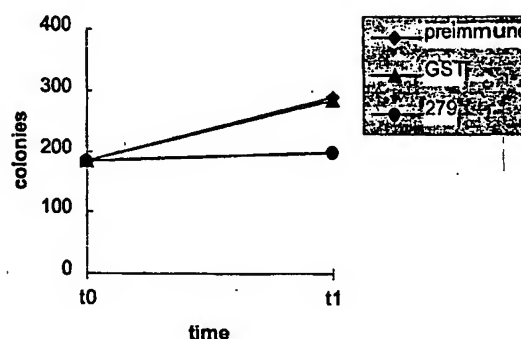
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay: positive

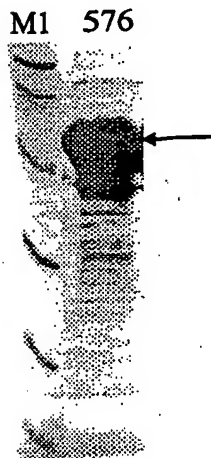
## 279

The predicted gene 279 was cloned in pGex vector and expressed in *E. coli*. The product of protein expression and purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 279-GST purification. Mice were immunized with the purified 279-GST and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that protein 279 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

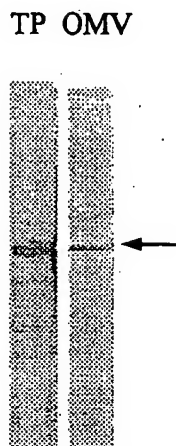
Fig. 3

576 (27.8 kDa)

## A) PURIFICATION



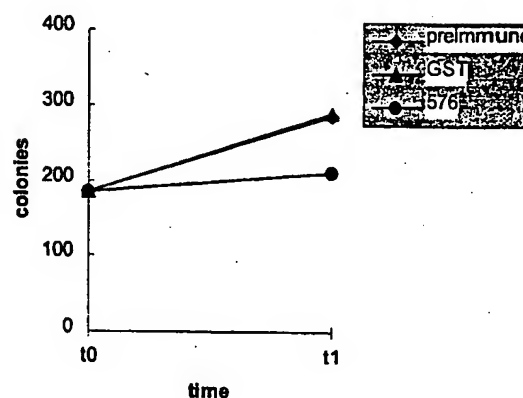
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay: positive

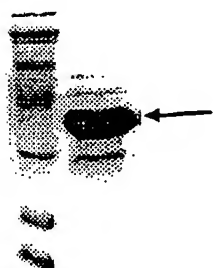
## 576

The predicted gene 576 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 576-GST fusion protein purification. Mice were immunized with the purified 576-GST and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 576 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

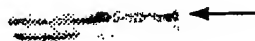
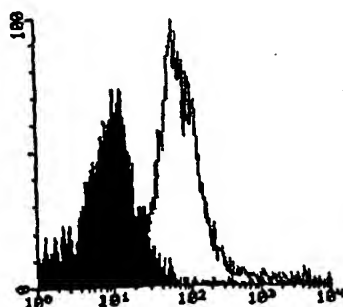
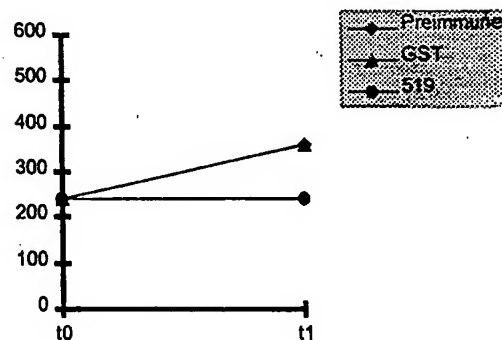


**519 (33 kDa)****Fig. 4****A) PURIFICATION**

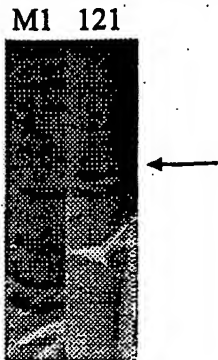
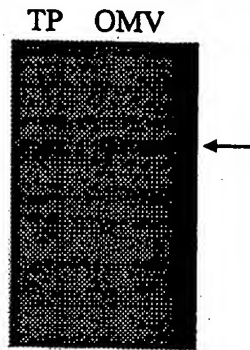
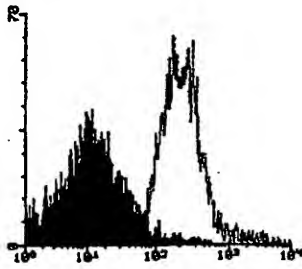
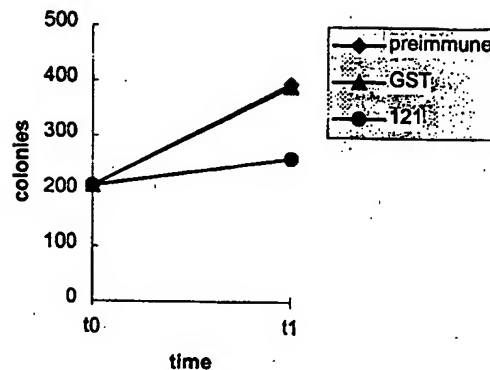
M1 519

**B) WESTERN BLOT**

TP OMV

**C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****519**

The predicted gene *519* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 519-His fusion protein purification. Mice were immunized with the purified 519-His and sera were used for Western blot (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 519 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

**121 (40 kDa)****A) PURIFICATION****B) WESTERN BLOT****C) FACS****D) BACTERICIDAL ASSAY****E) ELISA assay: positive****121**

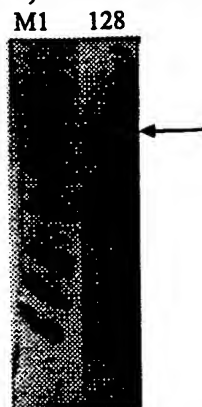
The predicted gene *121* was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 121-His fusion protein purification. Mice were immunized with the purified 121-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 121 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

**Fig. 5**

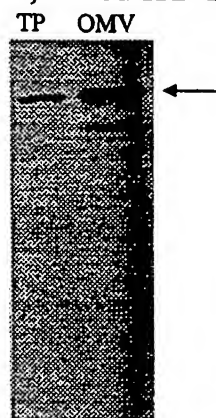
128 (101 kDa)

Fig. 6

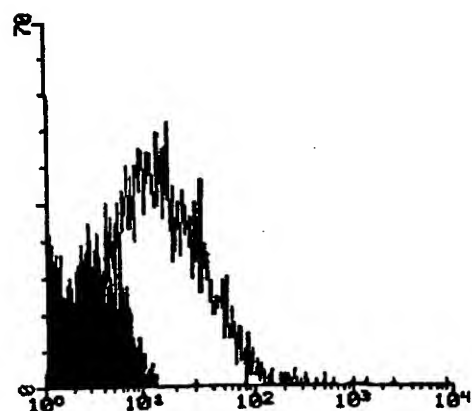
## A) PURIFICATION



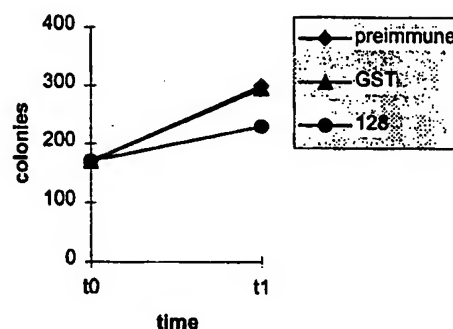
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY



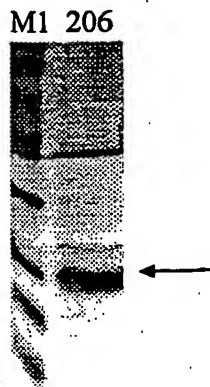
## E) ELISA assay: positive

## 128

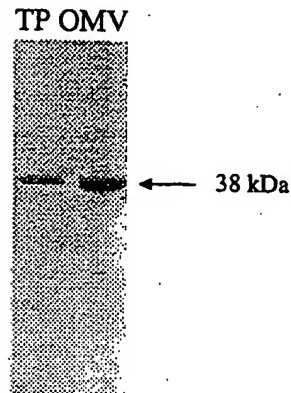
The predicted gene 128 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 128-His purification. Mice were immunized with the purified 128-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D) and ELISA assay (panel E). Results show that 128 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

Fig. 7

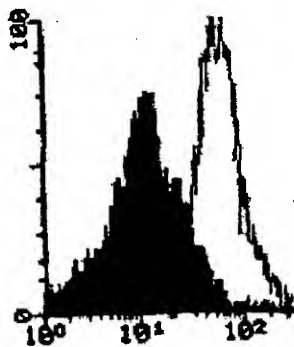
## A) PURIFICATION



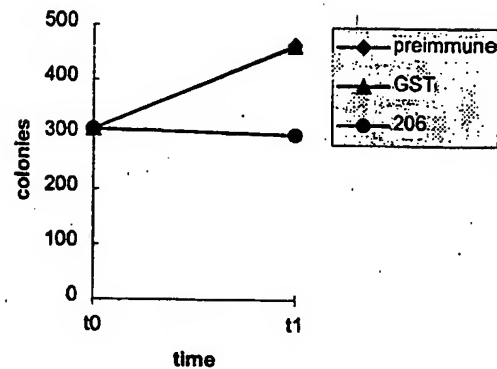
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY



## E) ELISA assay: positive

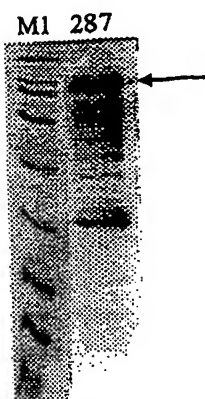
## 206

The predicted gene 206 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 206-His purification. Mice were immunized with the purified 206-His and sera were used for Western blot analysis (panel B). It is worth noting that the immunoreactive band in protein extracts from meningococcus is 38 kDa instead of 17 kDa (panel A). To gain information on the nature of this antibody staining we expressed ORF 206 in *E. coli* without the His-tag and including the predicted leader peptide. Western blot analysis on total protein extracts from *E. coli* expressing this native form of the 206 protein showed a reactive band at a position of 38 kDa, as observed in meningococcus. We conclude that the 38 kDa band in panel B) is specific and that anti-206 antibodies, likely recognize a multimeric protein complex. In panel C) is shown the FACS analysis, in panel D) the bactericidal assay, and in panel E) the ELISA assay. Results show that 206 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

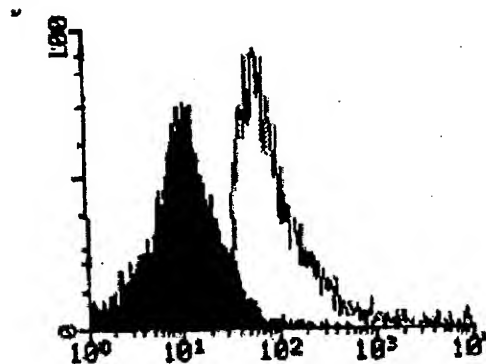
287 (78 kDa)

Fig. 8

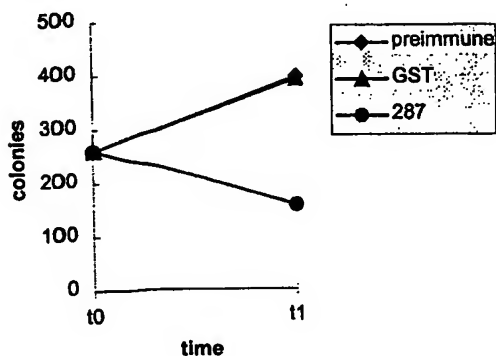
## A) PURIFICATION



## B) FACS



## C) BACTERICIDAL ASSAY

D) ELISA assay : positive

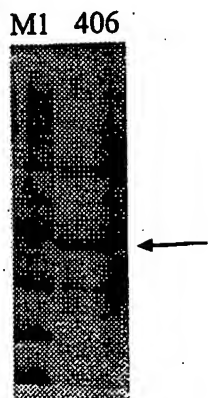
## 287

The predicted gene 287 was cloned in pGex vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 287-GST fusion protein purification. Mice were immunized with the purified 287-GST and sera were used for FACS analysis (panel B), bactericidal assay (panel C), and ELISA assay (panel D). Results show that 287 is a surface-exposed protein. Symbols: M1, molecular weight marker. Arrow indicates the position of the main recombinant protein product (A).

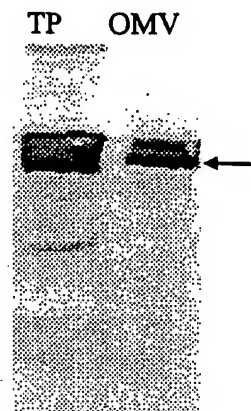
406 (33 kDa)

Fig. 9

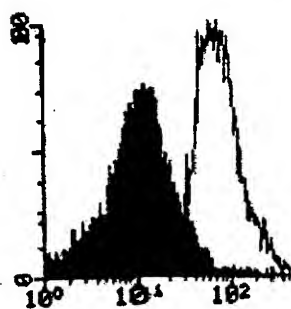
## A) PURIFICATION



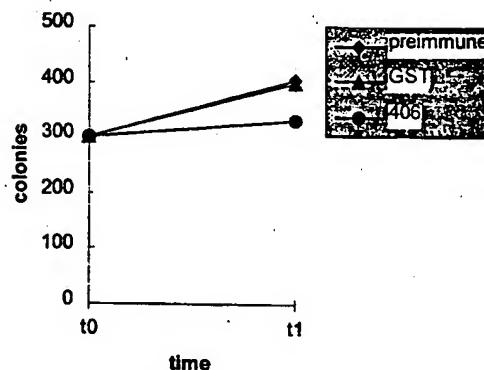
## B) WESTERN BLOT



## C) FACS



## D) BACTERICIDAL ASSAY

E) ELISA assay : positive

## 406

The predicted gene 406 was cloned in pET vector and expressed in *E. coli*. The product of protein purification was analyzed by SDS-PAGE. In panel A) is shown the analysis of 406-His fusion protein purification. Mice were immunized with the purified 406-His and sera were used for Western blot analysis (panel B), FACS analysis (panel C), bactericidal assay (panel D), and ELISA assay (panel E). Results show that 406 is a surface-exposed protein. Symbols: M1, molecular weight marker; TP, *N. meningitidis* total protein extract; OMV, *N. meningitidis* outer membrane vesicle preparation. Arrows indicate the position of the main recombinant protein product (A) and the *N. meningitidis* immunoreactive band (B).

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919

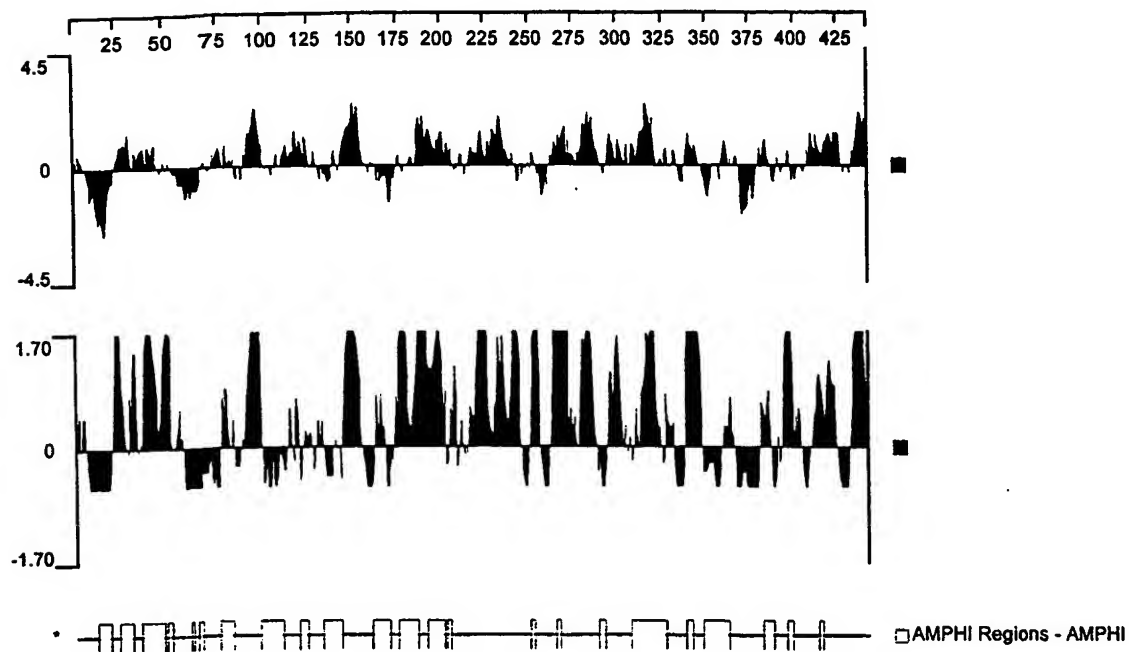
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 10

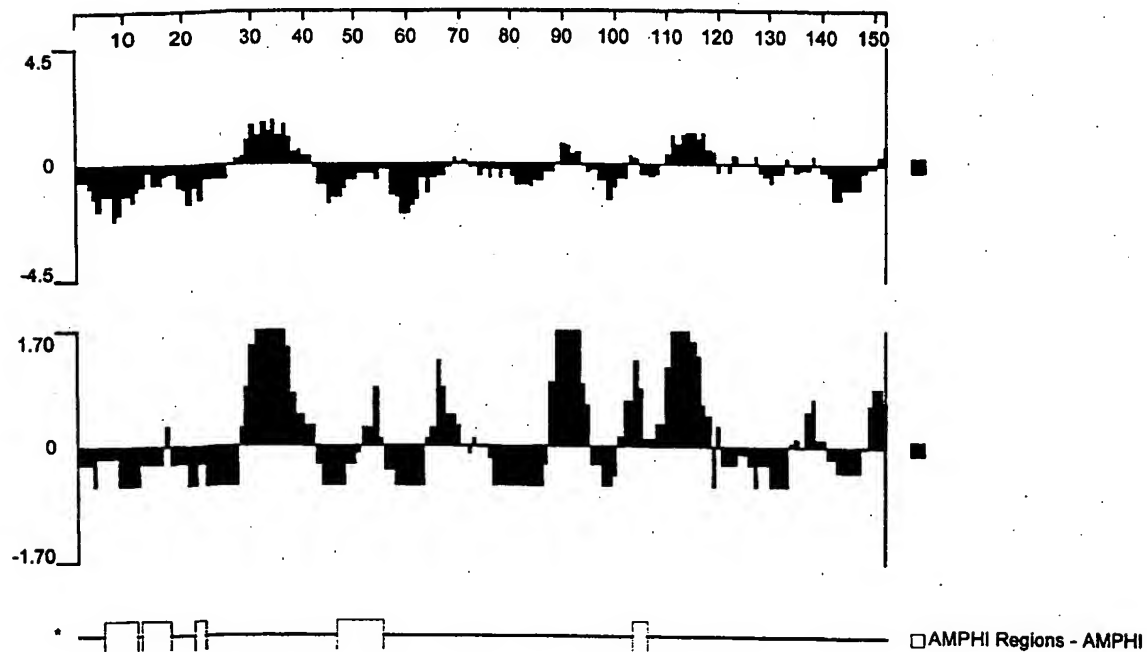
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 11



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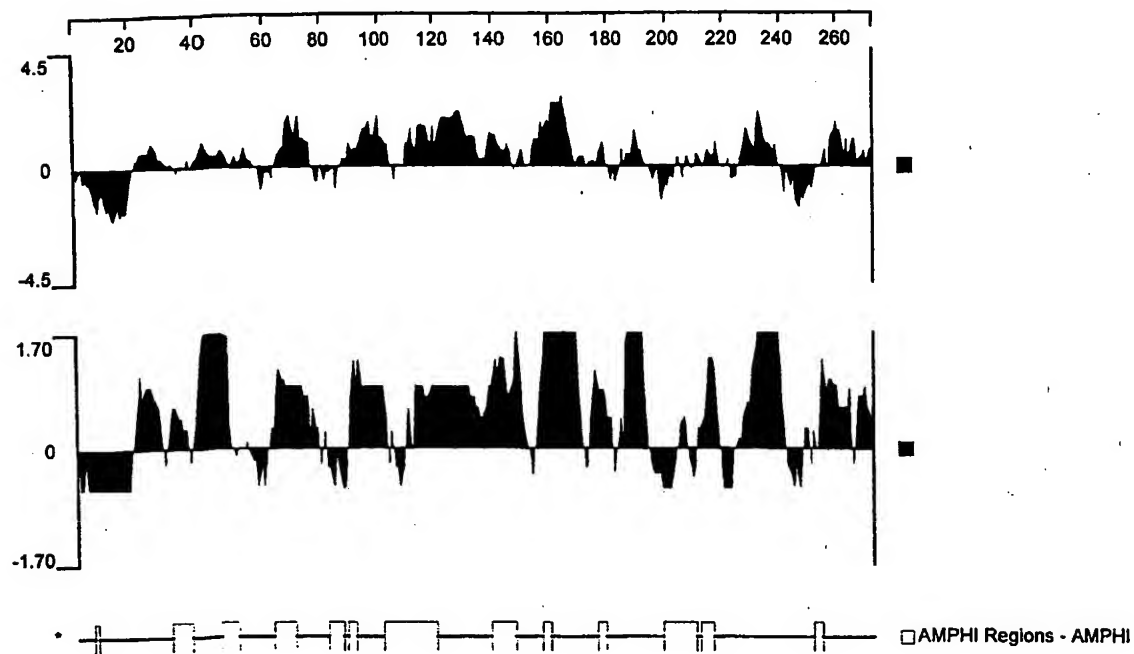
576-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 12

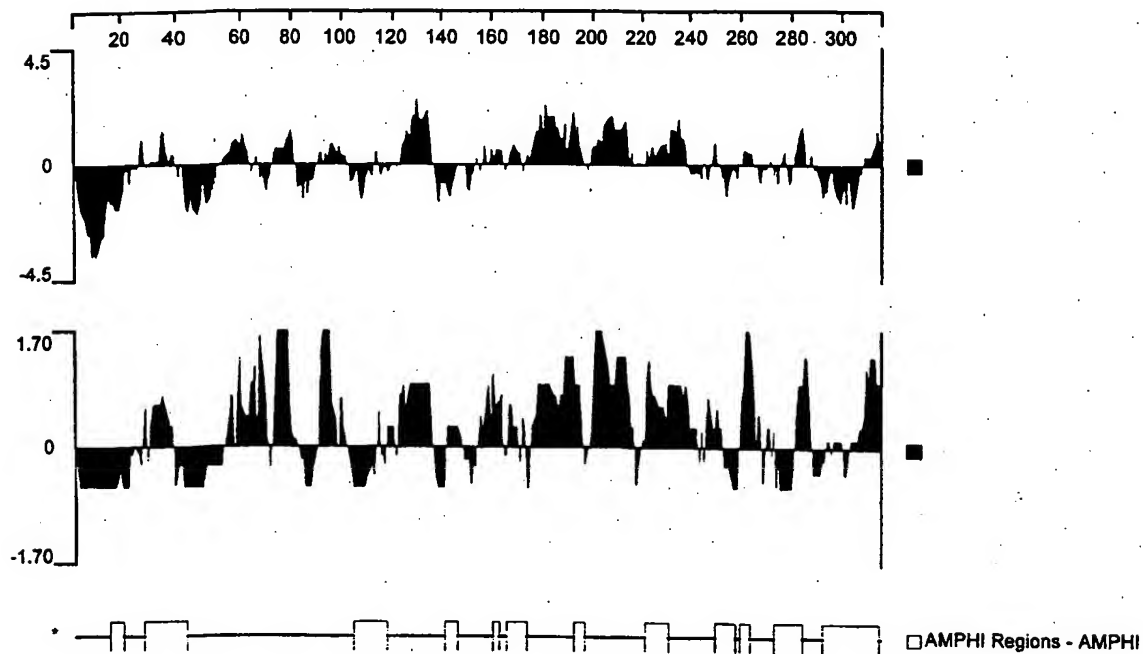
Hy drophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 13

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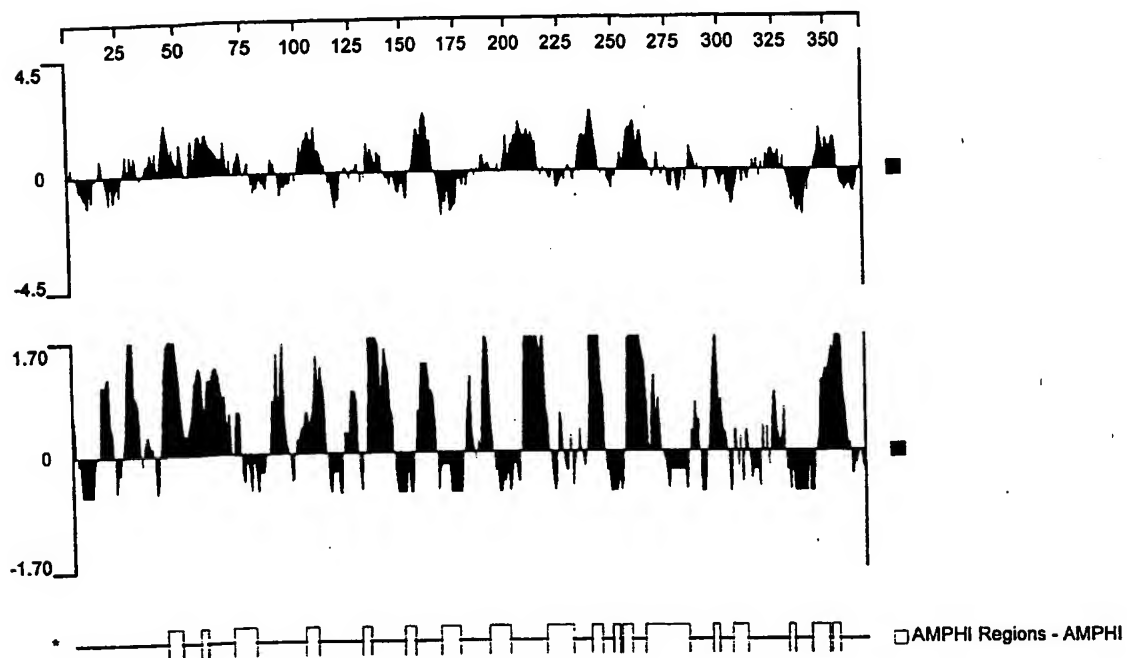
121-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 14

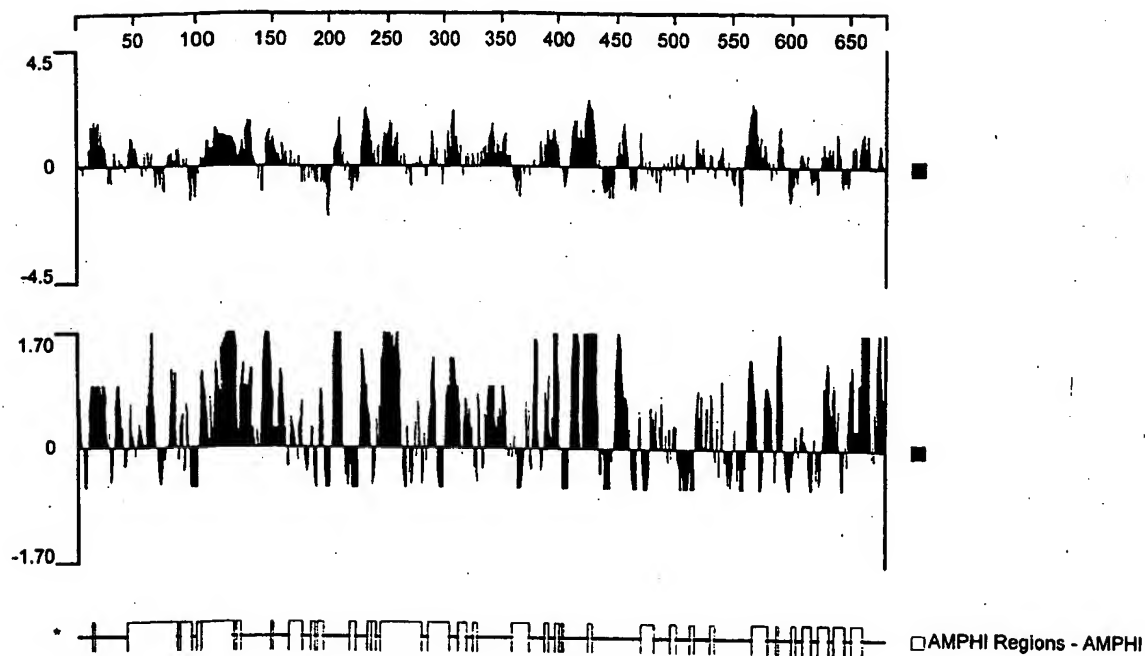
128-1Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 15

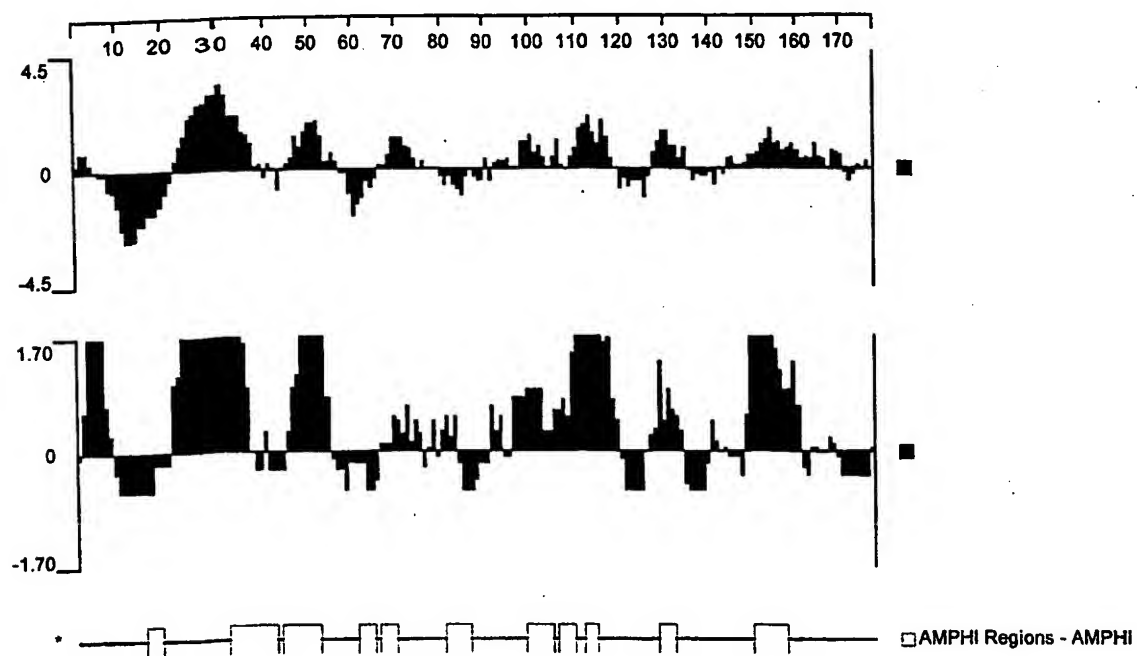
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 16

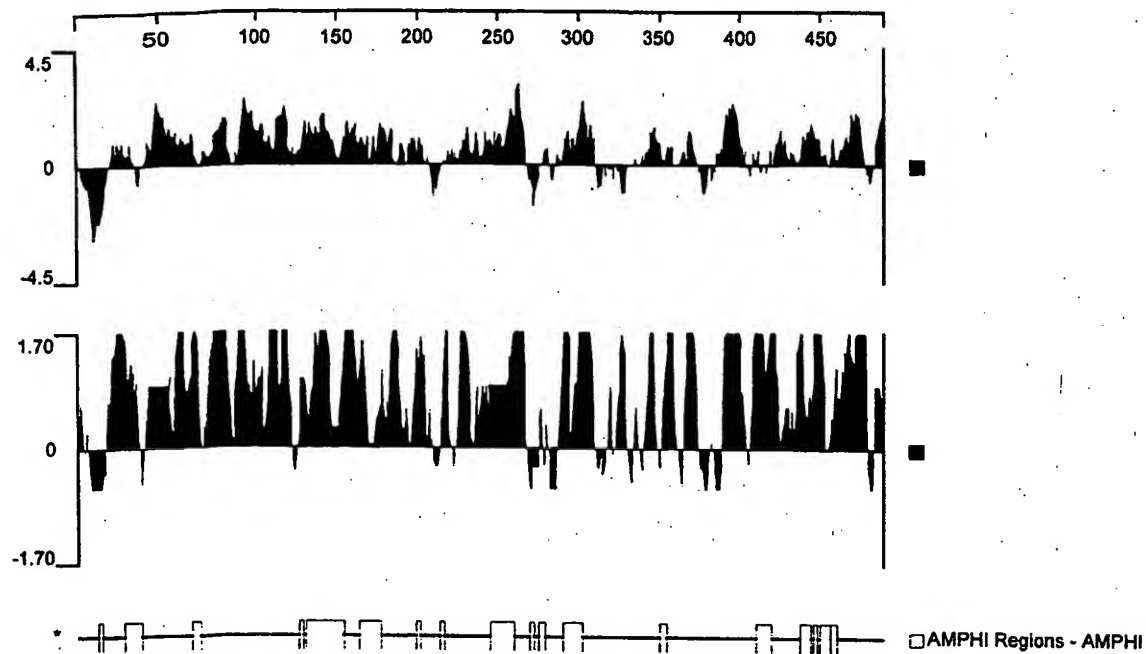
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 17

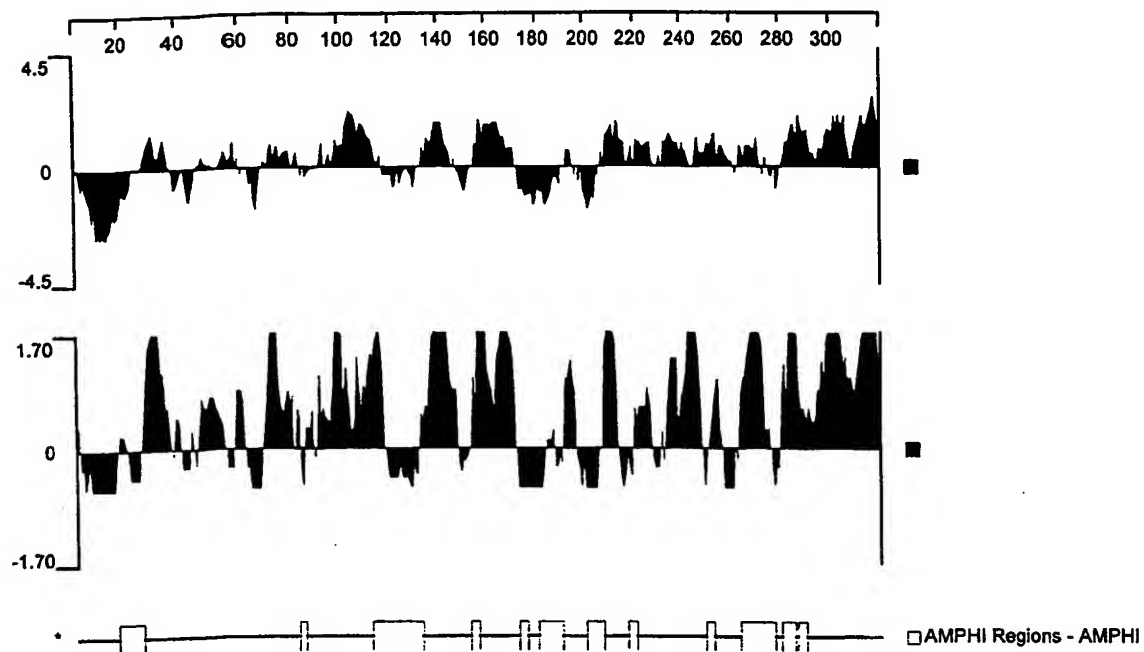
Hydrophilicity Plot, Antigenic Index and AMPHI Regions

Fig. 18

**Fig. 19A**





zo05_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo08_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
z2491	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo11_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo20_225	241	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo01_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo09_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo12_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo22_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo23_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo24_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo25_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo26_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo96_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo02_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo04_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo06_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo07_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo10_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo14_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo16_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo17_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo18_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo19_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo21_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo27_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo28_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo29_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo13_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo03_225	212	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo15_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
fa1090	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo32_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*
zo33_225	183	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDPSRFLN*

Fig. 19C

**Fig. 20A**

**Fig. 20B**

```

287_14 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVV...KETEA
287_2 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVV...KETEA
287_21 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVV...KETEA
z2491 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVV...KETEA
287_9 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVV...EDVGEEVLPKEKKDEEA
fa1090 1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSPKPAAPVV...ENAGEGVLPKEKKDEEA

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287_2 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGGAATDKPKNEDEGAQNDMPQNAADT
287_21 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGGAVTADNPKNEDEVAQNDMPQNAAGT
z2491 50 KEDAPQAGSQGGGAPSAQGGQDMAAVSEENTGNNGGAVTADNPKNEDEVAQNDMPQNAAGT
287_9 61 VSGAPQAD...QDATAGKGGQDMAAVSEENTGNNGGAATDNPKNEDEGAQNDMPQNAADT
fa1090 61 AGGAPQAD...QDATAGEGSDMAAVSEENTGNNGGAATDNPKNEDEGAQNDMPQNAADT

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287_2 110 DSLTPNHTPASNMPAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
287_21 110 DSSLTPNHTPDNMLLAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
z2491 110 DSSLTPNHTPDNMLLAGNMEQAQDAGESEOPANQPDMANADGMQGGDDPSAGGENAGNTA
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fa1090 117 .....

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287_21 170 AQTNOAENNOTAGSQNPASSINPSATNSGGDEGRITNNGSVVIDGPSQNTLTHCKGDS
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287_9 178 DQANOAENNOTAGSQNPASSINPSATNSGGDEGRITNNGSVVIDGPSQNTLTHCKGDS
fa1090 117 .ESANOTGNNOPAGSSDSAPAENPAPANCGSDEGRITNNGSVVIDGPSQNTLTHCKGDS

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287_2 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKKDGKNDGKNKRVGLVADSVQMKGINQYII
287_21 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKK....DGKNKRVGLVADSVQMKGINQYII
z2491 230 CSGNNFLDEEVOLKSEFEKLSDAKISNYKK....DGKNKRVGLVADSVQMKGINQYII
287_9 238 CORDFLDEEAPPKSEFEKLSDAKISNYKK....DEQRNFGVLVADRVKKGDTNKYII
fa1090 176 CNGDNFLDEEAPPKSEFEKLSDAKISNYKK....DEQRNFGVLVADRVKKGDTNKYII

287_14 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
287_2 290 FYKPKP...TSARFRRSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG
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fa1090 232 FYTDKPT.....RSARSRRSLPAEMPLIPVNQADTLIVDGEAVSLTGHSNIFAPEG

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287_21 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
z2491 344 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
287_9 353 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA
fa1090 285 NYRYLTYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENGRPSPLRGRFAA

287_14 408 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
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287_21 404 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
z2491 404 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
287_9 413 KVDFGSKSVDCIIDSGDLHMGTKQKFAVIDGNGFKGTWTENGCGDVSGFYGPAGEEVA
fa1090 345 KVDFGSKSVDCIIDSGDLHMGTKQKFAAIDGNGFKGTWTENGCGDVSGFYGPAGEEVA

```

FIG. 21A

287_14	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_2	468	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_21	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
z2491	464	GKYSYRPTDAEKGGFGVFAGKKEQD*
287_9	473	GKYSYRPTDAEKGGFGVFAGKKEQD*
fa1090	405	GKYSYRPTDAEKGGFGVFAGKKEQD*

FIG. 21B



z2491_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv26_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv22_519ass	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
fa1090_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv32_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv11_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv28_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv96_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv02_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv03_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv04_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv05_519	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv01_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv07_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv12_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv18_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv19_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv21_519ass	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv27_519	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv20_519ass	121	RMELDKTFEERDEINSTVVA	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv06_519ass	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
zv29_519ass	121	RMELDKTFEERDEINSTVVS	ALDEAAGAGWGVKVLRYEIKDLVPPQEILRSMQAQITAERE

FIG. 22A

z2491_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv26_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv22_519ass	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
fa1090_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv32_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv11_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv28_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv96_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv02_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv03_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv04_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv05_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv01_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv07_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv12_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv18_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv19_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv21_519ass	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv27_519	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv20_519ass	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv06_519ass	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR
zv29_519ass	1 81	KRARIAESEGRKIEQINLASGQREAEIQOSEGEAQAAVNASNAEKIARINRAKGEAESLR

z2491_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv26_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv22_519ass	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
fa1090_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv32_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv11_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv28_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv96_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv02_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv03_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv04_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv05_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv01_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv07_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv12_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv18_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv19_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv21_519ass	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv27_519	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv20_519ass	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv06_519ass	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
zv29_519ass	2 41	LVAEANAEAIROIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL

z2491_519	3 01	ISAGMKIIDSSKTAK*
zv26_519	3 01	ISAGMKIIDSSKTAK*
zv22_519ass	3 01	ISAGMKIIDSSKTAK*
fa1090_519	3 01	ISAGMKIIDSSKTAK*
zv32_519	3 01	ISAGMKIIDSSKTAK*
zv11_519	3 01	ISAGMKIIDSSKTAK*
zv28_519	3 01	ISAGMKIIDSSKTAK*
zv96_519	3 01	ISAGMKIIDSSKTAK*
zv02_519	3 01	ISAGMKIIDSSKTAK*
zv03_519	3 01	ISAGMKIIDSSKTAK*
zv04_519	3 01	ISAGMKIIDSSKTAK*
zv05_519	3 01	ISAGMKIIDSSKTAK*
zv01_519	3 01	ISAGMKIIDSSKTAK*
zv07_519	3 01	ISAGMKIIDSSKTAK*
zv12_519	3 01	ISAGMKIIDSSKTAK*
zv18_519	3 01	ISAGMKIIDSSKTAK*
zv19_519	3 01	ISAGMKIIDSSKTAK*
zv21_519ass	3 01	ISAGMKIIDSSKTAK*
zv27_519	3 01	ISAGMKIIDSSKTAK*
zv20_519ass	3 01	ISAGMKIIDSSKTAK*
zv06_519ass	3 01	ISAGMKIIDSSKTAK*
zv29_519ass	3 01	ISAGMKIIDSSKTAK*

Fig. 22B



**Fig. 23A**

**Fig. 23B**



fa1090	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm33asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm32asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm23asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm27bc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm09	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm10	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm24	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm25	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm14	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm04	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm11asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm08n	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm96	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm01	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm02	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm03	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm07	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm12	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm18	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm19	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm20	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm21	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm06	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm17	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm13	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm05	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
z2491	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm22	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm26	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm28	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm29asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm16	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm15	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
zm31asbc	361	DRHYITLGAPLFVATAHPVTRKALNRLIMAQDTGSAIKGAVRVDYFWGYGDEAGELAGK
fa1090	421	QKTTGYVWQLLPNGMKPEYRP*
zm33asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm32asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm23asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm27bc	421	QKTTGYVWQLLPNGMKPEYRP*
zm09	421	QKTTGYVWQLLPNGMKPEYRP*
zm10	421	QKTTGYVWQLLPNGMKPEYRP*
zm24	421	QKTTGYVWQLLPNGMKPEYRP*
zm25	421	QKTTGYVWQLLPNGMKPEYRP*
zm14	421	QKTTGYVWQLLPNGMKPEYRP*
zm04	421	QKTTGYVWQLLPNGMKPEYRP*
zm11asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm08n	421	QKTTGYVWQLLPNGMKPEYRP*
zm96	421	QKTTGYVWQLLPNGMKPEYRP*
zm01	421	QKTTGYVWQLLPNGMKPEYRP*
zm02	421	QKTTGYVWQLLPNGMKPEYRP*
zm03	421	QKTTGYVWQLLPNGMKPEYRP*
zm07	421	QKTTGYVWQLLPNGMKPEYRP*
zm12	421	QKTTGYVWQLLPNGMKPEYRP*
zm18	421	QKTTGYVWQLLPNGMKPEYRP*
zm19	421	QKTTGYVWQLLPNGMKPEYRP*
zm20	421	QKTTGYVWQLLPNGMKPEYRP*
zm21	421	QKTTGYVWQLLPNGMKPEYRP*
zm06	421	QKTTGYVWQLLPNGMKPEYRP*
zm17	421	QKTTGYVWQLLPNGMKPEYRP*
zm13	421	QKTTGYVWQLLPNGMKPEYRP*
zm05	421	QKTTGYVWQLLPNGMKPEYRP*
z2491	421	QKTTGYVWQLLPNGMKPEYRP*
zm22	421	QKTTGYVWQLLPNGMKPEYRP*
zm26	421	QKTTGYVWQLLPNGMKPEYRP*
zm28	421	QKTTGYVWQLLPNGMKPEYRP*
zm29asbc	421	QKTTGYVWQLLPNGMKPEYRP*
zm16	421	QKTTGYVWQLLPNGMKPEYRP*
zm15	421	QKTTGYVWQLLPNGMKPEYRP*
zm31asbc	421	QKTTGYVWQLLPNGMKPEYRP*

Fig. 23D

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